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(54) **METHOD FOR ISOLATING PLACENTAL TROPHOBLAST CELLS FROM CERVICAL EXFOLIATED CELLS OF PREGNANT WOMAN**

VERFAHREN ZUR TRENNUNG PLAZENTALER TROPHOBLASTZELLEN VON EXFOLIERTEN ZERVIKALZELLEN SCHWANGEREN FRAUEN

PROCÉDÉ DE SÉPARATION DE CELLULES TROPHOBLASTIQUES PLACENTAIRES À PARTIR DE CELLULES DU COL DE L'UTÉRUS EXFOLIÉES CHEZ LA FEMME ENCEINTE

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Description

TECHNICAL FIELD

[0001] The present invention belongs to the technical field of cell sorting. More specifically, the present invention relates to a method for isolating placental trophoblast cells from cervical exfoliated cells of a pregnant woman.

BACKGROUND

[0002] The three-level (pre-pregnancy, antenatal and newborn) prevention and control system is one of the important means to reduce birth defects and to improve population quality in China, among which prenatal screening and diagnosis is the most complex and most difficult part.

[0003] Currently, various disadvantages exist in clinically used prenatal diagnosic technologies such as, amniocentesis or cordocentesis, and non-invasive prenatal screening methods like fetal free nucleic acid sequencing. The amniocentesis and cordocentesis have high risks of infection during sampling and abortion, long analysis period, limited detection items and range. Moreover, the diagnosis time is limited within the middle and advanced stages of pregnancy, pregnant women have low acceptability of these two technologies, and the clinical treatment is difficult. The fetal free nucleic acid sequencing technology has extremely limited test range, and can only detect 3-5 designated chromosome aneuploid, and it's hard to avoid false positive and false negative cases using this method. Moreover, the technology has insufficient capacity in the detection of common mutations and the individual differences exist in the content of fetal free nucleic acids in maternal blood.

[0004] The applicant discloses a method for isolating trophoblast cells in patent application CN111304153A. In this method, by determining a specific antigen expressed on the surface of trophoblast cells and by using immunomagnetic beads carrying the corresponding specific antibody, the placental trophoblast cells are isolated from a cell suspension of a placental trophoblast sample and purified. Compared with the conventional amniocentesis and chorionic villus sampling, the technology has the advantages of non-invasive, earlier sampling time, low risk of infection and abortion, and similar reliability of test results. On the other hand, the technology still has space for the improvement of the applicable antibodies whose disclosed combinations are still limited, accuracy and specificity. The applicant team has carried out continuous research and development to the project.

SUMMARY

[0005] The objective of the present invention is to provide a method for isolating placental trophoblast cells from cervical exfoliated cells of a pregnant woman based on flow cytometry separation or microfluidics. The present invention not only overcomes the problems and defects of conventional methods, but also can achieve the synchronous labeling of a plurality of antigens as well as identification and sorting of characteristic fluorescence signals simultaneously; and the method has greatly improved accuracy and specificity superior to the previous immunomagnetic beads separation solution. Moreover, the method has advantages in the improvement of both cell quantity and quality. The number of cells obtained is larger than that of conventional methods, with good specificity and sensitivity.

[0006] The above objectives of the present invention are achieved by the following technical solutions:
a method for isolating trophoblast cells, including the following steps:

step (1) preparing a sample cell suspension from a solution containing cervical exfoliated cells;
step (2) adding a specific antibody to the sample cell suspension for incubation;
the specific antibody is an antibody combination corresponding to the specific antigen(s) expressed on the surface of or inside of trophoblast cells; preferably, the specific antibody combination is HLA-G+CK7, HLA-G+CK18, HLA-G+β-HCG, CD31+HPL, MMP9+CD31, HLA-G+HPL, HLA-G+MMP9, HLA-G+CD31, HLA-G+P, CD31+P, HLA-G+CDH5, CD31+CDH5, CD31+CK7+HLA-G, HLA-G+CK18+CD31, HLA-G+β-HCG+CD31, CD31+HPL+HLA-G, MMP9+CD31+HLA-G, CD31+P+HLA-G or HLA-G+CDH5+CD31;
step (3) performing sorting of a cell resuspension incubated in the step (2) by a flow cytometer to obtain isolated and purified placental trophoblast cells;
alternatively, performing fluorescence labeling and microfluidics cell sorting of a cell resuspension incubated in the step (2) by a microfluidic cell sorting chip to obtain isolated and purified placental trophoblast cells.

[0007] Preferably, the microfluidic cell sorting chip in the step (3) has a structure: including a substrate and a cover plate fitted therewith; the chip is made via the injection molding technology from base material, including but not limited to acrylic.

[0008] One side of the substrate is provided with a main channel, a side channel A and a side channel B, and the two side channels are close to left and right end portions of the main channel, correspondingly.

[0009] Another side of the substrate is provided with an inlet C, an inlet S, an outlet N and an outlet T; all the two inlets and the two outlets penetrate the substrate to communicate with the channels on the other side; and a position of the inlet C corresponds to the left end portion of the main channel; a position of the inlet S corresponds to the end portion of the side channel A; a position of the outlet N corresponds to the right end portion of the main channel; and a position of the outlet T corresponds to the end portion of the side channel B.

[0010] A deflection electrode device is further disposed in the main channel and at a convergence site of the outlet N and the outlet T.

[0011] Preferably, the main channel, the side channel A and the side channel B have a width not greater than 1000 μm and a depth not greater than 500 μm.

[0012] More preferably, the main channel, the side channel A and the side channel B have a width of 500-1000 μm.

[0013] More preferably, the main channel, the side channel A and the side channel B have a width of 1000 μm.

[0014] In the microfluidic cell sorting chip, the inlet C is used for feeding the mixed cell sample to be sorted; the inlet S is used for feeding a buffer solution; the outlet T is used for collecting target cells, and the outlet N is used for collecting non-target cells.

[0015] During the sorting process, the mixed sample containing target cells flows into the main channel of the chip from the inlet C, and the buffer solution flows into the side channel from the inlet S; the two are mixed at the intersection of the channels and then continuously flow along the same direction of the main channel. When the mixed cells flow through the deflection electrode device, the channel into which the cells are about to flow is selected by controlling the on/off of the electrode; the target cells are sorted to reach the outlet T, while the non-target cells continue to flow along the main channel to reach the outlet N, thus completing the sorting.

[0016] Moreover, preferably, a primary antibody in the step (2) is incubated in the following conditions: reacting for 30 - 90 min at 4°C, preferably, reacting for 60 min at 4°C; and a second antibody-fluorescent labeling complex is incubated in the following conditions: reacting for 20 min at 2°C - 8°C.

[0017] Preferably, the step (2) specifically includes: successively and specifically binding the primary antibody and the second antibody-fluorescent labeling complex to a target antigen step by step via incubation, wherein a washing and centrifugal separation technology is used to avoid cross contamination during the binding process.

[0018] Preferably, the step (3) specifically includes: feeding the incubated cell resuspension into the inlet C of the microfluidic cell sorting chip, feeding the buffer solution into the inlet S, then placing the microfluidic cell sorting chip in a cell sorter to carry out the sorting program, and collecting specimens at the outlet T at the end of the sorting program to obtain sorted trophoblast cells.

[0019] Preferably, a liquid-phase cell sorting system in the step (3) is 0.2% - 0.4% Triton-X-100, preferably, 0.3% Triton-X-100. More preferably, PBS is used for preparation.

[0020] Preferably, the sorting conditions of the flow cytometer in the step (3) are as follows: a sample loading rate is adjusted within 1000 - 2000 events/s, and a collecting rate is 5.0.

[0021] Preferably, an optimal system of the cell suspension in the step (1) is 1xPBS containing 0.2% - 0.4% FBS, preferably, 1xPBS containing 0.3% FBS.

[0022] Moreover, an application of the method in the construction of products for human STR authentication, human chromosome ploidy detection, thalassemia gene testing, epicophosis gene testing, whole exome sequencing, chromosome microdeletion/duplicate detection (a high-throughput sequencing method), or chromosome structure variation detection (a high-density chip method) is also described without being claimed by the claims.

[0023] The prevent invention has the following beneficial effects:

Compared with the conventional amniocentesis and chorion villus sampling, the method for isolating placental trophoblast cells based on flow cytometry separation or microfluidics provided by the present invention has the advantages of non-invasively obtaining specimens, earlier sampling time, low risk of infection and abortion, and the test result has higher reliability and broader coverage area. Whole genome nucleic acid samples of fetus can be obtained by such kind of specimen, which makes the detection and analysis of all the genetic diseases possible, and basically achieves the coverage of genetic diseases detection (chromosome ploidy, chromosome structure variation CNV, mitochondria, microdeletion/duplicate, single-gene mutation, SNP/STR genetic characteristics detection, and the like).

[0024] The method of the present invention can obtain considerable cells (thousands of cells, the designed minimum quality control standard is greater than 2000 positive cells), and can achieve the specimen detection by the conventional molecular assay technique without special operations. Moreover, the method of the present invention has no strict requirement for technicians and laboratory equipment, which reduces the technical thresholds and use costs and can be carried out in more medical institutions, capable of being popularized in wide range.

[0025] Meanwhile, the method provided by the present invention is a multi-labeling screening solution, which can achieve the synchronous labeling of a more plurality of antigens as well as identification and sorting of characteristic fluorescence signals simultaneously, and the accuracy has been greatly improved. Compared with the existing immunomagnetic beads and other technologies, the method of the present invention can both have the advantages of cell quantity and quality. The cells obtained are not only numerous, but also have minor injury, and the cells obtained have good

quality, good detection specificity and sensitivity.

BRIEF DESCRIPTION OF DRAWINGS

[0026]

FIG. 1 is a schematic diagram showing a substrate structure of a microfluidic cell sorting chip; figures (a) and (b) respectively represent the two sides of the substrate;
FIG. 2 shows a mono-fluorescence labeled positive cell population selected in flow cytometry sorting;
FIG. 3 shows a bifluorescence labeled positive cell population selected in flow cytometry sorting;
FIG. 4 is an FAM-labeled channel 1; "822-" represents the rest specimens after sorting; "822+" represents sorted specimens; "822" represents specimens before sorting;
FIG. 5 is an HEX-labeled channel 2;
FIG. 6 is a TAMRA-labeled channel 3;
FIG. 7 is a ROX-labeled channel 4;
FIG. 8 is a schematic diagram showing a test result of Y-STR of the Y-chromosome containing specimen in the sorted plasmoditrophoblast cells;
FIG. 9 is a test result of epicophosis genes of the sorted specimen;
FIG. 10 is a test result of thalassemia genes of the sorted specimen;
FIG. 11 shows a family genogram carrying detected family pathogenic mutations;
FIG. 12 is a schematic diagram showing whole chromosomes;
FIG. 13 is a schematic diagram showing abnormal chromosomes;
FIG. 14 is a picture showing positive cells sorted by the method of the present invention;
FIG. 15 is a picture showing comparison of positive cells and negative cells before and after sorting using the method of the present invention.
FIG. 16 is a picture showing positive cells sorted by the control method of immunomagnetic beads.

DETAILED DESCRIPTION OF EMBODIMENTS

[0027] The present invention will be further described in combination with the detailed embodiments of the description, and the embodiments are not used to limit the present invention in any form. Unless otherwise specified, the reagent, method and equipment used in the present invention are conventional reagent, method and equipment in the art.
[0028] Unless otherwise specified, the reagent and material used in the examples below are available on the market.

Example 1 Design of a microfluidic cell sorting chip

[0029] The schematic diagram of the microfluidic cell sorting chip for isolating trophoblast cells from cervical exfoliated cells of a pregnant woman is shown in FIG. 1.
[0030] The structure of the microfluidic cell sorting chip is designed and described below: the chip is prepared by including but not limited to acrylic as a base material; a pipe shape of FIG. 1 was formed on one side of the base material via the injection molding technology, with the pipe width not greater than 1000 μm, and depth not greater than 500 μm, and another side of the base material is used for fitting to form a complete chip.
[0031] Specifically, the microfluidic cell sorting chip includes a substrate and a cover plate fitted therewith.
[0032] As shown in FIG. 1, one side of the substrate is provided with a main channel, a side channel A and a side channel B, and the two side channels are respectively close to left and right end portions of the main channel; and all the channels have a width of 1000 μm.
[0033] Another side of the substrate is provided with an inlet C (a liquid inlet for cell samples), an inlet S (a liquid inlet for buffer solution), an outlet N (a liquid storage hole for non-target cells) and an outlet T (a liquid storage hole for target cells); all the two inlets and the two outlets penetrate the substrate to communicate with the channels; and a position of the inlet C corresponds to the left end portion of the main channel; a position of the inlet S corresponds to the end portion of the side channel A; a position of the outlet N corresponds to the right end portion of the main channel; and a position of the outlet T corresponds to the end portion of the side channel B.
[0034] The inlet C is used for feeding the mixed cell samples to be sorted; the inlet S is used for feeding the buffer solution; the outlet T is used for collecting the target cells, and the outlet N is used for collecting the non-target cells.
[0035] Moreover, the main channel is further provided with a deflection electrode device for cell sorting; the deflection electrode device is specifically located at the intersection of the outlet N and the outlet T; the on/off of the electrode may be controlled according to the presence of a flow cell signal. Negatively-charged cells are subjected to deflection in the electromagnetic field formed by electrodes to flow into a designated pipe leading to the outlet N or the outlet T.

[0036] During the sorting process, the mixed sample containing target cells flows into the main channel of the chip from the inlet C, and the buffer solution flows into the side channel from the inlet S; the two are mixed at the intersection of the channels and then continuously flow along the same direction of the main channel. When the mixed cells flow through the deflection electrode device, the channel into which the cells are about to flow is selected by controlling the on/off of the electrode; the target cells are sorted to reach the outlet T, while the non-target cells continue to reach the outlet N along with the main channel, thus completing the sorting.

[0037] At the end of the sorting, the chip is immediately discarded, and a new chip needs to be exchanged before each sorting to ensure a clean, controllable and cross contamination-free sorting environment.

Example 2 Isolation of trophoblast cells from cervical exfoliated cells of a pregnant woman based on the microfluidic cell sorting chip

[0038]

I. A method for isolating trophoblast cells includes the following steps:

step 1, a sample cell suspension was prepared from a solution containing cervical exfoliated cells; the specific method included the followings as shown in step (1) - step (5);
step 2, a specific antibody was added to the sample cell suspension for incubation; and the specific method included the followings as shown in step (6) - step (14);
step 3, fluorescence labeling and microfluidics cell sorting was performed on a cell resuspension incubated in the step 2 by the microfluidic cell sorting chip in Example 1; the specific method included the followings as shown in step (15) - step (18).

[0039] The combinations of specific antibodies are shown in Table 1:

Table 1: Combinations of antigens and antibodies expressed on the trophoblast cells

Antibody combinations	HLA-G+CK7, HLA-G+CK18, HLA-G+β-HCG, CD31+HPL, MMP9+CD31, HLA-G+HPL, HLA-G+MMP9, HLA-G+CD31, HLA-G+P, CD31+P, HLA-G+CDH5, CD31+CDH5, CD31+CK7+HLA-G, HLA-G+CK18+CD31, HLA-G+β-HCG+CD31, CD31+HPL+HLA-G, MMP9+CD31+HLA-G, CD31+P+HLA-G, HLA-G+CDH5+CD31	
The information of the corresponding antigens is shown below:		
Specific antigens on the surface of trophoblast cells	Corresponding receptors	Available monoclonal antibodies
HLA-G (human leucocyte antigen G)	LIR1/ILT2, LIR2/ILT4, p49/KIR2DL4, BY55	4H84(BD Biosciences)
β-HCG (human chorionic gonadotropin)	LH/HCG receptor	5H4-E2(Thermo Scientific)
Cytokeratin7 (CK-7)		OV-TL 12/30 (DAKO), mouse-anti-human cytokeratin 7 (CK-7) monoclonal antibody
Cytokeratin18 (CK-18)		mouse-anti-human CK18 monoclonal antibody (ab181597) (Abcam company)
Matrix metalloproteinase 9 (MMP9)	Type-IV, V, VII and X collagens, gelatins and elastic fibers	4H3 (R&D Systems)
VE-Cadherin (CDH5)		2158(Cell Signaling Technology)
Platelet endothelial cell adhesion molecule precursor PECAM1 (CD31)		89C2(Cell Signaling Technology)
Human placental lactogen (HPL)	Prolactin receptor	
Progesterone (P)	Progesterone receptor (PGR)	

[0040] II. Specifically, the sorting method of the trophoblast cells includes the following steps of:

step (1), a cell preserving solution (containing the cervical exfoliated cells) was mixed on an oscillating mixer evenly for 5 min;
step (2), the preserving solution was transferred into a 15 mL centrifugal tube, and 3 mL 1×PBS was added to the bottle of the preserving solution, and mixed evenly by oscillation, then the solution was transferred into the same 15 mL centrifugal tube;
step (3), the solution was centrifuged for 10 min at 3000 rpm, and supernatant was discarded;
step (4), 1 mL 1×PBST was added and mixed well and transferred to a 1.5 mL EP tube, and centrifuged for 5 min at 3000 rpm, and supernatant was discarded;
step (5), the step (4) was repeated twice to prepare a cell suspension;
step (6), 200 μL 0.3% Triton X-100 was added and mixed well, then permeabilizd at room temperature for 20 min;
step (7), the step (4) was repeated for three times;
step (8), addition of a primary antibody: 200 μL of mouse-anti-human CK7 monoclonal antibody, mouse-anti-human CK18 monoclonal antibody, mouse-anti-human β-HCG monoclonal antibody, mouse-anti-human MMP9 monoclonal antibody, mouse-anti-human CDH5 monoclonal antibody, mouse-anti-human P monoclonal antibody, mouse-anti-human hPL monoclonal antibody, rabbit-anti-human HLA-G monoclonal antibody, and rabbit-anti-human CD31 monoclonal antibody (Abcam company) which were diluted by proportions were respectively added, and mixed well, incubating for 60 min at 4°C;
step (9), the step (4) was repeated for three times;
step (10), addition of a secondary antibody-fluorescent labeling complex: 200 μL of goat-anti-rabbit and goat-anti-mouse antibodies which were diluted by proportions were mixed well, incubating for 60 min at 37°C;
step (11), the step (4) was repeated for three times, and 200 μL buffer (DPBS+0.1% BSA+2 mM EDTA) was used for resuspending;
step (12), reaction was performed for 20 min at 2°C - 8°C;
step (13), 1 mL 1×PBST was added and mixed well and transferred to a 1.5 mL EP tube, and centrifuged for 5 min at 3000 rpm and supernatant was discarded;
step (14), the step (13) was repeated for two to three times, and 200 μL 1×PBST was added for resuspending to obtain a cell resuspension;
step (15), the obtained cell resuspension was fed into the inlet C of the microfluidic cell sorting chip in Example 1, and 1×PBST was fed into the inlet S;
step (16), the microfluidic cell sorting chip was placed and fixed on an objective table of a cell sorter, and the cell sorter was turned on to set the designated program for operation;
step (17), at the end of the program, specimens at the outlet T were collected to obtain the sorted trophoblast cells;
step (18), specimens at the outlet N were collected to obtain the remaining cells obtained after trophoblast cells were removed from the cervical exfoliated cells.

Example 3 Method for isolating trophoblast cells from cervical exfoliated cells of a pregnant woman based on a flow cytometer

[0041] A method for sorting trophoblast cells includes the following steps:

step 1, a sample cell suspension was prepared from a solution containing cervical exfoliated cells; and the specific method was the same as those in step (1) - step (5) of Example 2;
step 2, a specific antibody was added to the sample cell suspension for incubation; and the specific method was the same as those in step (6) - step (14) of Example 2; combinations of the specific antibodies are the same as those in the Table 1 above;
step 3, a cell resuspension incubated in step 2 was subjected to fluorescence labeling and sorting by a flow cytometer (BDFACSAria type II, USA), including the following steps:

step 1), the flow cytometer was turned on for daily startup operation according to the instructions;
step 2), the instrument was subjected to liquid flow adjustment such that the breakpoint position of the liquid flow was located in the middle-upper part of the window;
step 3), sorting liquid path was adjusted to confirm the delay of liquid drops, and a sample loading rate was adjusted within 1000-2000 events/s;
step 4), 5 mL flow tubes were chosen as collection devices; the number of the sorted cells was 3000, and direction was left, and cell population to be sorted was added, and subjected to gating successively, and then loaded the collecting tubes;

step 5), the incubated cell suspension was put into a sample warehouse, and a collecting rate was set 5.0 and sample loading was performed;
step 6), voltage was adjusted within the scope of 300 - 500 V such that the compensation between fluorescent dyes was kept as small as possible; the gate position was adjusted such that positive cells were located in the center, and cells within the gate were collected; and the cells in the collecting tube were namely, the selected target cells.

[0042] The target cell population was obtained according to the given labeling combinations, as shown in FIGS. 2-3. FIG. 2 shows a sorting result of mono-fluorescence labeling, and FIG. 3 shows a sorting result of bifluorescence labeling.

Example 4 Application case of the method--- human STR authentication

[0043] 1. Trophoblast cells were sorted and isolated from a sample (cervical exfoliated cells) according to the method of the above Example 2.
2. The isolated trophoblast cells and cervical exfoliated cells of a pregnant woman were subjected to DNA extraction:

1) the sorted trophoblast cells (the trophoblast cells obtained in the step (17) of the cell sorting method in Example 2), and the cells obtained in the step (18) of the cell sorting method in Example 2 (the remaining cells obtained after trophoblast cells were removed from the cervical exfoliated cells) were respectively centrifuged for 3 min at 12000 rpm;
2) supernatant was discarded, and 200 μL solution P was added for resuspending precipitates;
3) 20 μL protease K and 200 μL solution L were added and mixed well;
4) the mixed solution was treated in a warm bath at 56°C for 20 min and overturned and mixed well;
5) 200 μL absolute ethyl alcohol was added and mixed well, and then, the mixed solution was transferred to an adsorption column, and centrifuged at 10000 rpm for 1 min, then waste solution in the collecting tube was discarded;
6) 500 μL W1 was added and centrifuged at 10000 rpm for 1 min, then waste solution in the collecting tube was discarded;
7) 500 μL W2 was added and centrifuged at 10000 rpm for 1 min, then waste solution in the collecting tube was discarded;
8) 500 μL W2 was added and centrifuged at 10000 rpm for 1 min, then waste solution in the collecting tube was discarded;
9) the blank tube was centrifuged at 12000 rpm for 3 min, then the collecting tube was discarded;
10) the adsorption column was put into a new 1.5 mL centrifugal tube, uncovered and standing for 2 min, then 50 μL TE was added and centrifuged at 12000 rpm for 2 min after standing for 5 min, and the adsorption column was discarded;
11) the extracted DNA concentration and purity were determined.

3. The isolated trophoblast cells and cervical exfoliated cells of a pregnant woman were subjected to DNA extraction, and then subjected to PCR amplification with Microread D-21 human STR authentication kit; the PCR products were subjected to capillary electrophoresis with a 3500xL sequencer, and the instrument was subjected to fluorescent calibration with G5-Matrix Standard, and corresponding Panels and bins files were compiled, and software GeneMapper ID version 3.0 was used for result analysis.
4. STR detection
1) PCR amplification, and the amplification system is shown in Table 2:

Table 2: PCR amplification system

Reagent	Volume (μL)
2.5× Buffer D	10
5× Primer MIX	5
Polymerase MIX I	0.55
DNA	1
H_2O	Up to 25

PCR reaction procedure: PCR reaction was performed for 10 min at 50°C and for 4 min at 96°C (5 sec at 94°C and 1 min + 10 sec at 60°C) × 27 cycles, for 30 min at 60°C, and preserved at 15°C.
2) STR test result
8.7 μL Hidi and 0.3 μL internal reference were mixed well according to the instructions, and added with 1 mL amplified

product, then the treated PCR product was subjected to capillary electrophoresis with a 3500xL sequencer, and the instrument was subjected to fluorescent calibration with G5-Matrix Standard, and corresponding Panels and bins files were compiled, and software GeneMapper ID version 3.0 was used for result analysis. Results are shown in FIGS. 4-7. The results show that besides the DNA of the pregnant woman, there was exactly another individual DNA information, and the DNA information has a strong genetic relationship with the pregnant woman.

3) Y-STR detection

The specimen of Y chromosome detected in STR was subjected to Y-STR detection with a Microread 40Y kit. Results are shown in FIG. 8, and the results show that there exists male DNA in the specimen.

Example 5 Application case of the method---detection of epicophosis-susceptible genes

[0044] Cervical exfoliated cells of a pregnant woman (sample source: Guangzhou Hybribio Medical Laboratory) were subjected to epicophosis-susceptible gene testing with a commercial kit (an epicophosis-susceptible gene kit (PCR+flow-through hybridization), Chaozhou Hybribio Biochemistry Co., Ltd., Registration Certificate No. for Medical Device of the People's Republic of China: 20153401698) according to the method of Example 2; specifically, 9 mutation sites (mtDNA1494, mtDNA1555, SLC26A4-IVS7(-2), SLC26A4-2168, GJB2-35, GJB2-176, GJB2-235, GJB2-299 and GJB3-538) of the epicophosis-related genes (GJB2, GJB3, SLC26A4 and mtDNA) were subjected to testing.

[0045] The DNA extraction method of the cervical exfoliated cells of a pregnant woman in Example 4 was used, and then a commercial kit (epicophosis-susceptible gene kit (PCR+flow-through hybridization), Chaozhou Hybribio Biochemistry Co., Ltd., Registration Certificate No. for Medical Device of the People's Republic of China: 20153401698) was used for subsequent testing. Specific operations are specifically shown in the instructions. Raw data are shown in FIG. 9; and result analysis are shown in Table 3.

Table 3 Epicophosis result analysis

155M homozygosity	176M homozygosity	235 M homozygosity
299 M homozygosity	1494 M homozygosity	1555 M homozygosity
7445 M homozygosity	538 M homozygosity	2168 M homozygosity
IVS- M homozygosity	1229 M homozygosity	Normal sample
Blank control	Blank control	Blank control

[0046] The results indicate that the test results are consistent with the clinical test results.

Example 6 Application case of the method---detection of thalassemia-related genes

[0047] Cervical exfoliated cells of a pregnant woman (sample source: remaining nucleic acid samples of the humanized specimen detected by Hybribio Medical Laboratory) were subjected to epicophosis-susceptible gene testing with a commercial kit (α- and β-thalassemia gene kit (PCR+ membrane hybridization method), Chaozhou Hybribio Biochemistry Co., Ltd., SFDA Certified No.: 3400399, 2012) according to the method of Example 2; specifically, 3 common α-thalassemia deletion types ($--^{SEA}$, $-\alpha^{3.7}$, $-\alpha^{4.2}$), 2 α-thalassemia mutant types (CS and QS) and 11 β-thalassemia mutant types (CD14-15, CD17, CD27-28, CD41-42, CD43, CD71-72, -28, -29, IVS-I-1, IVS-II-654 and β EN) were subjected to testing.

[0048] The DNA extraction method of the cervical exfoliated cells of a pregnant woman in Example 4 was used, and then a commercial kit (α- and β-thalassemia gene kit (PCR+ membrane hybridization method), Chaozhou Hybribio Biochemistry Co., Ltd., SFDA Certified No.: 3400399, 2012) was used for subsequent testing. Specific operations are specifically shown in the instructions. Raw data are shown in FIG. 10; and result analysis is shown in Table 4.

Table 4 Thalassemia result analysis

Southeast Asia deletion (--SEA/--SEA)	Left deletion ($-\alpha4.2/\alpha\alpha$)	QS mutation heterozygote
Left deletion ($-\alpha4.2/\alpha\alpha$)	41-42M heterozygote	17M heterozygote
Normal sample	Normal sample	Right deletion ($-\alpha3.7/-\alpha3.7$)
Right deletion ($-\alpha3.7/-\alpha3.7$)	Normal sample	Left deletion ($-\alpha4.2/\alpha\alpha$)
Normal sample	Normal sample	654 M heterozygote

[0049] The results indicate that the test results are consistent with the clinical test results.

Example 7 Application case of the method---whole exome sequencing

[0050]

1. Cervical exfoliated cell specimen and amniotic fluid specimen of a pregnant woman were obtained in a known epicophosis family (father, mother (16-week pregnancy), eldest child (deaf son) and youngest son (deaf son)) according to the method in Example 2. The pregnant woman and other family members were subjected to whole blood specimen collection and DNA extraction (after the cervical exfoliated cells of the pregnant woman were sorted, the specimen was obtained by the extraction method of Example 4; the amniotic fluid and the whole blood specimens were extracted by a human whole blood genome DNA extraction kit (Hybribio, China) (sample source: a humanized specimen detected by Hybribio Medical Laboratory)); and the obtained human genome DNA was subjected to whole exome sequencing (WES) with a whole exome kit (iGeneTech Biotechnology (Beijing) Co., Ltd., Art. No.: T086V4): The genome DNA was processed into 300bp fragments with a transposase Tn5 to construct a DNA library; adapters P5, P7, index1, 2 were added at both terminals; a proper length of DNA fragments was chosen, amplified and purified, then hybridized with the exon probe library with biotin; strong binding force of the biotin to streptavidin was used to bind streptavidin-carrying magnetic beads with the probe which had been bound to the target library; the magnetic beads were adsorbed and supernatant was removed, and DNA on the magnetic beads was eluted, and the library was subjected to PCR amplification, and quality evaluation; and sequencing on a machine was performed.
2. Whole exome sequencing result
Whole exome sequencing was performed with a high-throughput sequencing technology, and the detected pathogenic or suspected pathogenic site was verified with Sanger sequencing. The test sample was an amniotic fluid specimen (16-week pregnancy); two brothers were deaf and parents were normal. CDH23 gene c.8363T>C (p.Leu2788Pro) heterozygous mutation and GJB2 gene c. 109G>A (p.Val27Ile) heterozygous mutation were detected in the sample. Family genogram is shown in FIG. 11.

[0051] The results indicate that pathogenic mutation was effectively detected from the sorted exfoliated cell specimen, which is completely consistent with the amniotic fluid specimen. Pathogenesis and pathogenic mutation-carrying situations can be found from the test results.

Example 8 Application case **of the method---detection of whole genome DNA copy number variation** (CNV)

[0052]

1. The whole genome DNA copy number variation was detected with a CytoOneArray chromosome chip and a supporting kit from Phalanx Biotech according to the theory (aCGH) of comparative genomic hybridization:

the sorted trophoblast cells by the method of Example 2 were extracted by the DNA extraction method of the cervical exfoliated cells of the pregnant woman in Example 4; the obtained human genome DNA was subjected to fragmentation, amplification pretreatment, amplification and PCR product purification, then labeled by two different fluorescent dyes (normal sample was labeled by Cy3, showing green, and the patient sample was labeled by Cy5, showing red);
the fluorescent product was poured into the chip after being purified, and the chip was washed and scanned to obtain results.

2. Test results of the whole genome DNA copy number variation (CNV)
The schematic diagram of whole chromosomes is shown in FIG. 12 and the schematic diagram of abnormal chromosomes is shown in FIG. 13. In FIG. 13, the horizontal axis represents the schematic diagram of a chromosome zone, and longitudinal axis shows a signal ratio of the sample to the standard sample (represented by a log2 ratio). When the chromosome CNV has a significant difference, it is represented by different colors. The region (Gain) where chromosome is amplified is represented by blue, and the region (Loss) where chromosome is deleted is represented by red. The length and value of the black line respectively represent the mean size and signal of each Segment.

[0053] One abnormity is detected in the sample, namely, 22q11.21 deletion; the start-end positions [UCSC hg19] of the abnormal fragment are arr22q11.21 (19006943_21461068)x1 with a size of 2.454 Mb. Related disease area is Pathogenic (pathogenicity, ACMG classification); and such abnormal fragment covers 106 ISCA genes, such as TBX1, CRKL, GP1BB, SLC25A1, DGCR10, TSSK1A, GSC2 and CLTCL1. The regional anomaly is located at 22q11.2 recurrent

(DGS/VCFS) region (includes TBX1). The deletion of 22q11.2 proximal (A-D) region is related to the DiGeorge / Velocardioffacial (DGS/VCFS) syndrome which is generally clinically featured by congenital heart disease, heart abnormity, characteristic facial features, DD/ID, behavior disorders, immune deficiency and hypocalcemia (PMID 25217958). The regional anomaly is located at 22q11.2 recurrent region (central, B/C-D) (includes CRKL). The clinical phenotypes possibly caused by the region deletion includes: deformed facial features, growth restriction/short stature, central nervous system abnormity/attack, developmental retardation, dysgnosia, skeletal anomalies, cardiovascular defects, urogenital system anomalies, immune deficiency/repeated infection (PMID 25123976).

[0054] The results indicate that the sorted cell specimen can be effectively subjected to chromosome structure variation detection and corresponding mutations can be detected.

Example 9 Comparison between the method for isolating trophoblast cells from cervical exfoliated cells of a pregnant woman based on the microfluidic cell sorting chip and the method of immunomagnetic beads

[0055]

(I) Experimental sample:
Two solutions containing cervical exfoliated cells from a humanized specimen detected by Hybribio Medical Laboratory.
(II) Immunomagnetic beads sorting served as a control experiment to compare the differences of the effects of the two methods.

[0056] The method of the present invention was the same as that in Example 2.

[0057] The process for sorting trophoblast cells by the immunomagnetic beads includes the following steps:

step (1) the specimen of the collected cervical exfoliated cell of the pregnant woman was mixed well via oscillation for 5 min;
step (2) the preserving solution was transferred into a 15 mL centrifugal tube, and 3 mL cell separating solution was added to the bottle of the preserving solution, and mixed evenly by oscillation, then the remaining solution was transferred into the same 15 mL centrifugal tube;
step (3) the solution was centrifuged for 10 min at 3000 rpm and supernatant was discarded;
step (4) 1 mL 1 ×PBST was added and mixed well and transferred to a 1.5 mL EP tube, and centrifuged for 5 min at 3000 rpm and supernatant was discarded;
step (5) the step (4) was repeated twice;
step (6) 200 μL 0.5% Triton X-100 was added and mixed well, then permeabilized at room temperature for 20 min;
step (7) the step (4) was repeated for three times;
step (8) 200 μl primary antibody was added and mixed well, incubating over night at 4°C;
step (9) the step (4) was repeated for three times;
step (10) 200 μl secondary antibody was added and mixed well for reaction for 1 h at 37°C;
step (11) the step (4) was repeated for three times, and 200 μL buffer (DPBS+0.1% BSA+2 mM EDTA) was used for resuspending;
step (12) 25 μl beads were fully mixed with 50 μl buffer well, and 600 g were centrifuged for 10 min, and supernatant was discarded, and the remaining solution was resuspended with 25 μl buffer, and then added to the mixed solution in the step (11);
step (13) reaction was performed for 20 min at 2°C-8°C;
step (14) 1 mL buffer was added and mixed well, standing on a magnetic frame for 2 min, then supernatant was discarded (200 μl was preserved for comparison);
step (15) the step (14) was repeated for two to three times;
step (16) 200 μl buffer preheated at 37°Cwas added for resuspending, and 4 μl Release Buffer was added and mixed well;
step (17) 15 min later at room temperature, the solution was pipetted for 5-10 times with a sample loading pipette, standing on the magnetic frame for 2 min, and supernatant was collected;
step (18) 200 μl buffer was added and pipetted for 5-10 times, standing on the magnetic frame for 2 min, then supernatant was collected;
step (19) the step (18) was repeated for three times to finally obtain the trophoblast cells.

(III) Result

[0058] The sorted positive cells were subjected to photo shooting with a SUNNY RX50 fluorescence microscope, as

shown in FIGS. 14-16. FIG. 14 is a picture showing positive cells sorted by the method of the present invention; FIG. 15 is a picture showing comparison of positive cells and negative cells before and after being sorted by the method of the present invention; FIG. 16 is a picture showing positive cells sorted by the immunomagnetic beads. It can be obviously seen from the comparison that there is an obvious difference in the order of magnitudes of the cell population after being sorted by the two methods; the method of the present invention is significantly superior to the immunomagnetic beads. Statistics show that the number of positive cells sorted by the method of the present invention may be up to about 3000-13,000.

[0059] The examples described above are merely several embodiments of the present invention, and described more specifically, but may be not construed as limiting the scope of the patent

[0060] Therefore, the protection scope of the present invention shall be subjected to the claims attached.

Claims

1. A method for isolating trophoblast cells, **characterized in that**, the method comprises the following steps:

   step (1) preparing a sample cell suspension from a solution containing cervical exfoliated cells, wherein the cells are suspended in 1x PBS containing 0.2%-0.4% FBS
   step (2) adding a specific antibody to the sample cell suspension for incubation; a primary antibody is incubated in the following conditions: reacting for 30-90 min at 4°C; and a second antibody-fluorescent labeling complex is incubated in the following conditions: reacting for 20 min at 2°C - 8°C;
   wherein the specific antibody is an antibody combination specifically recognizing an specific antigen expressed on the surface of or inside of corresponding trophoblast cells, namely, a specific antibody combination is HLA-G+CK7, HLA-G+CK18, HLA-G+β-HCG, CD31+HPL, MMP9+CD31, HLA-G+HPL, HLA-G+MMP9, HLA-G+CD31, HLA-G+P, CD31+P, HLA-G+CDH5, CD31+CDH5, CD31+CK7+HLA-G, HLA-G+CK18+CD31, HLA-G+β-HCG+CD31, CD31+HPL+HLA-G, MMP9+CD31+HLA-G, CD31+P+HLA-G or HLA-G+CDH5+CD31; and
   step (3) performing fluorescence labeling and microfluidics cell sorting of a cell resuspension incubated in the step (2) by a microfluidic cell sorting chip to obtain isolated and purified placental trophoblast cells;
   wherein a liquid-phase cell sorting system is 0.2% - 0.4% Triton-X-100;
   the microfluidic cell sorting chip comprises a substrate and a cover plate fitted therewith;
   wherein one side of the substrate is provided with a main channel, a side channel A and a side channel B, and the two side channels are respectively close to left and right end portions of the main channel;
   and wherein another side of the substrate is provided with an inlet C, an inlet S, an outlet N and an outlet T; all the two inlets and the two outlets penetrate the substrate to communicate with the channels on the other side; and a position of the inlet C corresponds to the left end portion of the main channel; a position of the inlet S corresponds to the end portion of the side channel A; a position of the outlet N corresponds to the right end portion of the main channel; and a position of the outlet T corresponds to the end portion of the side channel B;
   and a deflection electrode device is further disposed in the main channel and at a convergence site of the outlet N and the outlet T; and
   each of the main channel, the side channel A and the side channel B has a width not greater than 1000 μm and a depth not greater than 500 μm.

2. The method according to claim 1, wherein the step (2) specifically comprises:

   successively and specifically binding the primary antibody and the second antibody-fluorescent labeling complex to a target antigen step by step by incubation,
   wherein a washing and centrifugal separation technology is used to avoid cross contamination during the binding process.

3. The method according to claim 1, wherein the step (3) specifically comprises: feeding the incubated cell resuspension into the inlet C of the microfluidic cell sorting chip, feeding a buffer solution into the inlet S, then placing the microfluidic cell sorting chip in a cell sorter to carry out the sorting program, and collecting specimens at the outlet T at the end of the sorting program to obtain sorted trophoblast cells.

Patentansprüche

1. Verfahren zum Isolieren von Trophoblastenzellen, **dadurch gekennzeichnet, dass** das Verfahren die folgenden

Schritte umfasst:

Schritt (1) Vorbereiten einer Probenzellsuspension aus einer Lösung, die zervikale exfolierte Zellen enthält, wobei die Zellen in 1xPBS suspendiert sind, das 0,2% - 0,4% FBS enthält;

Schritt (2) Zugeben eines spezifischen Antikörpers zu der Probenzellsuspension zur Inkubation; ein primärer Antikörper wird unter den folgenden Bedingungen inkubiert: Reagieren für 30-90 min bei 4°C; und ein zweiter Antikörper-Fluoreszenz-Markierungskomplex wird unter den folgenden Bedingungen inkubiert: Reagieren für 20 min bei 2°C - 8°C;
wobei der spezifische Antikörper eine Antikörperkombination ist, die spezifisch ein Antigen erkennt, das auf der Oberfläche oder im Inneren von entsprechenden Trophoblastenzellen exprimiert wird, d.h. eine spezifische Antikörperkombination ist HLA-G+CK7, HLA-G+CK18, HLA-G+β-HCG, CD31+HPL, MMP9+CD31, HLA-G+HPL, HLA-G+MMP9, HLA-G+CD31, HLA-G+P, CD31+P, HLA-G+CDH5, CD31+CDH5, CD31+CK7+HLA-G, HLA-G+CK18+CD31, HLA-G+ß-HCG+CD31, CD31+HPL+HLA-G, MMP9+CD31+HLA-G, CD31+P+HLA-G oder HLA-G+CDH5+CD31; und

Schritt (3) Durchführen von Fluoreszenzmarkierung und mikrofluidischer Zellsortierung einer Zellresuspension, die in Schritt (2) inkubiert wurde, durch einen mikrofluidischen Zellsortierungschip, um isolierte und gereinigte plazentare Trophoblastenzellen zu erhalten;
wobei ein Flüssigphasen-Zellsortierungssystem 0,2% - 0,4% Triton-X-100 ist;
der mikrofluidische Zellsortierungschip ein Substrat und eine damit ausgestattete Abdeckplatte umfasst;
wobei eine Seite des Substrats mit einem Hauptkanal, einem Nebenkanal A und einem Nebenkanal B versehen ist und die beiden Nebenkanäle jeweils nahe linken und rechten Endabschnitten des Hauptkanals sind;
und wobei eine andere Seite des Substrats mit einem Einlass C, einem Einlass S, einem Auslass N und einem Auslass T versehen ist; alle der beiden Einlässe und der beiden Auslässe das Substrat durchdringen, um mit den Kanälen auf der anderen Seite in Verbindung zu stehen; und eine Position des Einlasses C dem linken Endabschnitt des Hauptkanals entspricht; eine Position des Einlasses S dem Endabschnitt des Nebenkanals A entspricht; eine Position des Auslasses N dem rechten Endabschnitt des Hauptkanals entspricht; und eine Position des Auslasses T dem Endabschnitt des Nebenkanals B entspricht;
und eine Ablenkelektrodenvorrichtung ferner in dem Hauptkanal und an einer Konvergenzstelle des Auslasses N und des Auslasses T angeordnet ist; und
jeder des Hauptkanals, des Nebenkanals A und des Nebenkanals B eine Breite von nicht mehr als 1000 μm und eine Tiefe von nicht mehr als 500 μm aufweist.

2. Verfahren nach Anspruch 1, wobei der Schritt (2) insbesondere umfasst: sukzessives und spezifisches Binden des primären Antikörpers und des zweiten Antikörper-Fluoreszenz-Markierungskomplexes an ein Zielantigen Schritt für Schritt durch Inkubation, wobei eine Wasch- und Zentrifugaltrenntechnologie verwendet wird, um Kreuzkontamination während des Bindungsprozesses zu vermeiden.

3. Verfahren nach Anspruch 1, wobei der Schritt (3) insbesondere umfasst: Einspeisen der inkubierten Zellresuspension in den Einlass C des mikrofluidischen Zellsortierungschips, Einspeisen einer Pufferlösung in den Einlass S, dann Platzieren des mikrofluidischen Zellsortierungschips in einem Zellsortierer, um das Sortierungsprogramm durchzuführen, und Sammeln von Proben am Auslass T am Ende des Sortierungsprogramms, um sortierte Trophoblastenzellen zu erhalten.

Revendications

1. Procédé pour isoler des cellules de trophoblaste, **caractérisé en ce que** le procédé comprend les étapes suivantes :

étape (1) préparer une suspension de cellules échantillon à partir d'une solution contenant des cellules exfoliées du col de l'utérus, dans lequel les cellules sont mises en suspension dans du PBS 1x contenant 0,2 % à 0,4 % de FBS ;
étape (2) ajouter un anticorps spécifique à la suspension de cellules échantillon pour incubation ; un anticorps primaire est incubé dans les conditions suivantes : réagir pendant 30 à 90 min à 4 °C ; et un second complexe anticorps-marquage fluorescent est incubé dans les conditions suivantes : réagir pendant 20 min à 2 °C à 8 °C ;
dans lequel l'anticorps spécifique est une combinaison d'anticorps reconnaissant spécifiquement un antigène exprimé sur la surface ou à l'intérieur de cellules de trophoblaste correspondantes, à savoir, une combinaison d'anticorps spécifique est HLA-G+CK7, HLA-G+CK18, HLA-G+β-HCG, CD31+HPL, MMP9+CD31, HLA-G+HPL, HLA-G+MMP9, HLA-G+CD31, HLA-G+P, CD31+P, HLA-G+CDH5, CD31+CDH5, CD31+CK7+HLA-

G, HLA-G+CK18+CD31, HLA-G+β-HCG+CD31, CD31+HPL+HLA-G, MMP9+CD31+HLA-G, CD31+P+HLA-G ou HLA-G+CDH5+CD31 ; et

étape (3) effectuer un marquage par fluorescence et un tri cellulaire microfluidique d'une remise en suspension cellulaire incubée dans l'étape (2) par une puce de tri cellulaire microfluidique pour obtenir des cellules de trophoblaste placentaires isolées et purifiées ;

dans lequel un système de tri cellulaire en phase liquide est Triton-X-100 à 0,2 % à 0,4 % ;

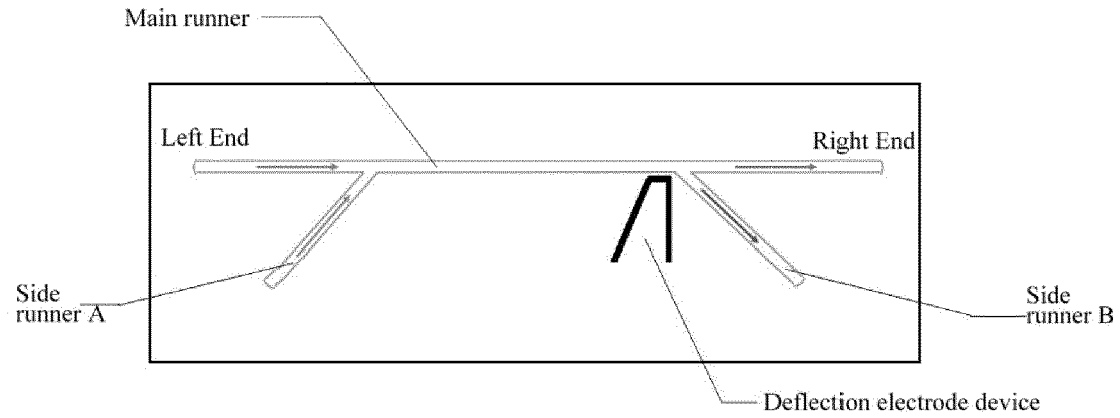
la puce de tri cellulaire microfluidique comprend un substrat et une plaque de couverture ajustée avec celui-ci ; dans lequel un côté du substrat est pourvu d'un canal principal, d'un canal latéral A et d'un canal latéral B, et les deux canaux latéraux sont respectivement proches des parties d'extrémité gauche et droite du canal principal ; et dans lequel un autre côté du substrat est pourvu d'une entrée C, d'une entrée S, d'une sortie N et d'une sortie T ; toutes les deux entrées et les deux sorties pénètrent dans le substrat pour communiquer avec les canaux de l'autre côté ; et une position de l'entrée C correspond à la partie d'extrémité gauche du canal principal ; une position de l'entrée S correspond à la partie d'extrémité du canal latéral A ; une position de la sortie N correspond à la partie d'extrémité droite du canal principal ; et une position de la sortie T correspond à la partie d'extrémité du canal latéral B ;

et un dispositif d'électrode de déviation est en outre disposé dans le canal principal et au niveau d'un site de convergence de la sortie N et de la sortie T ; et

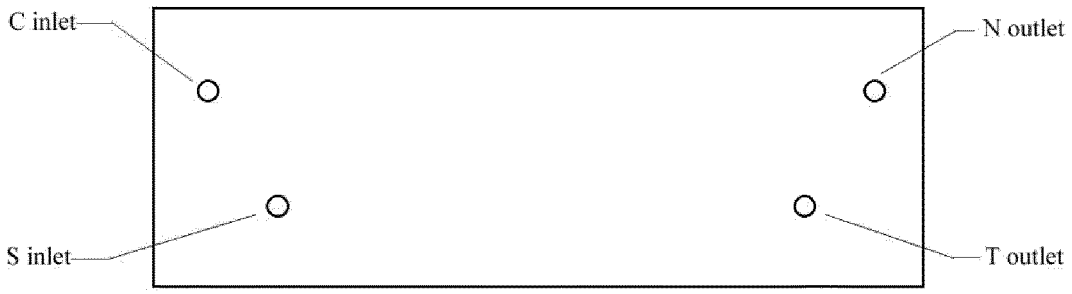
chacun du canal principal, du canal latéral A et du canal latéral B a une largeur non supérieure à 1000 μm et une profondeur non supérieure à 500 μm.

2. Procédé selon la revendication 1, dans lequel l'étape (2) comprend spécifiquement : lier successivement et spécifiquement l'anticorps primaire et le second complexe anticorps-marquage fluorescent à un antigène cible étape par étape par incubation, dans lequel une technologie de lavage et de séparation centrifuge est utilisée pour éviter une contamination croisée pendant le processus de liaison.

3. Procédé selon la revendication 1, dans lequel l'étape (3) comprend spécifiquement : introduire la remise en suspension cellulaire incubée dans l'entrée C de la puce de tri cellulaire microfluidique, introduire une solution tampon dans l'entrée S, puis placer la puce de tri cellulaire microfluidique dans un trieur cellulaire pour exécuter le programme de tri, et collecter des spécimens à la sortie T à la fin du programme de tri pour obtenir des cellules de trophoblaste triées.


Main runner
Left End
Right End
Side runner A
Side runner B
Deflection electrode device

(a)


C inlet
N outlet
S inlet
T outlet

(b)

FIG. 1

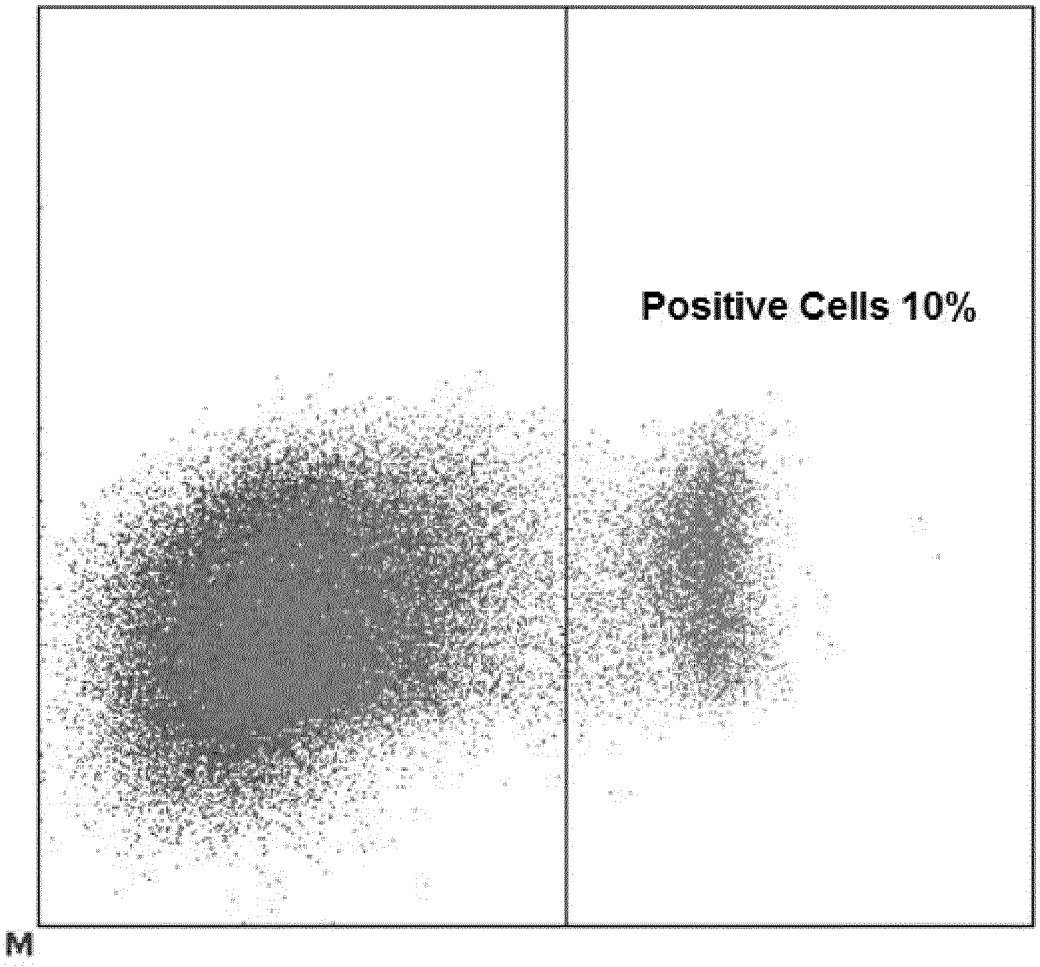


FIG. 2

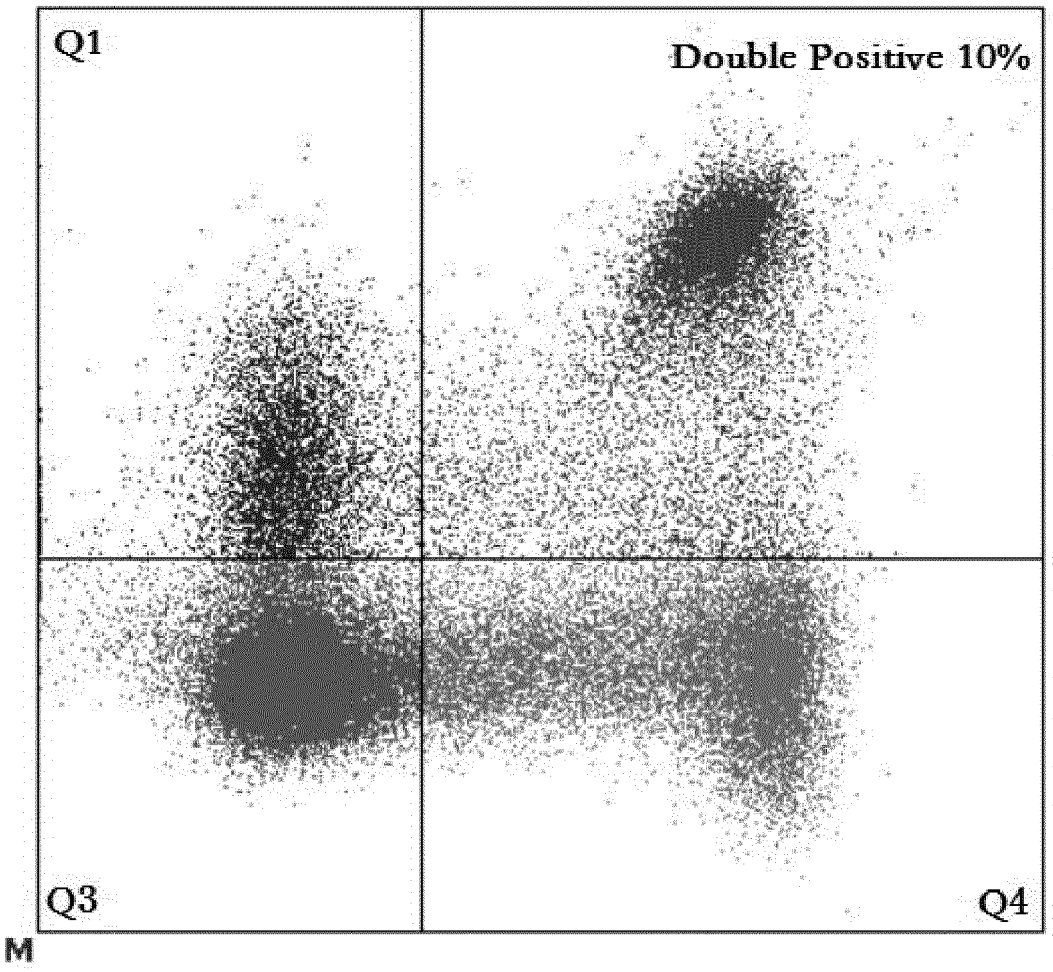
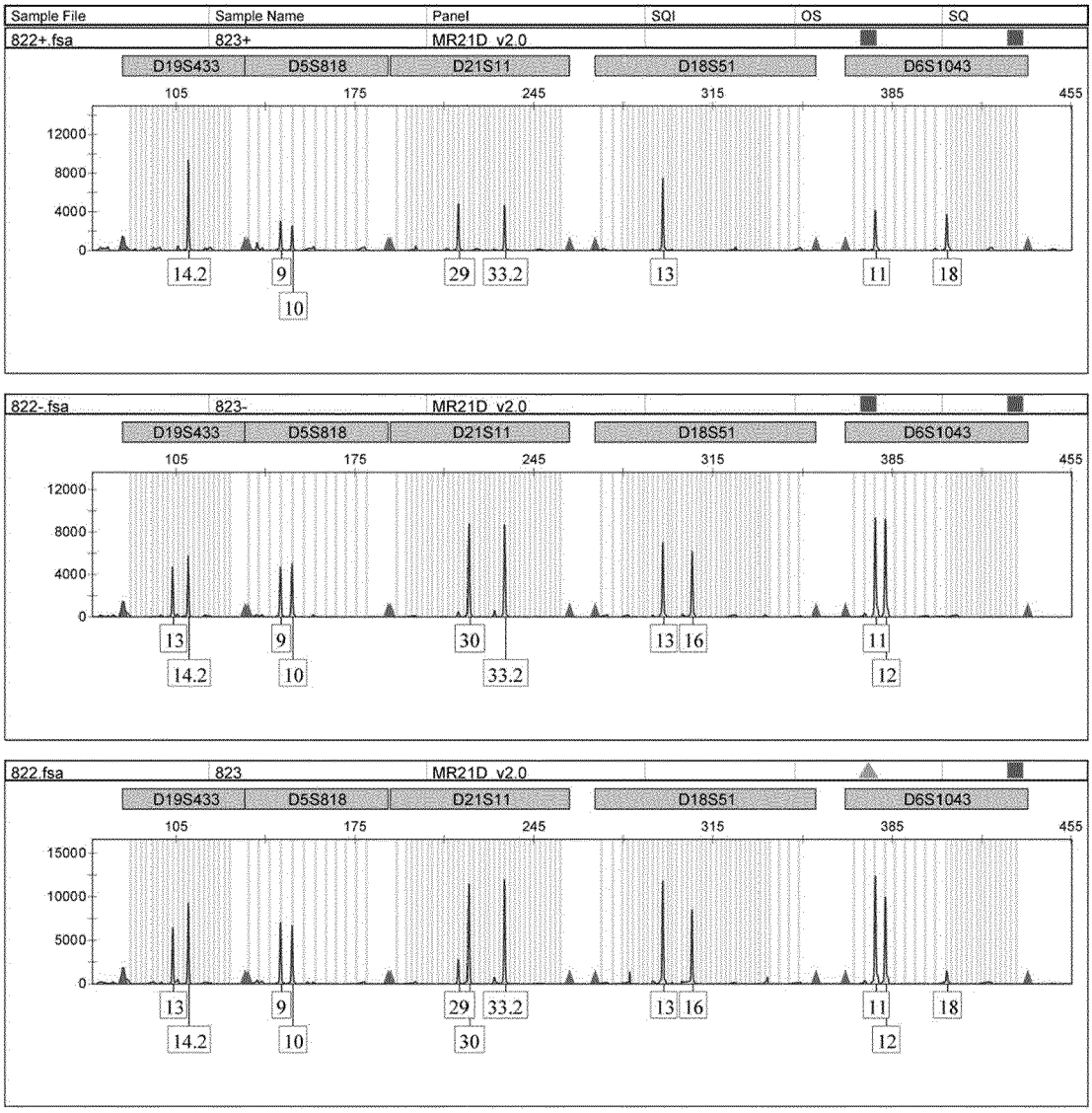


FIG. 3


Sample File
Sample Name
Panel
SQI
OS
SQ
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823+
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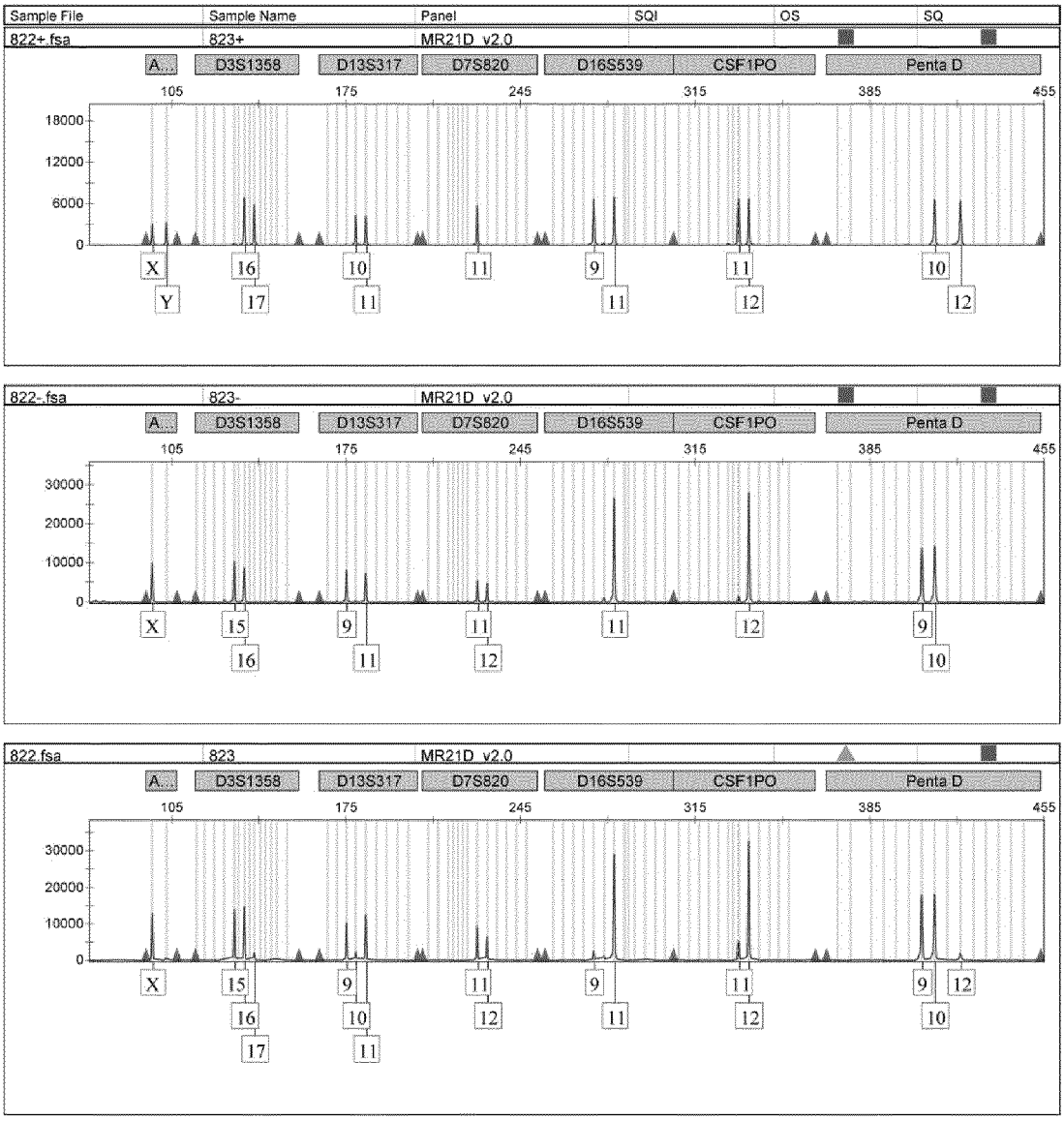
D19S433
D5S818
D21S11
D18S51
D6S1043
105
175
245
315
385
455
12000
8000
4000
0
14.2
9
10
29
33.2
13
11
18
822-.fsa
823-
MR21D_v2.0
13
14.2
9
10
30
33.2
13
16
11
12
822.fsa
823
MR21D_v2.0
15000
10000
5000
0
13
14.2
9
10
29
30
33.2
13
16
11
12
18

FIG. 4


Sample File
Sample Name
Panel
SQI
OS
SQ
822+.fsa
823+
MR21D_v2.0
A...
D3S1358
D13S317
D7S820
D16S539
CSF1PO
Penta D
105
175
245
315
385
455
18000
12000
6000
0
X
Y
16
17
10
11
11
9
11
11
11
12
10
12
822-.fsa
823-
MR21D_v2.0
30000
20000
10000
0
X
15
16
9
11
11
12
11
12
9
10
822.fsa
823
MR21D_v2.0
30000
20000
10000
0
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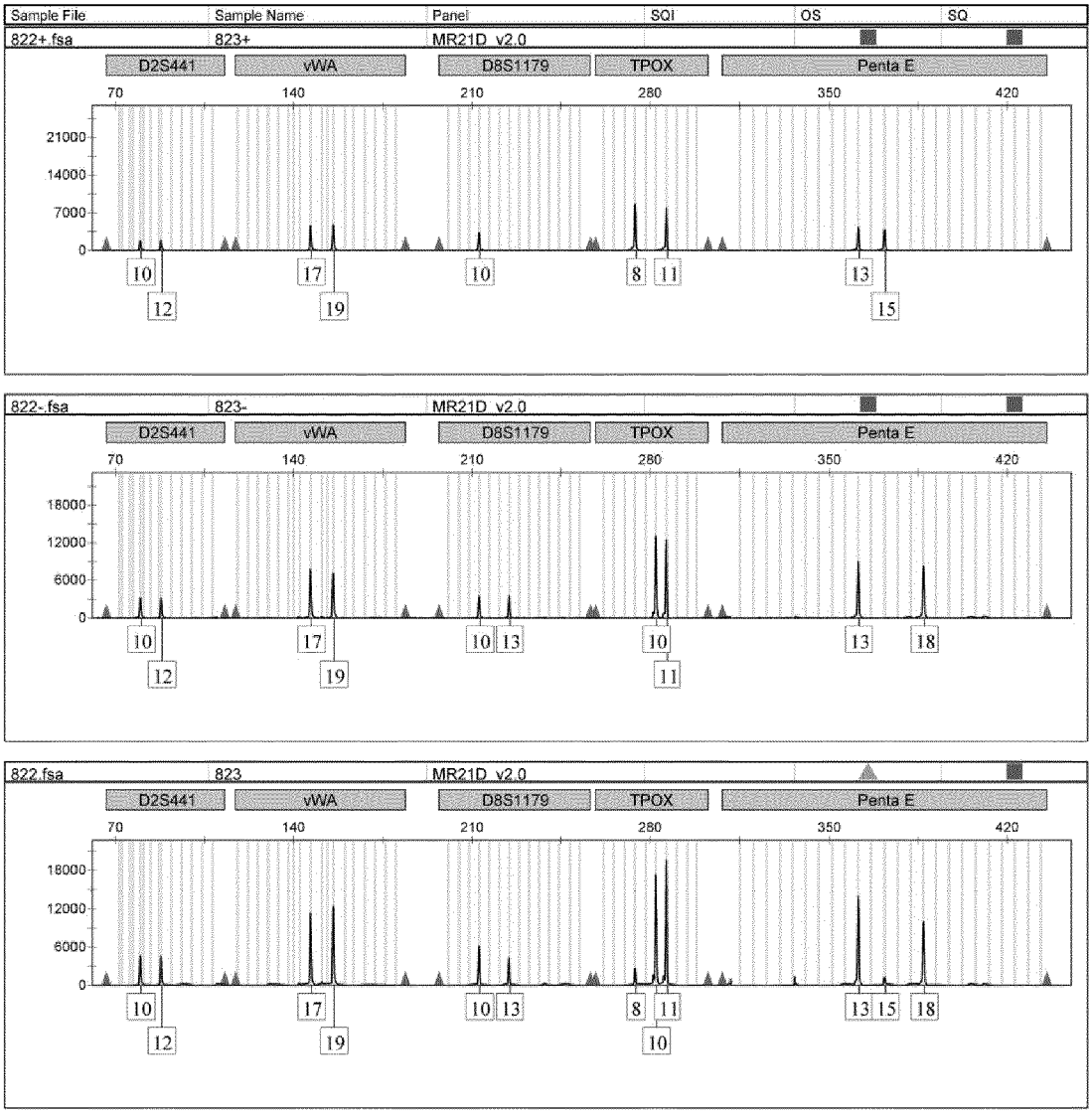
17
9
10
11
11
12
9
11
11
12
11
9
12
10

FIG. 5


Sample File
Sample Name
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SQI
OS
SQ
822+.fsa
823+
MR21D_v2.0
D2S441
vWA
D8S1179
TPOX
Penta E
70
140
210
280
350
420
21000
14000
7000
0
10
12
17
19
10
8
11
13
15
822-.fsa
823-
MR21D_v2.0
18000
12000
6000
0
10
12
17
19
10
13
10
11
13
18
822.fsa
823
MR21D_v2.0
18000
12000
6000
0
10
12
17
19
10
13
8
11
10
13
15
18

FIG. 6

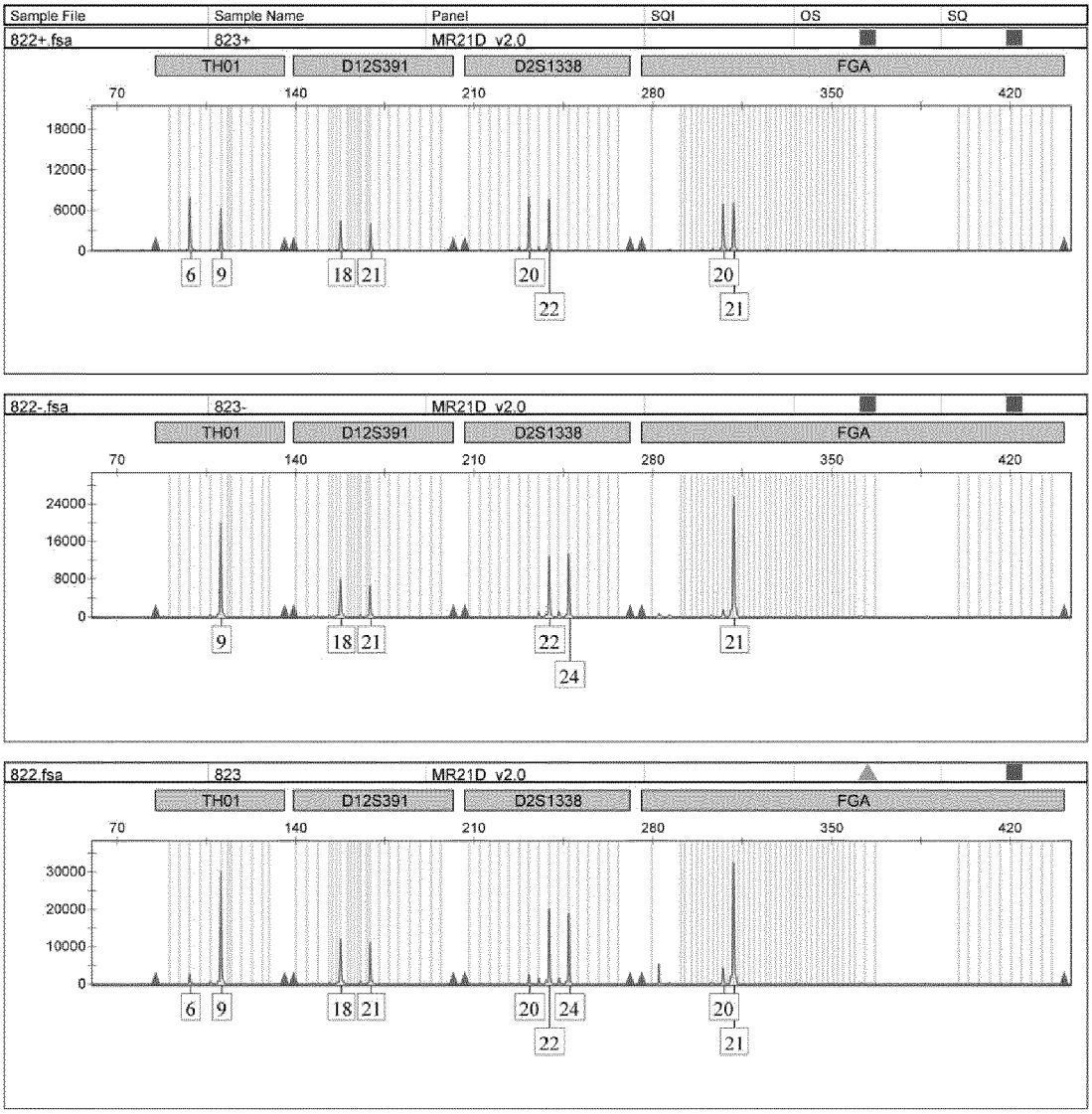
Sample File
Sample Name
Panel
SQI
OS
SQ
822+.fsa
823+
MR21D_v2.0
TH01
D12S391
D2S1338
FGA
70
140
210
280
350
420
18000
12000
6000
0
6
9
18
21
20
22
20
21
822-.fsa
823-
MR21D_v2.0
TH01
D12S391
D2S1338
FGA
24000
16000
8000
0
9
18
21
22
24
21
822.fsa
823
MR21D_v2.0
TH01
D12S391
D2S1338
FGA
30000
20000
10000
0
6
9
18
21
20
24
22
20
21

FIG. 7

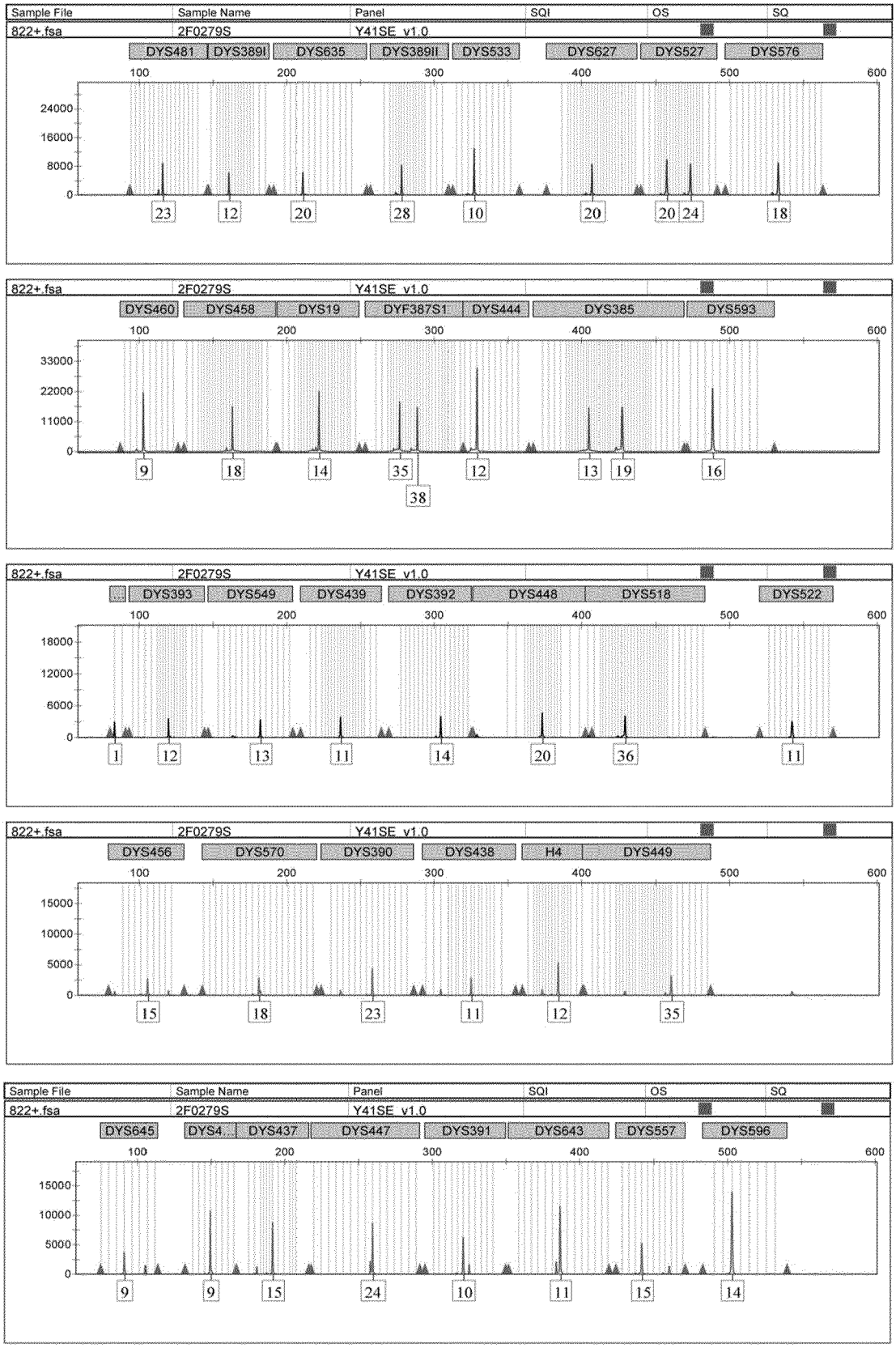
Sample File
Sample Name
Panel
SQI
OS
SQ
822+.fsa
2F0279S
Y41SE_v1.0
DYS481
DYS389I
DYS635
DYS389II
DYS533
DYS627
DYS527
DYS576
23
12
20
28
10
20
20
24
18
DYS460
DYS458
DYS19
DYF387S1
DYS444
DYS385
DYS593
9
18
14
35
38
12
13
19
16
DYS393
DYS549
DYS439
DYS392
DYS448
DYS518
DYS522
1
12
13
11
14
20
36
11
DYS456
DYS570
DYS390
DYS438
H4
DYS449
15
18
23
11
12
35
DYS645
DYS4
DYS437
DYS447
DYS391
DYS643
DYS557
DYS596
9
9
15
24
10
11
15
14

FIG. 8

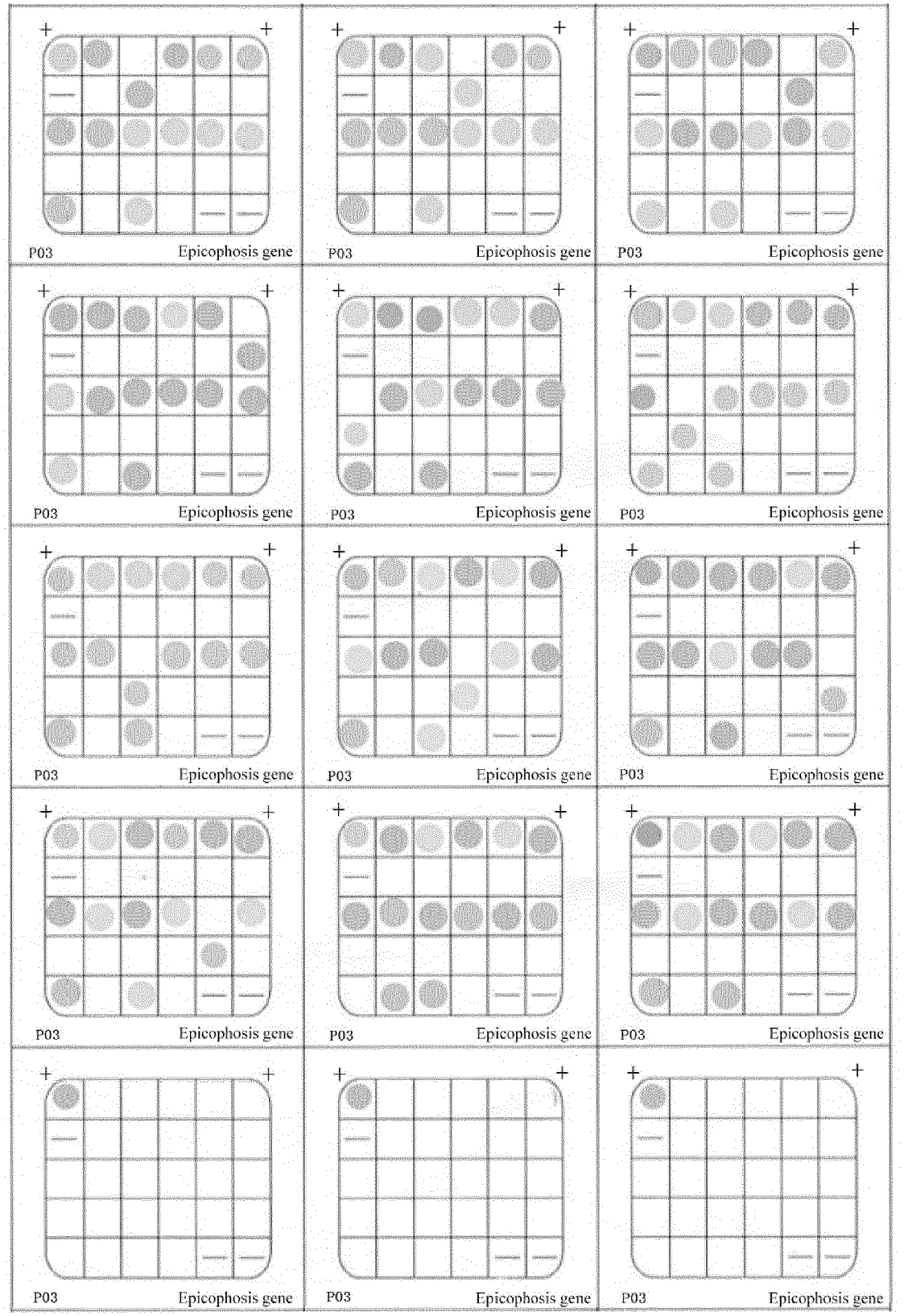

FIG. 9

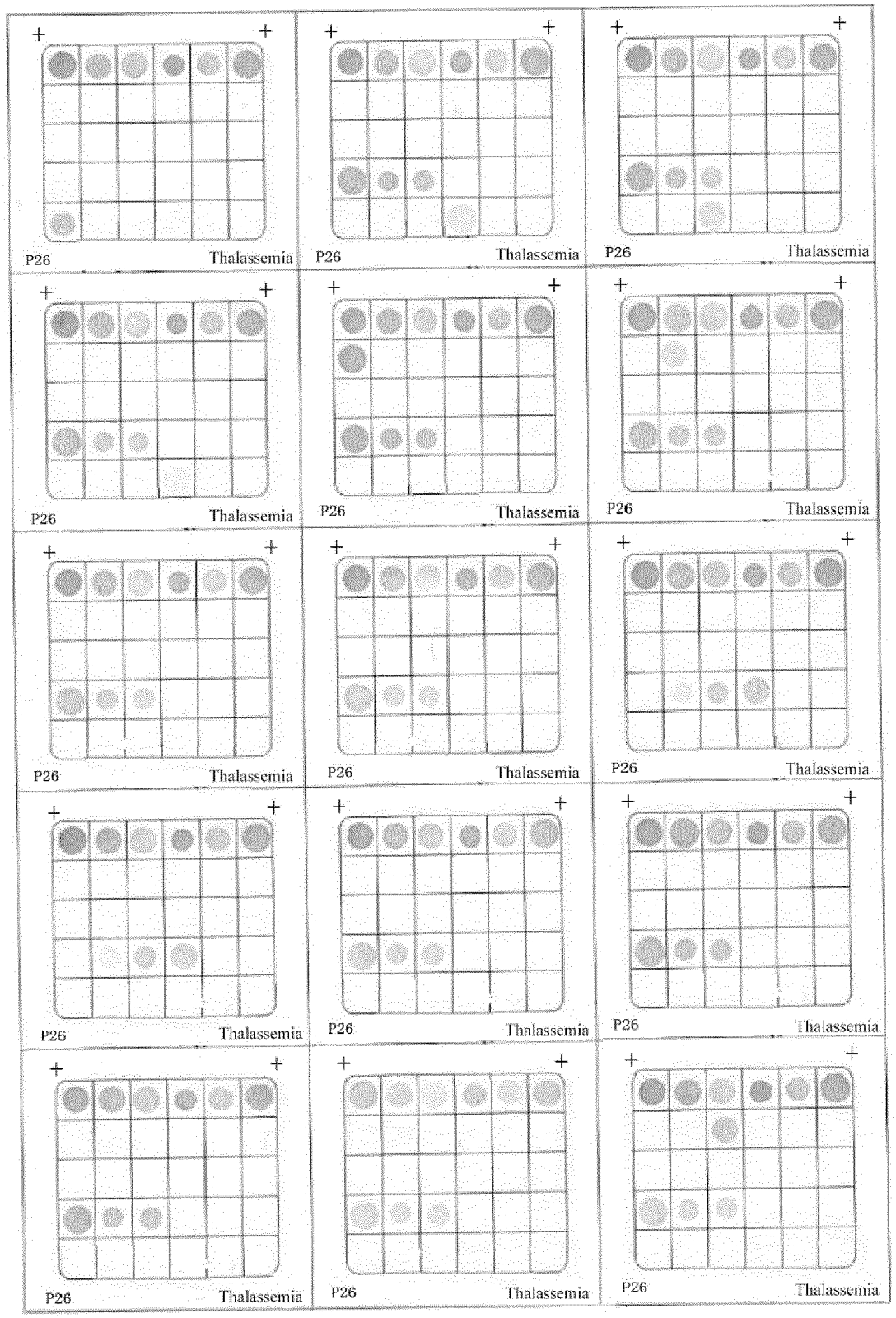

FIG. 10

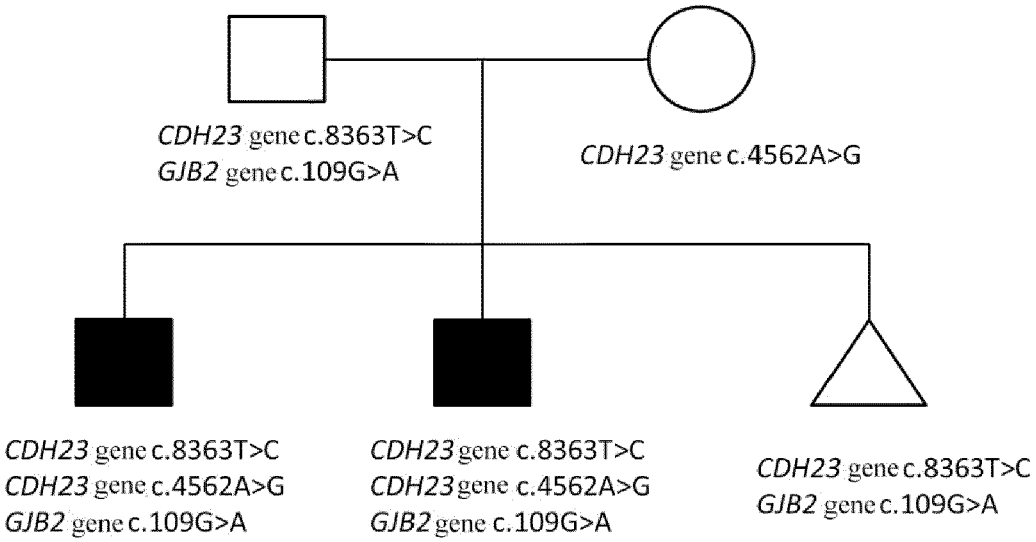
CDH23 gene c.8363T>C
GJB2 gene c.109G>A
CDH23 gene c.4562A>G
CDH23 gene c.8363T>C
CDH23 gene c.4562A>G
GJB2 gene c.109G>A
CDH23 gene c.8363T>C
CDH23 gene c.4562A>G
GJB2 gene c.109G>A
CDH23 gene c.8363T>C
GJB2 gene c.109G>A

FIG. 11

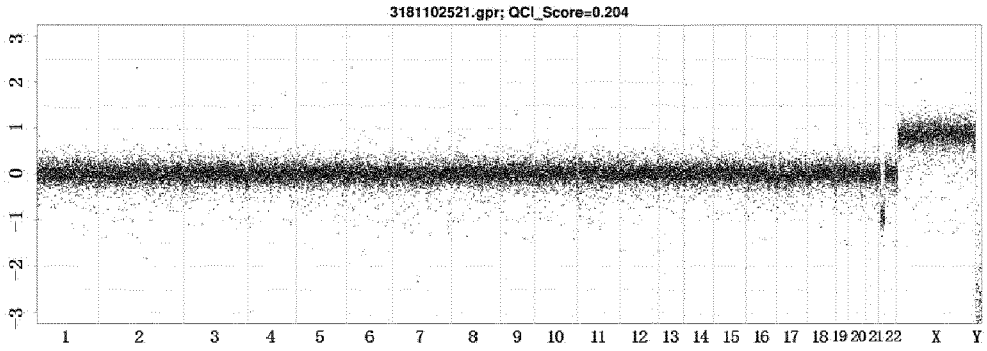
3181102521.gpr; QCI_Score=0.204
3
2
1
0
−1
−2
−3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y

FIG. 12

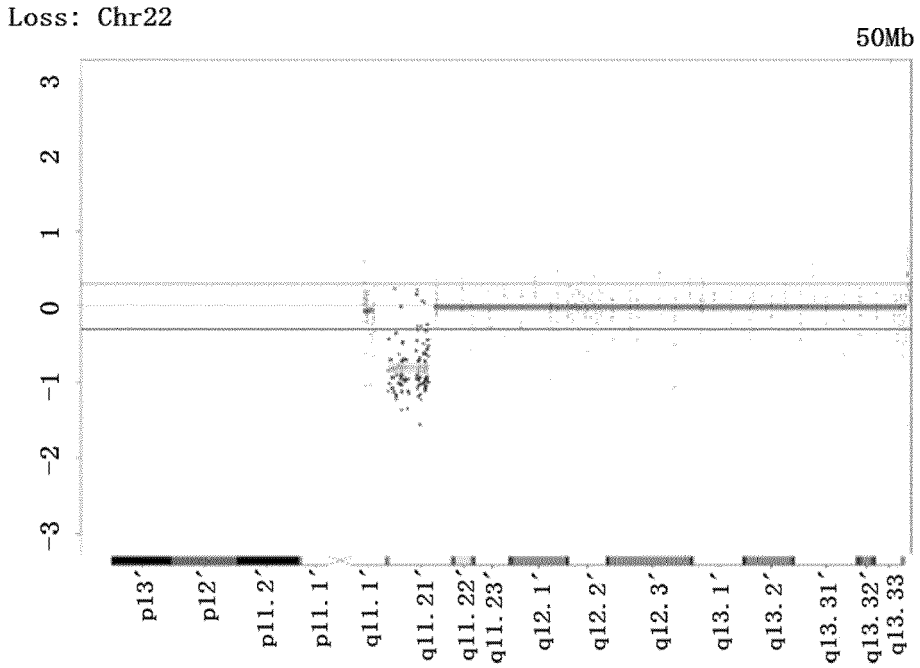
Loss: Chr22
50Mb
3
2
1
0
−1
−2
−3
p13′
p12′
p11.2′
p11.1′
q11.1′
q11.21′
q11.22′
q11.23′
q12.1′
q12.2′
q12.3′
q13.1′
q13.2′
q13.31′
q13.32′
q13.33

FIG. 13

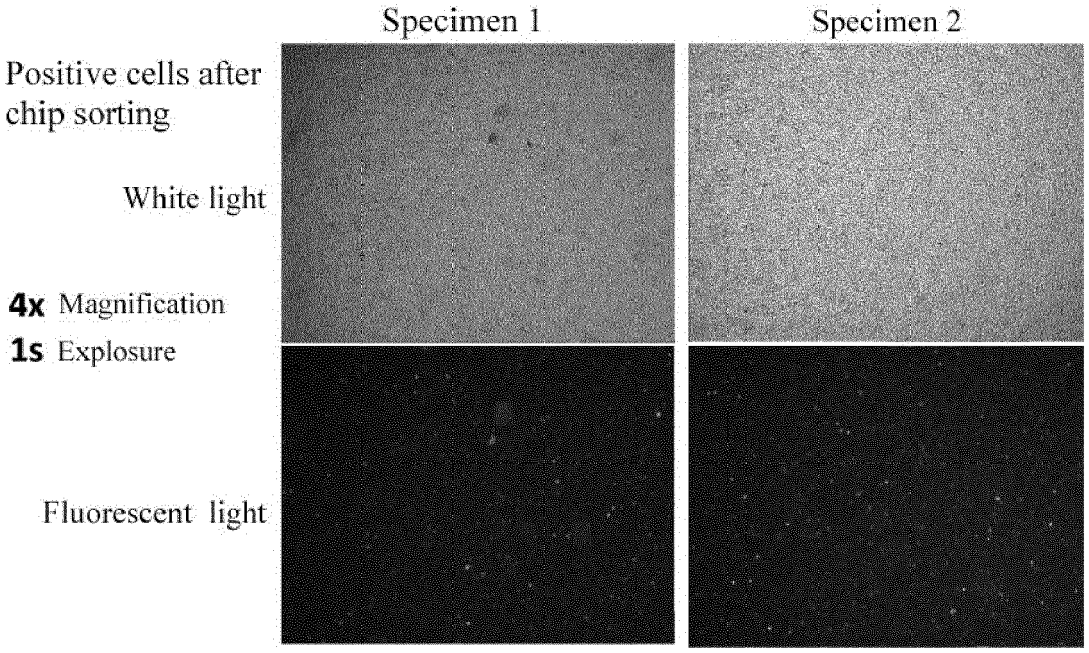
Specimen 1
Specimen 2
Positive cells after chip sorting
White light
4x Magnification
1s Explosure
Fluorescent light

FIG. 14

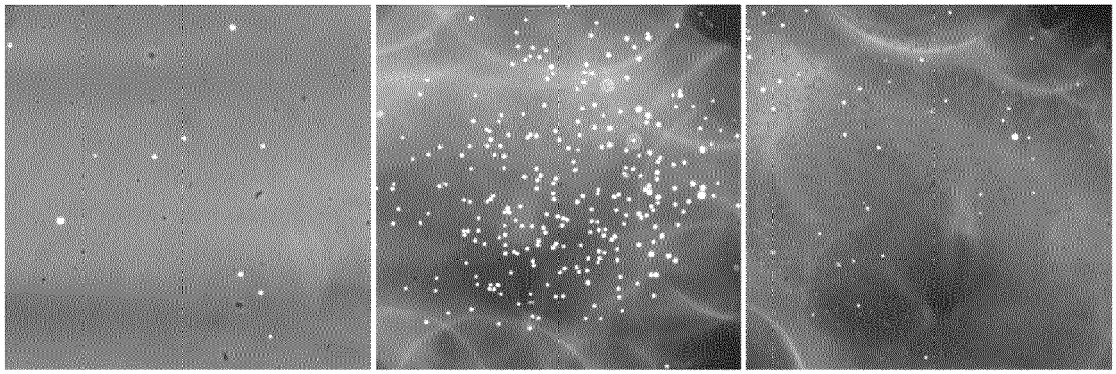
Cell mixture before sorting
Positive cell result after sorting
Negative cell result after sorting

FIG. 15

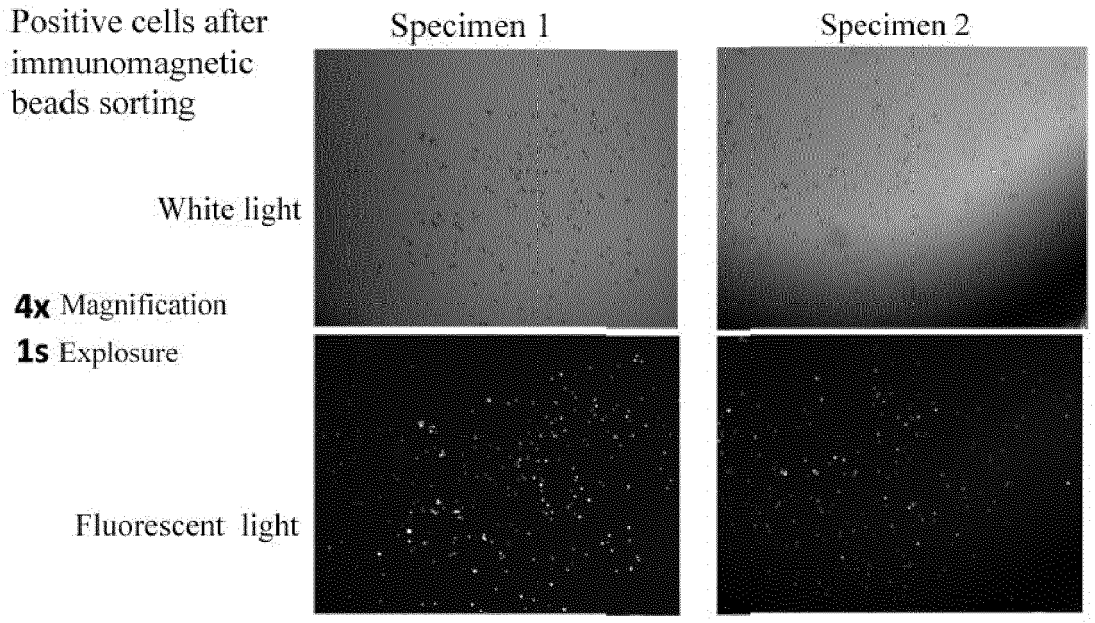
Positive cells after immunomagnetic beads sorting
Specimen 1
Specimen 2
White light
4x Magnification
1s Explosure
Fluorescent light

FIG. 16

REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- CN 111304153 A **[0004]**