

Title (en)
METHOD FOR THE HIGHLY PARALLEL ANALYSIS OF METHYLATION STATUS

Title (de)
VERFAHREN ZUR HOCHPARALLELEN ANALYSE VON METHYLIERUNGSSTATUS

Title (fr)
PROCEDE D'ANALYSE HAUTEMENT PARALLELE D'ETAT DE METHYLATION

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Application
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Abstract (en)
[origin: WO0181620A2] The invention relates to a method for the highly parallel characterization of polymorphisms, especially SNPs, which can be used for the simultaneous or separate detection of DNA methylations. A set of probes that is provided with at least one detectable marking characteristic of the corresponding probe is bound to an addressed surface, the bond of the probes to the surface being photochemically, chemically or enzymatically cleavable. A nucleic acid to be analyzed is then bound to said probes, the probes are modified in an allele-specific enzymatic reaction and a part of the probes that is irrelevant for the analysis of the allele-specific reaction is removed. The allele-specific products are analyzed by means of the detectable markings and the alleles present in the analyzed nucleic acid probe are determined.

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Cited by
US11410750B2; US11685958B2; US11725251B2; US11795513B2

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