CLAIMS

1. A method for determining the integrity of the human genome of a sample to be analysed by whole genome amplification (WGS) and/or the quality of a library of DNA sequences obtained by deterministic restriction site whole genome amplification (DRS-WGA) of the human genome of the sample comprising the steps of:

(a) providing the library of DNA sequences,

(b) amplifying the library of DNA sequences by PCR using:

- at least one first primer pair which hybridises to a DNA sequence of the library having a length from 1000 bp to 5000 bp and encompassing the D5S2117 region of chromosome 5q of the genome,

- at least one second primer pair which hybridises to a DNA sequence of the library having a length from 1000 bp to 5000 bp and encompassing exons 2 and 3 of the TRP53 gene of the genome, and

- at least one third primer pair which hybridises to a DNA sequence of the library having a length from 1000 bp to 5000 bp and encompassing the KRT19 pseudo-gene 1 of the genome,

the step of amplifying giving rise to a first PCR product from 50 bp to 1000 bp, a second PCR product from 50 bp to 1000 bp having a size other than the first PCR product, and a third PCR product from 50 bp to 1000 bp

having a size other than the first and second PCR products;

(c) detecting the first, second and third PCR products;

(d) correlating the presence of the first, second and third PCR products with the integrity of the genome of the sample and/or the quality of the library of DNA sequences.

2. The method according to claim 1, wherein the forward primer of the at least one first primer pair is SEQ ID NO:4 and the reverse primer of the at least one first primer pair is SEQ ID NO:3.

3. The method according to claim 1 or 2, wherein the forward primer of the at least one second primer pair is SEQ ID NO:6 and the reverse primer of the at least one second primer pair is SEQ ID NO:5.

4. The method according to any of claims 1 to 3, wherein the forward primer of the at least one third primer pair is SEQ ID NO:8 and the reverse primer of the at least one third primer pair is SEQ ID NO:7.

5. The method according to any of claims 2 to 4, wherein step (b) further uses at least one fourth primer pair which hybridises to a DNA sequence of the library having a length from 80 bp to 300 bp, the step of amplifying giving rise to a fourth PCR product from 50 bp to 200 bp having a size other than the first, the second

and the third PCR products;

- step (c) further comprises detecting the fourth PCR product;

- step (d) further comprises correlating the presence of the fourth PCR product with the integrity of the genome of the sample and/or the quality of the library of DNA sequences.

6. The method according to claim 5, wherein the DNA sequence of the library to which the at least one fourth primer pair hybridises encompasses Codon 12/13 of the KRAS gene.

7. The method according to claim 6, wherein the forward primer of the at least one fourth primer pair is SEQ ID NO:17 and the reverse primer of the at least one first primer pair is SEQ ID NO:18.

8. A kit for implementing the method according to any of claims 1 to 7 comprising:

- at least one first primer pair which hybridises to a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing the D5S2117 region of chromosome 5q of the genome,

- at least one second primer pair which hybridises to a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing exons 2 and 3 of the TRP53 gene of the genome, and

- at least one third primer pair which hybridises to

a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing the KRT19 pseudo-gene 1 of the genome,

wherein the first, second and third primer pairs give rise, when amplified by PCR, to PCR products having different size from one another.

9. The kit according to claim 8, further comprising at least one fourth primer pair which hybridises to a DNA sequence of the library having a length from 80 bp to 300 bp,

wherein the first, second, third and fourth primer pairs give rise, when amplified by PCR, to PCR products having different size from one another.

10. Use of a kit comprising:

- at least one first primer pair which hybridises to a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing the D5S2117 region of chromosome 5q of the genome,

- at least one second primer pair which hybridises to a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing exons 2 and 3 of the TRP53 gene of the genome, and

- at least one third primer pair which hybridises to a DNA sequence of the human library having a length from 1000 bp to 5000 bp and encompassing the KRT19 pseudo-gene 1 of the genome,

wherein the first, second and third primer pairs give rise, when amplified by PCR, to PCR products having different size from one another,

in predicting the success of a genetic analysis assay after amplification of single cell genomic DNA by DRS-WGA.

11. Use according to claim 10, wherein the genetic analysis assay is selected from the group consisting of Sanger sequencing for mutation analysis, assessment of specific copy number changes, quantitative PCR for gene amplification, metaphase Comparative Genomic Hybridisation (CGH), and array Comparative Genomic Hybridisation (CGH).