

What is claimed is :

1. A method for determining chromosome abnormalities comprising:
 - a first step of extracting a unique read from sequenced sequencing data of a target chromosome;
 - a second step of setting a threshold line for determining chromosome aneuploidy by linear discriminant analysis (LDA) by dividing and labeling normality and aneuploidy of chromosome data pre-verified for the normality and aneuploidy; and
 - a third step of determining whether there is aneuploidy of the unique read-target chromosome gene extracted in the first step by the threshold line set in the second step;
 - wherein after the first step,
 - the method for determining chromosome abnormalities further comprising:
 - a 1-1 step of calculating $UR(x) \%$ (percentage of reads uniquely matched to a chromosome X) and $UR(y) \%$ (percentage of reads uniquely matched to a chromosome Y) represented by the following Formulas from the extracted unique read;
$$UR(x) \% = \text{Number of reads of chromosome X (chrX)} / \text{total number of (autosomes) reads} \times 100$$
$$UR(y) \% = \text{Number of reads of chromosome Y (chrY)} / \text{total number of (autosomes) reads} \times 100$$
 - a 1-2 step of discriminating gender from the $UR(x) \%$ and the $UR(y) \%$; and
 - a 1-3 step of discriminating gender from the number of reads of the region matched to a Y-specific region in the step of discriminating the gender from the $UR(x) \%$ and the $UR(y) \%$.
2. The method for determining chromosome abnormalities of claim 1, wherein in the second step of performing initial learning by the LDA method by discriminant-labeling the normality and the aneuploidy of the pre-verified chromosome data and setting the threshold line for determining chromosome aneuploidy, a minimum value of the aneuploidy chromosome data among the pre-verified chromosome data is set as the threshold line.

3. The method for determining chromosome abnormalities of claim 1, wherein in the step of extracting the unique read, the read which is divided into a 90 kb bin region and has the GC content of 0.35 to 0.55 or less is extracted.
4. The method for determining chromosome abnormalities of claim 1, wherein the chromosome is at least one chromosome selected from the group consisting of chromosome 13, chromosome 18, chromosome 21, chromosome 3, chromosome 7, and chromosome 12, a chromosome X or a chromosome Y.
5. The method for determining chromosome abnormalities of claim 4, wherein when the chromosome is a chromosome X, the chromosome abnormalities are determined as XXX or XO.
6. The method for determining chromosome abnormalities of claim 4, wherein when the target chromosome is a chromosome Y, the chromosome abnormalities are determined as XXY or XYY.
7. The method for determining chromosome abnormalities of claim 1, wherein the first to third steps are repeated N times.
8. The method for determining chromosome abnormalities of claim 7, wherein the determination of the aneuploidy for a chromosome data D_n used at the time of the N-th determination is a threshold value derived from a chromosome data D_{n-1} used at the time of the N-1-th determination.
9. The method for determining chromosome abnormalities of any one of claims 1 to 8 wherein the sequenced sequence data is obtained by a next-generation sequencing platform.

10 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by a sequencing platform including the use of a polymerase chain reaction.

11 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by a sequencing platform including the use of sequencing by synthesis.

12 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by a sequencing platform including the use of ions, for example, hydrogen ion release.

13 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by a sequencing platform including the use of a semiconductor-based sequencing method.

14 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by a sequencing platform including the use of a nanopore-based sequencing method.

15 The method for determining chromosome abnormalities of claim 9, wherein the next-generation sequencing platform is selected from a Roche 454 (i.e., Roche 454 GS FLX), a SOLiD system from Applied Biosystems (i.e., SOLiDv4), GAIIx, HiSeq 2500 and MiSeq sequencers from Illumina, Ion Torrent semiconductor sequencing platforms from Life Technologies, PacBio RS from Pacific Biosciences, and 3730xl from Sanger.

16 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by an Ion Torrent platform from Life Technologies or MiSeq from Illumina.

17 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by an Ion Torrent personal genome machine (Ion Torrent PGM) from Life Technologies.

18 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is obtained by multiplex capable iteration based on an Ion Torrent platform from Life Technologies, Ion Proton having PI or PII chips, S5 and its further derivative devices and components thereof.

19 The method for determining chromosome abnormalities of any one of claims 1 to 8, wherein the sequenced sequence data is normalized or not.