

with corresponding cost savings.

The method for analyzing LoH from a sample according to the present invention allows to infer LoH regions across the genome from low-pass whole genome sequencing data down to the single-cell resolution, using very few samples, as it may be the case where only few (down to a single one) CTCs are available, with the additional optional possibility to run the analysis without a normal control, and with a relatively small number of reads.

Further, particular embodiments of the method enable to increase the resolution in LoH calling by introducing certain processing steps in the library preparation process, without incremental sequencing costs.

The method according to the invention surprisingly advances the state of the art with performances previously thought unachievable by the skilled in the art. In particular, the method allows to:

- identify LoH on a single-cell by low-pass whole-genome sequencing with as low as 0.01-0.04 mean coverage (250,000-1,000,000 single-end 150bp reads of the human genome);
- obtain the above point without a control sample;
- obtain the above points with the further possibility of obtaining additional genetic material for investigation of other characteristics of said single-cell, as well as the possibility to reliably reanalyse a single cell for verification, in virtue of the use of an inherent WGA in the process.

In addition, the method according to the present invention allows to determine whole-genome copy number profile and LoH even from minute amount of cells, FFPE or tissue biopsies.