

【ABSTRACT】

The present invention relates to a method for detecting a gene rearrangement on the basis of next generation sequencing (NGS) and, more specifically, to a method for arranging and extracting read data generated by NGS, analyzing the sequence similarity of the extracted read data so as to detect a gene rearrangement present in a cancer sample and, further, detecting the direction of the gene rearrangement, micro-homology sequences and external insertion sequences and positions. According to the method for detecting a gene rearrangement by using NGS, a gene rearrangement can be detected and the direction of the gene rearrangement, micro-homology sequences, external insertion sequences and the position of gene rearrangement can be accurately differentiated into units of base pairs through the reads obtained from the NGS. In addition, a search can be performed even in concordant read pairs, which have not been searched for by a conventional method, such that accuracy is high, and the time required for the detection can be reduced because only regions of genes related to a specific cancer or tumor can be searched for as the priority. Therefore, the method of the present invention is useful for effectively detecting a gene rearrangement in a cancer sample.