thereby generating a plurality of amplicons comprising a plurality of target gene sequences corresponding to the plurality of target genes that are capable of undergoing genomic alteration;

(c) removing target capture primers that have not been incorporated into the plurality of amplicons generated in step (b) using at least one nuclease, thereby generating a purified mixture of the plurality of amplicons comprising the plurality of target gene sequences;

(d) amplifying the plurality of amplicons in the purified mixture obtained from step (c) by using universal indexed adapter primers to generate a sequencing library, wherein each amplicon of the sequencing library comprises two barcode sequences;

(e) purifying the sequencing library obtained from step (d);

(f) subjecting the purified sequencing library from step (e) to multiplex sequencing on a next-generation sequencing platform to obtain a plurality of sequencing reads;

(g) mapping the plurality of sequencing reads obtained from step (f) to a first reference genome;

(h) grouping the sequencing reads where the barcode sequences of the sequencing reads are identical into a consensus cluster;

(i) performing a sequence alignment of each consensus cluster obtained from step (h) with all consensus clusters having at least one overlapping barcode sequence, then determining the presence of a consensus base in each sequence alignment result to generate a consensus sequencing read;

(j) mapping each of the consensus sequencing read from step (i) with a second reference genome;

(k) identifying the differences between the sequencing read and the reference genome from step (j) to thereby determine the presence of genomic alteration in the nucleic acid present in the biological sample.

[0007] In an example, the present disclosure refers to a kit for detecting genomic alterations within a biological sample according to the method disclosed herein, comprising a plurality of target capture primer pairs specific to a plurality of target genes that are capable of undergoing genomic alteration as defined in step (b) of the first aspect, and instructions for use in the method disclosed herein.

BRIEF DESCRIPTION OF DRAWINGS

[0008] The invention will be better understood with reference to the detailed description when considered in conjunction with the non-limiting examples and the accompanying drawings, in which: