to a sequence spanning an exon-exon junction of each control housekeeping gene,

wherein each forward primer of the plurality of forward and reverse primer pairs specific to the plurality of control housekeeping genes is complementary to a sequence about 100 base pairs downstream of the sequence spanning the exon-exon junction of each control housekeeping gene,

wherein each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of control housekeeping genes comprises a barcode sequence on its 5' end, wherein the barcode sequence of each reverse primer corresponding to each control housekeeping gene is different; or

(iii) each forward and each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of control housekeeping genes is complementary to consecutive sequences spanning an exon-exon junction of each control housekeeping gene,

wherein each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of control housekeeping genes comprises a barcode sequence on its 5' end, wherein the barcode sequence of each reverse primer corresponding to each control housekeeping gene is different, and/or

(III) a plurality of primer sets specific to a plurality of **target genes related to protein expression**,

wherein each primer set comprises a plurality of forward and reverse primer pairs specific to each target gene related to protein expression, wherein:

(i) each forward primer of the of the plurality of forward and reverse primer pairs specific to each target gene related to protein expression is complementary to a sequence spanning an exon-exon junction of each target gene related to protein expression,

wherein each reverse primer of the of the plurality of forward and reverse primer pairs specific to each target gene related to protein expression is complementary to a sequence about 100 base pairs downstream of the sequence spanning the exon-exon junction of each target gene related to protein expression,

wherein each reverse primer of the plurality of forward and reverse primer pairs specific to each target gene related to protein expression comprises a barcode sequence on its 5' end, wherein the barcode sequence of each reverse primer corresponding to each target gene related to protein expression is different,

(ii) each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of target genes related to protein expression is complementary to a sequence spanning an exon-exon junction of each target gene related to protein expression,

wherein each forward primer of the plurality of forward and reverse primer pairs specific to the plurality of target genes related to protein expression is complementary to a sequence about 100 base pairs downstream of the sequence spanning the exon-exon junction of each target gene related to protein expression,

wherein each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of target genes related to protein expression comprises a barcode sequence on its 5' end, wherein the barcode sequence of each reverse primer corresponding to each target gene related to protein expression is different; or

(iii) each forward and each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of target genes related to protein expression is complementary to consecutive sequences spanning an exon-exon junction of each target gene related to protein expression,

wherein each reverse primer of the plurality of forward and reverse primer pairs specific to the plurality of target genes related to protein expression comprises a barcode sequence on its 5' end, wherein the barcode sequence of each reverse primer corresponding to each target gene related to protein expression is different,

thereby generating a plurality of amplicons;

(c) purifying the plurality of amplicons from step (b);

(d) amplifying the purified product from step (c) by using universal indexed adapter primers to generate a sequencing library;

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

[0008] In another example, the present disclosure refers to a kit for detecting genomic alteration and/or detecting gene expression and/or quantifying a level of gene expression using RNA in a biological sample according to the method disclosed herein, wherein the kit comprises:

- a plurality of forward and reverse primer pairs specific to a plurality of **target genes that are capable of undergoing genomic alteration** as defined in the method disclosed herein,
- a plurality of forward and reverse primer pairs specific to a plurality of **control housekeeping genes** as defined in the method disclosed herein, and
- a plurality of primer sets specific to a plurality of **target genes related to protein expression** as defined in the method disclosed herein.

BRIEF DESCRIPTION OF THE DRAWINGS

[0009] 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:

[0010] **Fig. 1** is a general overview of the cfRNA-based detection method of a gene fusion event resulting from the intronic DNA rearrangement between two genes as described herein. Primers (represented by arrows) are designed to flank exonic junctions of genes known to undergo fusions. Primers (→) are designed such that the if a fusion product is present, the resulting amplicon would be of ~100 base pairs in length to be compatible with the observed cfRNA fragment size in plasma samples.

[0011] **Fig. 2**, comprising **Figs. 2A and 2B**, illustrates examples of primer design of the disclosed method, wherein **Fig. 2A** illustrates examples of primer design for capturing control housekeeping genes (left panel) and expression genes (right panel) in cfRNA. At least one primer of a primer pair spans an exon-exon junction, to prevent unintended amplification of cfDNA and the resulting amplicons are approximately 100 base pairs in length. It should be noted that the primer pairs for the housekeeping genes differ from that of the expression genes, and **Fig. 2B** illustrates an example of a forward primer and a reverse primer designed to bind to two different exons, intervened by an intron >5000 base pairs in length.

[0012] **Fig. 3**, comprising **Figs. 3A and 3B**, shows the size and concentration analysis of cfRNA from plasma total nucleic acid extracts from cancer patients and healthy individuals, wherein **Fig. 3A** shows the size and concentration analysis of cfRNA from plasma total nucleic acid extracts from a cancer patient (sample A), **Fig. 3B** shows the size and concentration analysis of cfRNA from plasma total nucleic acid extracts from another cancer patient (sample