

ABSTRACT

**METHOD FOR IDENTIFICATION AND QUANTIFICATION OF NUCLEIC ACID
EXPRESSION, SPLICE VARIANT, TRANSLOCATION, COPY NUMBER, OR
METHYLATION CHANGES**

The present invention relates to methods and devices for identifying and quantifying, including low abundance, nucleotide base mutations, insertions, deletions, translocations, splice variants, miRNA variants, alternative transcripts, alternative start sites, alternative coding sequences, alternative non-coding sequences, alternative splicings, exon insertions, exon deletions, intron insertions, or other rearrangement at the genome level and/or methylated nucleotide bases.

Figure 1