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(54) Title: METHOD FOR IDENTIFICATION AND RELATIVE QUANTIFICATION OF NUCLEIC ACID SEQUENCE, MUTATION, COPY NUMBER, OR METHYLATION CHANGES

(57) Abstract: The present invention relates to methods for identifying and/or quantifying 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 or hydroxymethylated nucleotide bases, as well as markers to identify early cancer, monitor cancer treatment, and identify early cancer recurrence.