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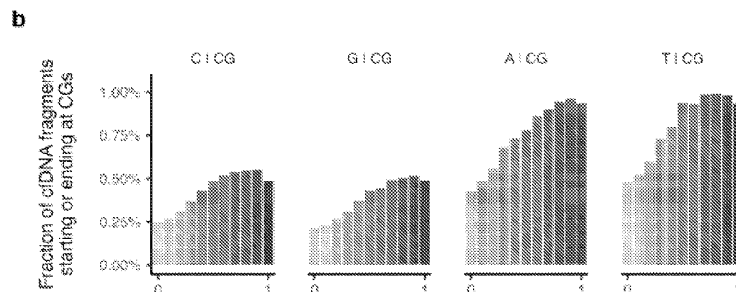
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(54) Title: DNA METHYLATION AND GENE EXPRESSION AS DETERMINANTS OF GENOME-WIDE CELL-FREE DNA
FRAGMENTATION



FIGS. 2B

(57) Abstract: Analysis of cell-free DNA (cfDNA) fragment ends in patients with cancer provide a direct link between epigenetic changes and cfDNA fragmentation for non-invasive disease detection and treatment of patients. In some embodiments, the methods for the diagnosing and treatment of cancer include detecting methylation and expression differences affecting cell free (cfDNA) size and coverage in patients. In certain aspects, it includes a method for determining circulating cfDNA fragmentation in a sample provided, comprising assaying genomic sequences to identify cfDNA endpoints; analyzing frequency of cfDNA breakpoints at a plurality of positions in the genomic sequences; thereby, determining circulating cfDNA fragmentation.

[Continued on next page]

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