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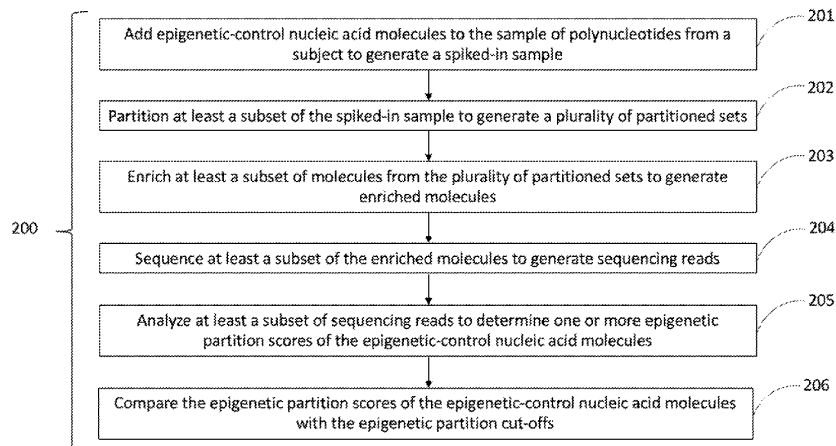


FIG. 2

(57) Abstract: In an aspect, a method for evaluating the partitioning of nucleic acid molecules in a sample of polynucleotides based on epigenetic state, comprising: (a) adding a set of epigenetic-control nucleic acid molecules to the nucleic acid molecules in the sample of polynucleotides, whereby producing a spiked-in sample; (b) partitioning nucleic acid molecules of the spiked-in sample into plurality of partitioned sets; (c) enriching a subset of molecules from the plurality of partitioned sets to generate enriched molecules, wherein the enriched molecules comprises a group of epigenetic-control nucleic acid molecules and a group of nucleic acid molecules from the sample of polynucleotides; (d) sequencing the enriched molecules to produce sequencing reads; (e) analyzing the sequencing reads to generate one or more epigenetic partition scores of the epigenetic-control nucleic acid molecules; and (f) comparing the one or more epigenetic partition scores with one or more epigenetic partition cut-offs.

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