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(54) Title: DETECTING HOMOLOGOUS RECOMBINATION DEFICIENCIES BASED ON METHYLATION STATUS OF CELL-FREE NUCLEIC ACID MOLECULES

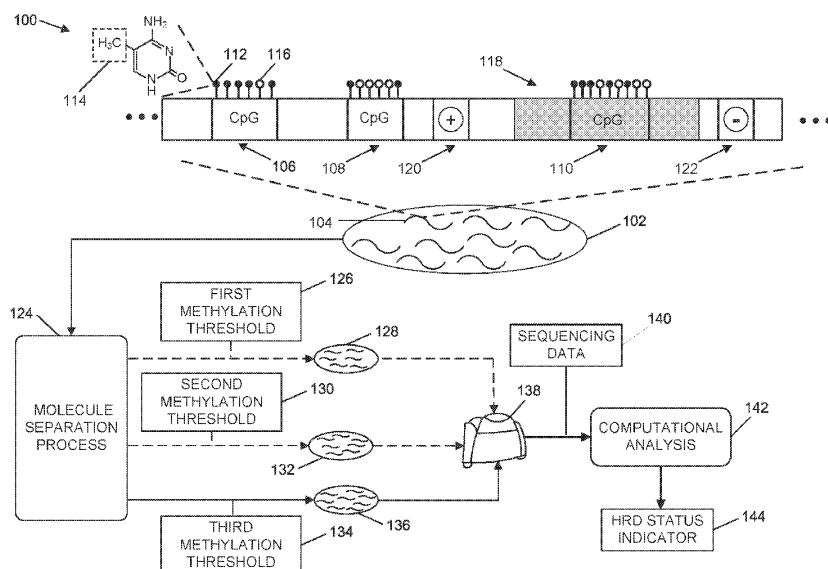


Figure 1

(57) Abstract: In implementations described herein, methylation information is determined with respect to classification regions of a reference genome that are related to the presence of a homologous recombination repair deficiency in a subject. The methylation information can be analyzed using a number of computational techniques to provide metrics related to the presence or absence of a homologous recombination repair deficiency in a given subject.

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