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- (71) **Applicant: GUARDANT HEALTH, INC.** [US/US]; 505 Penobscot Drive, Redwood City, California 94063 (US).
- (72) **Inventors: NANCE, Tracy;** 505 Penobscot Drive, Redwood City, California 94063 (US). **HELMAN, Elena;** 505 Penobscot Drive, Redwood City, California 94063 (US). **CHUDOVA, Darya;** 505 Penobscot Drive, Redwood City, California 94063 (US).
- (74) **Agent: HOTT, Timothy A.;** Guardant Health, Inc., 505 Penobscot Drive, Redwood City, California 94063 (US).
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(54) **Title:** METHODS AND SYSTEMS FOR DIFFERENTIATING SOMATIC AND GERMLINE VARIANTS

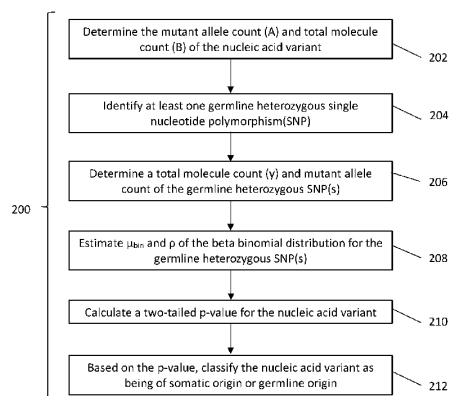


Fig. 2

- 202 Déterminer le nombre d'allèles mutants (A) et le nombre total de molécules (B) du variant d'acide nucléique
- 204 Identifier au moins un polymorphisme nucléotidique simple (SNP) hétérozygote de lignée germinale
- 206 Déterminer un nombre total de molécules (y) et un nombre d'allèles mutants dudit SNP hétérozygote de lignée germinale
- 208 estimer μ_B et p de la distribution bêta binomiale pour l'edit SNP hétérozygote de lignée germinale
- 210 Calculer une valeur p bilatérale pour le variant d'acide nucléique
- 212 Sur la base de la valeur p, classer le variant d'acide nucléique comme étant d'origine somatique ou de lignée germinale

(57) **Abstract:** In an aspect, a method of identifying a somatic or germline origin of a nucleic acid variant from a sample of nucleic acid molecules comprises: determining quantitative measures for the nucleic acid variant comprising a total allele count and minor allele count for the nucleic acid variant; identifying an associated variable of the nucleic acid variant; determining a quantitative value for the associated variable; generating a statistical model for expected germline mutant allele counts at a genomic locus of the nucleic acid variant; generating a probability value (p-value) for the nucleic acid variant based at least in part on the statistical model, the quantitative value, and at least one of the quantitative measures; and classifying the nucleic acid variant as (i) being of somatic origin when the p-value is below a predetermined threshold value, or as (ii) being of germline origin when the p-value is at or above the predetermined threshold value.

[Continued on next page]

SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN,
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