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(54) Title: CANCER DETECTION THROUGH INTEGRATED ANALYSIS OF WHOLE GENOME SEQUENCING

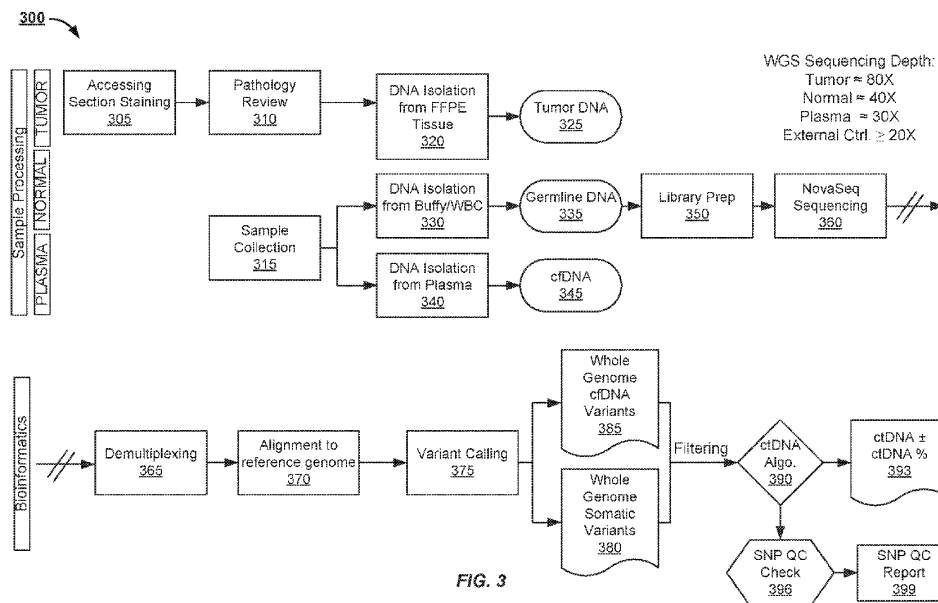


FIG. 3

(57) Abstract: The present disclosure pertains to techniques that leverage machine learning models to identify tumor-specific mutations through an integrated analysis of next generation sequencing data. In a particular aspect, a computer-implemented method is provided that includes generating sequence reads from one or more samples collected from the same patient, generating variant call files by analyzing the sequence reads corresponding respectively to the one or more samples, comparing variant call files to generate a list of candidate somatic variants, generating, by a classification machine learning model, scores for each of the candidate somatic variants in the list of candidate somatic variants, where the scores are generated based on a plurality of classifications generated by the classification machine learning model, determining, based on the scores, a ctDNA status for the patient, where the ctDNA status is either positive or negative, and generating a report that provides the ctDNA status for the patient.

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KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY,
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