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(54) Title: METHODS AND SYSTEMS FOR ADJUSTING TUMOR MUTATIONAL BURDEN BY TUMOR FRACTION AND COVERAGE

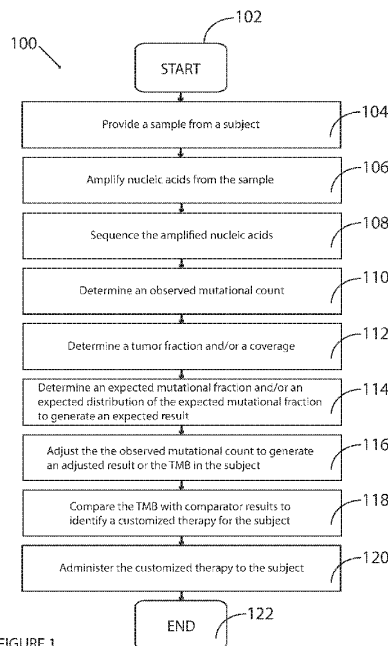


FIGURE 1

(57) Abstract: Provided herein are methods for detecting tumor mutational burden (TMB) in subjects. In one aspect, the methods include determining observed mutational counts from sequence information obtained from nucleic acids in samples from the subjects and determining a tumor fraction and/or a coverage of the nucleic acids to generate sequencing parameters. The methods also include determining an expected mutational fraction and/or an expected distribution of the expected mutational fraction given the sequencing parameters to generate an expected result, and adjusting the observed mutational count given the expected result to generate an adjusted result, thereby detecting the TMB in the subject. Other aspects are directed to methods of selecting customized therapies for treating cancer in subjects, and methods of treating cancer in subjects. Yet other aspects include related systems and computer readable media used to detect TMB in subjects.

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