

ABSTRACT

Provided are a base mutation detection method, device and storage medium based on sequencing data. The method includes: determining an initial frequency of sequencing data of samples to be detected being a specific base at an interested locus; calculating, based on the
5 initial frequency, an expected value of each sample to be detected being the specific base at the interested locus; updating, by using each expected value, the initial frequency of the sequencing data of the samples to be detected being the specific base at the interested locus; further calculating, by using the updated initial frequency, the expected value of each sample to be detected being the specific base at the interested locus, further updating, by using each
10 new expected value, the initial frequency of the sequencing data of the samples to be detected being the specific base at the interested locus, and repeating the foregoing iteration until the expected value of each sample to be detected being the specific base at the interested locus converges; and determining, based on each converging expected value, a base mutation type and a mutation confidence at the interested locus of each of the samples to be detected.
15 (Fig.1)