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(54) Title: MULTI-PASS SOFTWARE-ACCELERATED GENOMIC READ MAPPING ENGINE

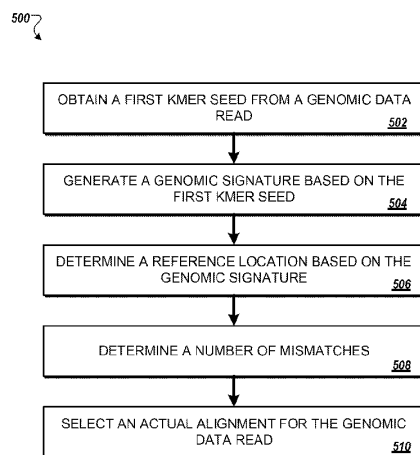


FIG. 5

(57) Abstract: Methods, systems, and apparatus, including computer programs encoded on computer-storage media, for software-accelerated genomic data read mapping. In some implementations, software-accelerated genomic data read mapping includes obtaining a first k-mer seed from a genomic data read; generating a genomic signature based on a first k-mer seed; determining a reference sequence location using a hash data structure based on the genomic signature; determining a number of mismatches; based on determining the number of mismatches includes one or more mismatches, obtaining, by the one or more computers, a set of k-mer seeds from the genomic data read; and based on the set of k-mer seeds from the genomic data read, selecting, by the one or more computers, an actual alignment for the genomic data read.

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