Auxiliary Request 9

1. A method for detecting a true mutation in a nucleic acid molecule, comprising: amplifying a double-stranded nucleic acid library, wherein the double-stranded nucleic acid library comprises a plurality of target nucleic acid molecules and a plurality of double-stranded cyphers, wherein the nucleic acid library comprises molecules having a formula of X^a-Y-X^b (in 5' to 3' order), wherein:

(a) X^a comprises a first cypher;

(b) Y comprises a target nucleic acid molecule, and

(c) X^b comprises a second cypher,

wherein the target nucleic acid molecules are fragments of genomic DNA,

wherein each of the plurality of target nucleic acid molecules is associated with a unique pair of double-stranded first and second cyphers, wherein each of the plurality of cyphers comprise a length ranging from about 5 nucleotides to about 50 nucleotides, provided that the double-stranded sequence of the X^a cypher for each target nucleic acid molecule is different from the double-stranded sequence of the X^b cypher, wherein each strand of the plurality of target nucleic acid molecules and plurality of double-stranded cyphers are amplified;

sequencing each amplified strand of the plurality of target nucleic acid molecules and plurality of cyphers to obtain sequencing reads for the plurality of target nucleic acid molecules and plurality of cyphers, and of their reverse complements;

grouping sequencing reads of target nucleic acid molecules comprising identical cypher pairs into families of sequencing reads, and

detecting the true mutation over a background rate of artifact mutations, said detecting comprising identifying as a true mutation a mutation present in substantially all reads in a family of sequencing reads.