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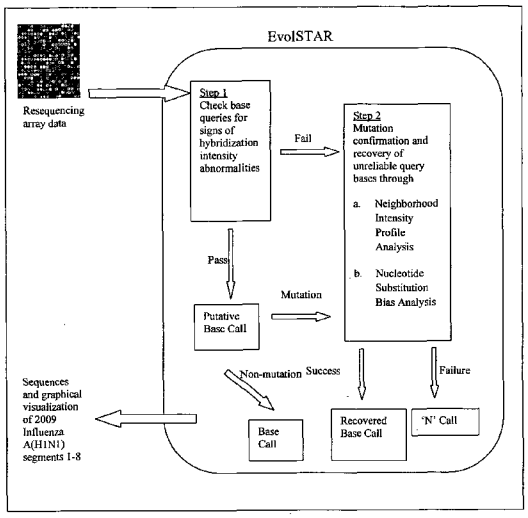

FIGURE 1

(57) Abstract: A method of sequencing a first polynucleotide strand having a first polynucleotide sequence, the first polynucleotide strand resembling a second polynucleotide strand having a known second polynucleotide sequence, the method employing a data set which, for one or more fragment(s) of the second polynucleotide sequence, contains: for each position along each said fragment: (i) first probe data describing the hybridization intensity of the first polynucleotide strand with a respective first probe designed to bind to a portion of the second polynucleotide strand centered at said position; and (ii) second probe data describing the respective hybridization intensities of the first polynucleotide strand with each of a set of second probes, each said second probe being designed to bind with a respective mutation of the corresponding portion of the second polynucleotide sequence which is formed by mutating the corresponding portion of the second polynucleotide sequence at said position, the data set including said second probe data for every possible said mutation; the method comprising: for each said position, obtaining from the dataset a first numerical parameter characterizing the hybridization intensity of the first polynucleotide strand with the corresponding first probe in comparison to the hybridization intensities of the first polynucleotide strand with the corresponding second probes; said first numerical parameter being indicative of whether a nucleic acid of the first polynucleotide sequence is equal to a nucleic acid the second polynucleotide sequence at said position.

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