



US006404907B1

(12) **United States Patent**
Gilchrist et al.

(10) **Patent No.: US 6,404,907 B1**
(45) **Date of Patent: Jun. 11, 2002**

- (54) **METHOD FOR SEQUENCING NUCLEIC ACIDS WITH REDUCED ERRORS**
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- (*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

- (21) Appl. No.: **09/345,613**
- (22) Filed: **Jun. 25, 1999**

Related U.S. Application Data

- (60) Provisional application No. 60/090,887, filed on Jun. 26, 1998.
- (51) **Int. Cl.⁷** **G06K 9/00**
- (52) **U.S. Cl.** **382/129; 382/173; 382/190;**
435/6
- (58) **Field of Search** 435/6; 436/86,
436/89; 364/500; 392/129, 173, 190

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(57) **ABSTRACT**

Nucleic acid polymers are sequenced by obtaining forward and reverse data sets for forward and reverse strands of a sample nucleic acid polymer. The apparent base sequences of these forward and reverse sets are determined and the apparent sequences are compared to identify any deviations from perfect complementarity. Any such deviation presents a choice between two bases, only one of which is correct. A confidence algorithm is applied to the peaks in the data sets associated with a deviation to arrive at a numerical confidence value for each of the two base choices. These confidence values are compared to each other and to a predetermined threshold, and the base represented by the peak with the better confidence value is assigned as the “correct” base, provided that its confidence value is better than the threshold. The confidence value takes into account at least one, and preferably more than one of several specific characteristics of the peaks in the data set that were not complementary.

9 Claims, 6 Drawing Sheets

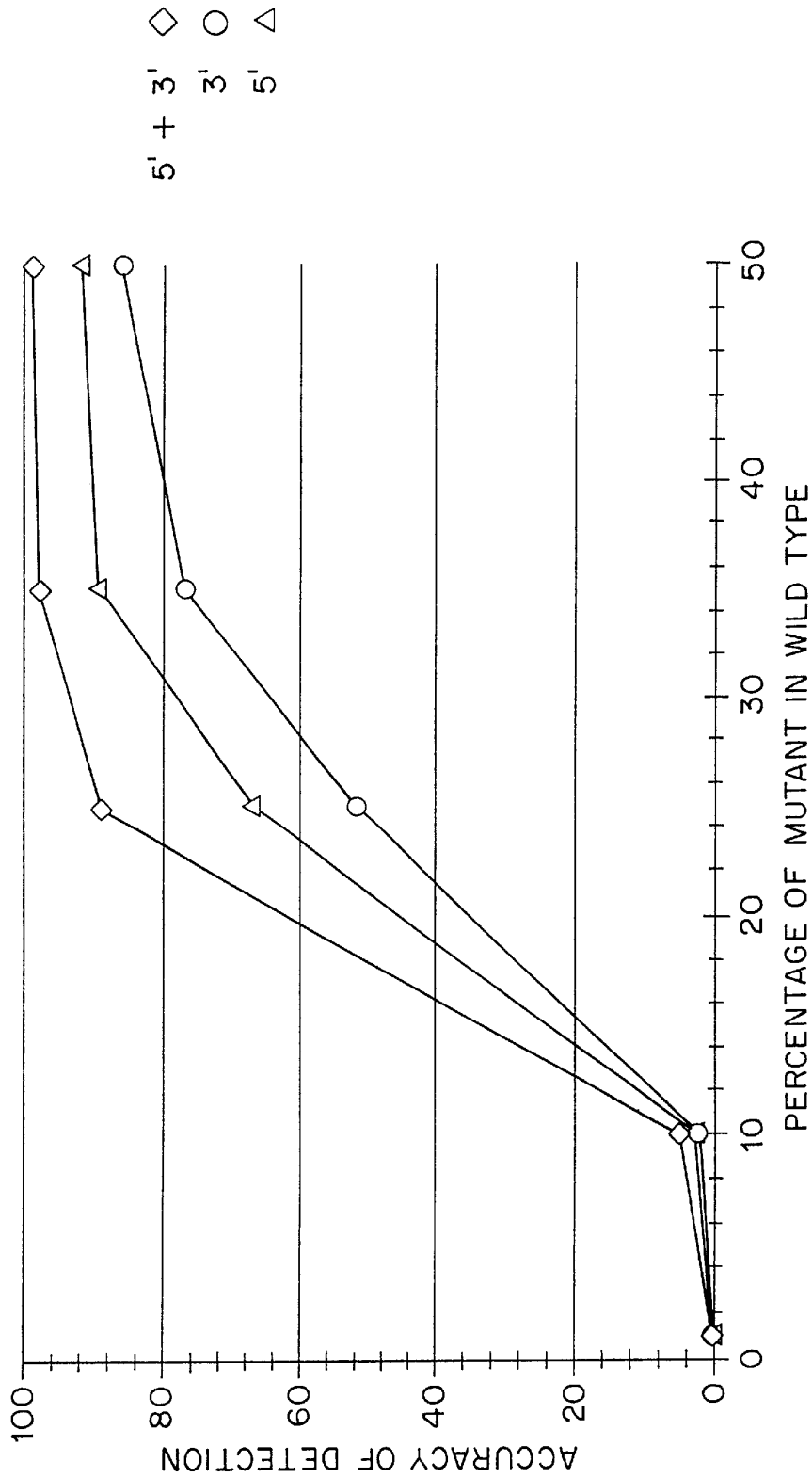


FIG. 2

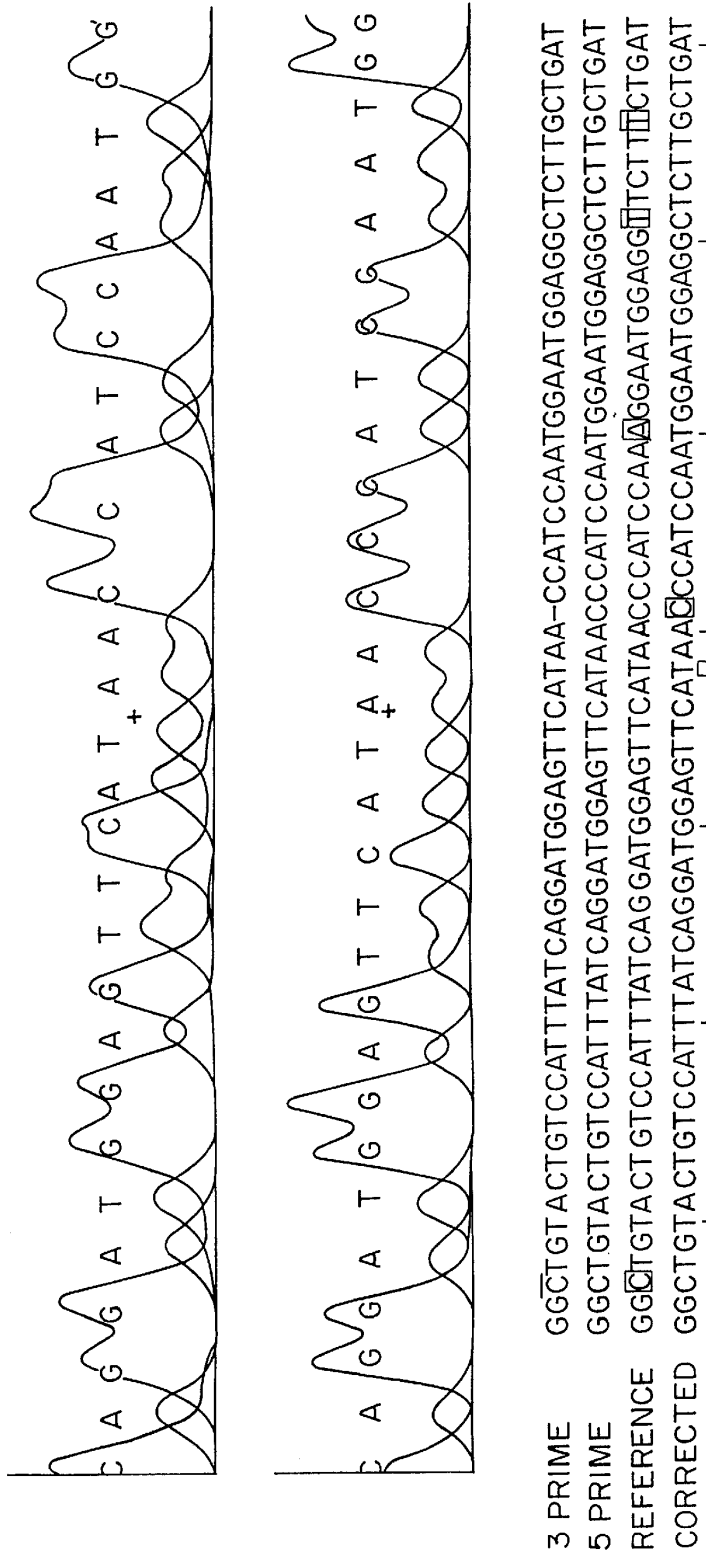


FIG. 3

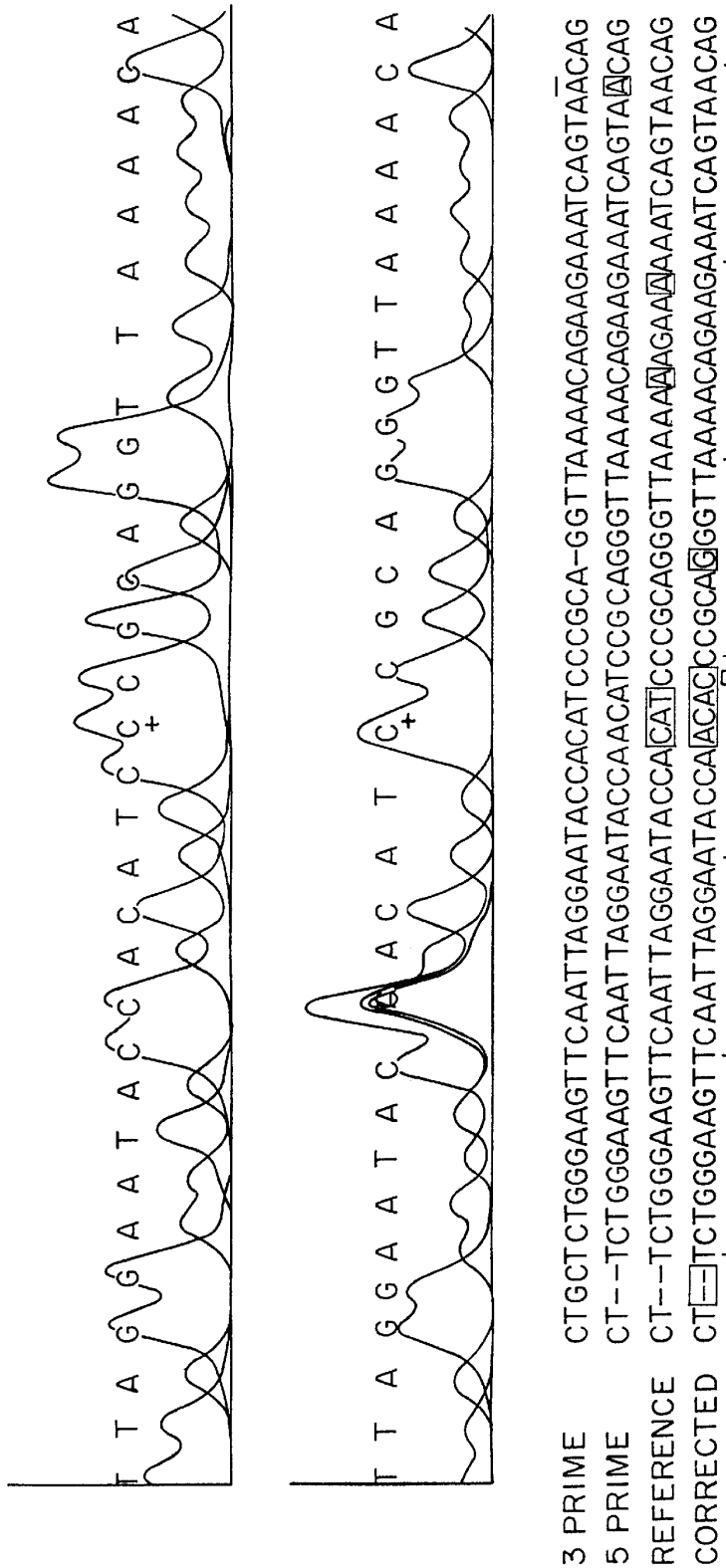


FIG. 4

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