



[54] MASSIVELY PARALLEL SIGNATURE SEQUENCING BY LIGATION OF ENCODED ADAPTORS

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[73] Assignee: Lynx Therapeutics, Inc., Hayward, Calif.

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Related U.S. Application Data

[63] Continuation-in-part of application No. 08/862,610, May 23, 1997, abandoned, which is a continuation-in-part of application No. 08/689,587, Aug. 12, 1996, abandoned, which is a continuation-in-part of application No. 08/659,453, Jun. 6, 1996, abandoned.

[51] Int. Cl.⁷ C12Q 1/68; C07H 21/02

[52] U.S. Cl. 435/6; 536/24.2

[58] Field of Search 435/6, 91.52; 536/24.2, 536/24.3, 26.6; 935/77, 78

[56] References Cited

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Table with 4 columns: Patent No., Date, Inventor, and Reference No. (e.g., 4,237,224 12/1980 Cohen et al. 435/68)

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Table with 4 columns: Patent No., Date, Country/Office, and Reference No. (e.g., 0 246 864 B1 11/1987 European Pat. Off.)

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[57] ABSTRACT

The invention provides a method of nucleic acid sequence analysis based on the ligation of one or more sets of encoded adaptors to the terminus of a target polynucleotide. Encoded adaptors whose protruding strands form perfectly matched duplexes with the complementary protruding strands of the target polynucleotide.

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The invention provides a method of nucleic acid sequence analysis based on the ligation of one or more sets of encoded adaptors to the terminus of a target polynucleotide. Encoded adaptors whose protruding strands form perfectly matched duplexes with the complementary protruding strands of the target polynucleotide are ligated, and the identity of the nucleotides in the protruding strands is determined by an oligonucleotide tag carried by the encoded adaptor. Such determination, or "decoding" is carried out by specifically hybridizing a labeled tag complement to its corresponding tag on the ligated adaptor.

29 Claims, 10 Drawing Sheets



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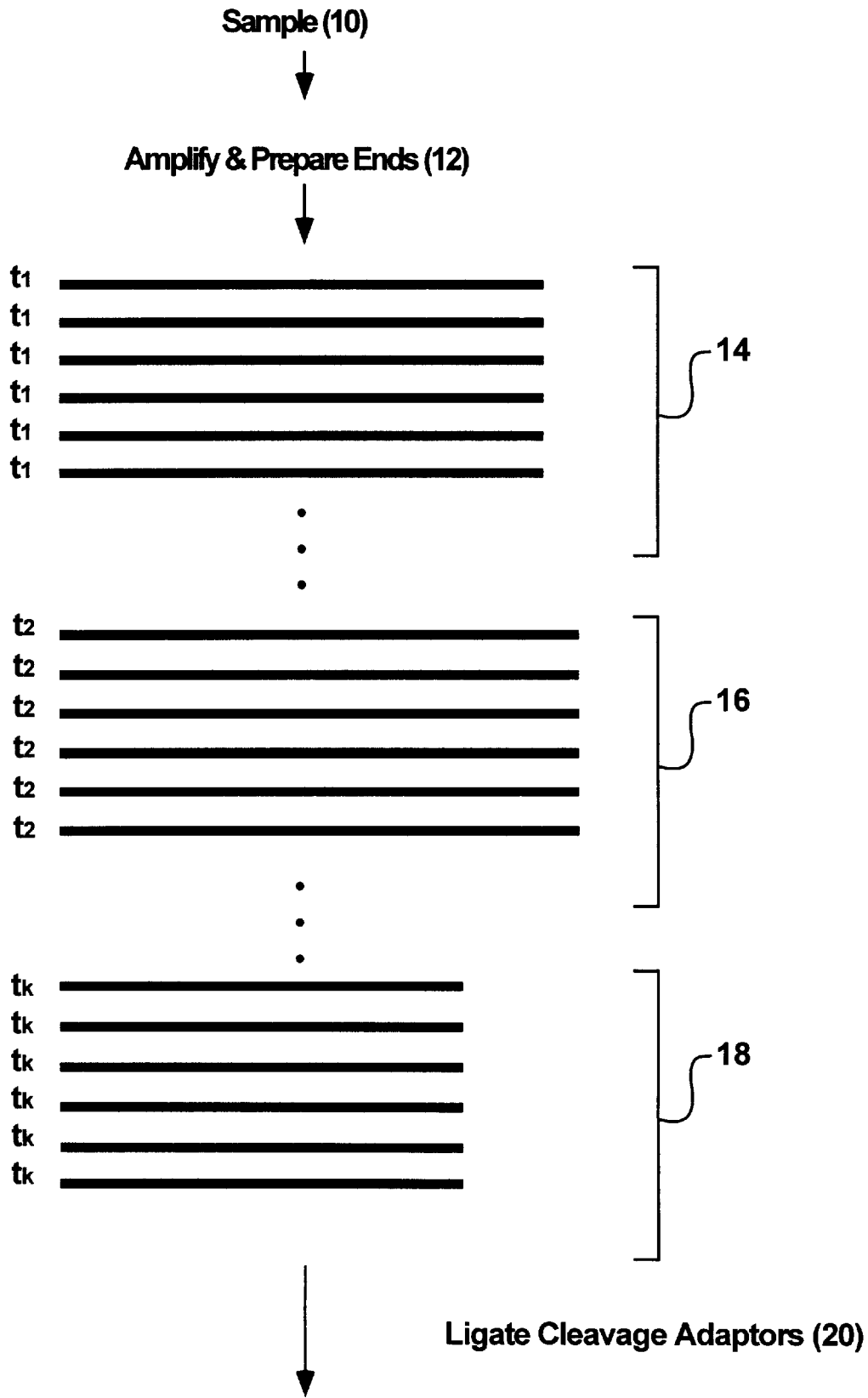
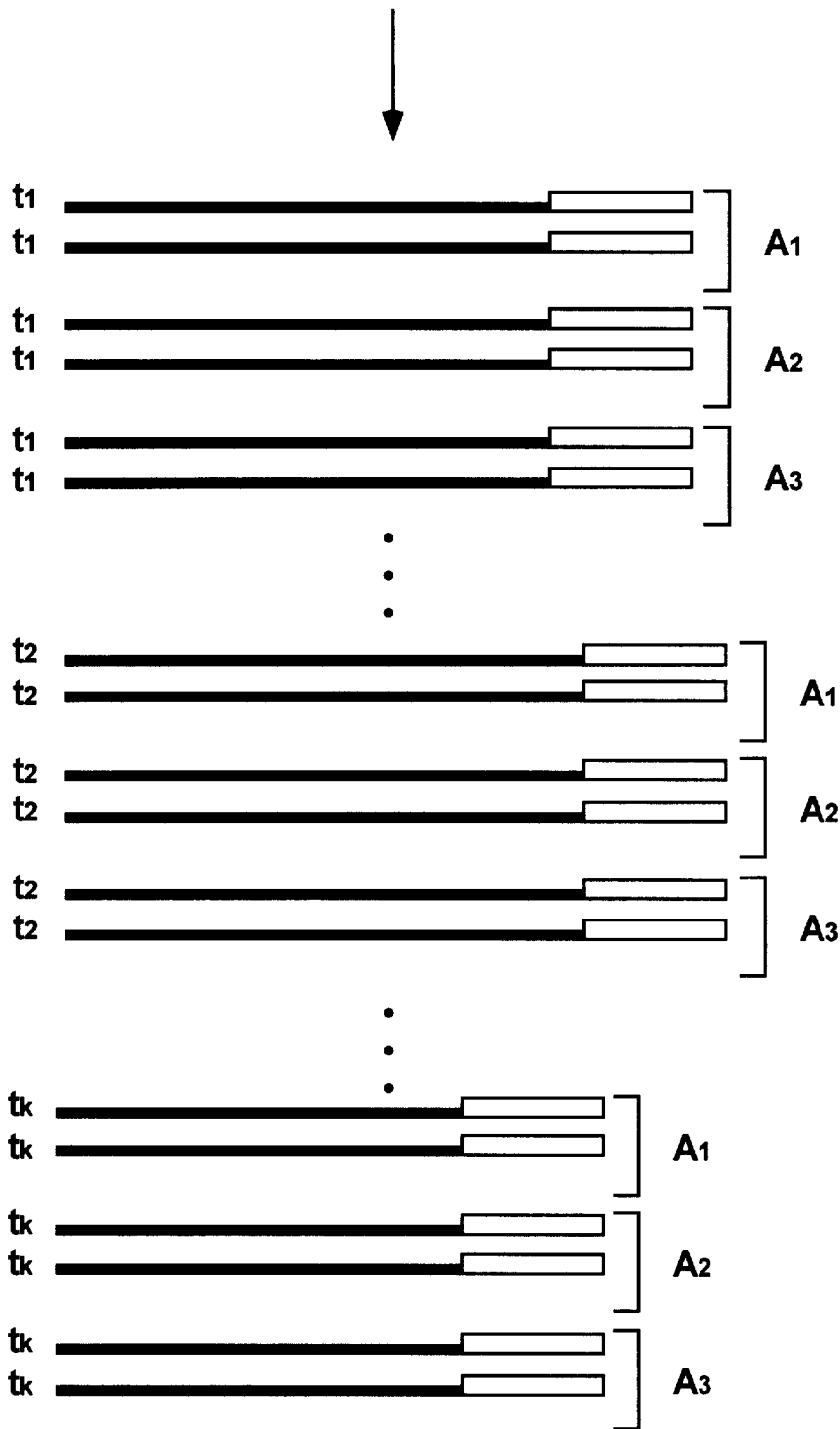


Fig. 1A



Cleave with A1 endonuclease &
Ligate first Set of encoded probes (22)

Fig. 1B

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