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(54) **Title:** METHOD FOR IMPROVING NUCLEIC ACID SEQUENCING QUALITY BY ELIMINATING NUCLEIC ACIDS WITH DEAMINATED BASES FROM LIBRARY AND METHOD FOR SEQUENCING IN WHICH COMPLEXES OF PRIMERS, POLYMERASES AND LABELLED PROBES ARE BOUND TO CONCATEMERS

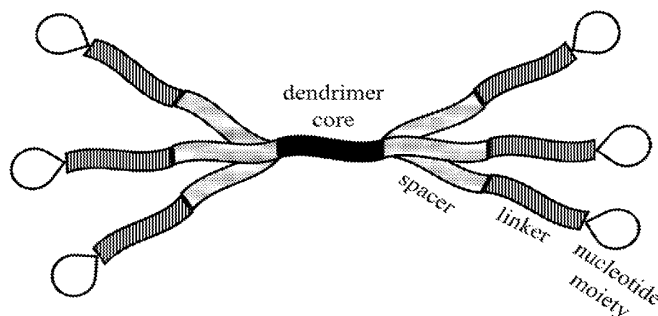


FIG. 4

(57) **Abstract:** The present disclosure provides methods for reducing sequencing errors comprising one or any combination of: (i) removing deaminated bases in any nucleic acid molecule throughout a library preparation workflow which includes immobilised splints which bind to the library, the use of a compaction oligonucleotide, optionally with an intervening sequence, formation of closed circular nucleic acids, creating gaps using glycosylase and lyase activities at positions with deaminated bases. The library may be sequenced using pairwise sequencing, e.g. with dark sequencing and/or sequencing using a multivalent labelled probe for the formation of an avidity molecule and soluble primer and polymerase. Method for sequencing concatemers in which the concatemers are contacted with polymerases, soluble primers and a multivalent labelled molecule which forms a complex with the polymerase. Detecting polymerase position and nucleobase bound to the polymerase in the complex. These methods generate higher quality base calls during downstream sequencing workflows.

[Continued on next page]

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Declarations under Rule 4.17:

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- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

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