

## CLAIMS

### WHAT IS CLAIMED IS:

1. A DNA molecule, comprising:
  - a nucleic acid segment obtained or derived from a biological sample, wherein the nucleic acid segment is DNA;
  - a pair of partial Y-adapters, each comprising an error-correcting unique identifier ligated to the nucleic acid segment at a double-stranded region end of each partial Y-adapter to produce a ligation product, wherein the pair of partial Y-adapters flanks the nucleic acid segment, wherein each of the pair of error-correcting unique identifiers is a DNA segment, wherein the pair of error-correcting unique identifiers collectively provides a unique identification of the nucleic acid segment against other nucleic acid segments represented in a set of sequencing reads; and
  - a pair of error-correcting dual index sample barcodes grafted onto the ligation product by a polymerase chain reaction, wherein each of the pair of error-correcting dual index sample barcodes are each DNA segment, and wherein the pair of error-correcting dual index sample barcodes flank the ligation product and collectively provides a unique identification of the biological sample against other biological samples represented in a set of sequencing reads.
2. The DNA molecule of claim 1, wherein the nucleic acid segment is complementary DNA (cDNA).
3. The DNA molecule of claim 1 or 2, wherein the nucleic acid segment is obtained or derived from a cell-free DNA sample.
4. A collection comprising a plurality of the DNA molecules according to any one of claims 1 to 3.
5. A method to prepare a DNA library for sequencing, the method comprising:
  - ligating onto a plurality of nucleic acid segments pairs of partial Y-adapters to flank each of the plurality of nucleic acid segments by a pair of partial Y-adapters, thereby producing a plurality of ligation products,

wherein each of the plurality of nucleic acid segments is DNA, and wherein the plurality of nucleic acid segments is obtained or derived from a biological sample,

wherein each of the pair of partial Y-adapters comprises an error-correcting unique identifier and sequences for a primer to anneal in a grafting polymerase chain reaction, and

wherein the pair of error-correcting unique identifiers on each of the plurality of nucleic acid segments collectively provides a unique identification of the nucleic acid segments against other nucleic acid segments in the plurality of nucleic acid segments; and

grafting onto each of the plurality of ligation products a pair of error-correcting dual index sample barcodes to flank the ligation product by the error-correcting dual index sample barcodes, wherein the error-correcting dual index sample barcodes collectively provide a unique identification of the biological sample.

6. The method of claim 5, wherein the nucleic acid segment is complementary DNA (cDNA).

7. The method of claim 5 or 6, wherein the biological sample comprises a cell-free DNA sample.

8. The method according to any one of claims 5 to 7, wherein the error-correcting dual index sample barcodes collectively provide the unique identification of the biological sample against other biological samples represented in the DNA library.

9. A DNA molecule, comprising:

a nucleic acid molecule sourced from a biological sample, wherein the nucleic acid molecule is DNA or cDNA;

a pair of partial Y-adapters, each comprising an error-correcting unique identifier, ligated to the nucleic acid molecule at a double-stranded region end of each partial Y-adapter to produce a ligation product, wherein the pair of partial Y-adapters flanks the nucleic acid molecule, wherein the error-correcting unique identifiers are each DNA molecules and the combination of the error-correcting unique identifiers provides an identification of the nucleic acid molecule in a sequencing result; and

a pair of error-correcting dual index sample barcodes grafted onto the ligation product by a polymerase chain reaction, wherein the error-correcting dual index sample barcodes are each DNA

molecules and flank the ligation product, and wherein the combination of the error-correcting dual index sample barcodes provides an identification of the biological sample in a sequencing result.

10. A method to prepare DNA library for sequencing, comprising:

ligating onto a collection of nucleic acid molecules pairs of partial Y-adapters at the double-stranded region end of each partial Y-adapter such that each nucleic acid molecule is flanked by a pair of partial Y-adapters, wherein each nucleic acid molecule is DNA or cDNA and the collection of nucleic acid molecules is sourced from a biological sample,

wherein each partial Y-adapter includes an error-correcting unique identifier and sequences for a primer to anneal in a grafting polymerase chain reaction, and

wherein each flanking combination of the two error-correcting unique identifiers on each nucleic acid molecule identifies the ligation of the pair of partial Y-adapters to that nucleic acid molecule; and

grafting onto each ligation product a pair of error-correcting dual index sample barcodes and the sequence of a universal primer such that the ligation product is flanked by the error-correcting

dual index sample barcodes and the sequence of the universal primer, wherein the combination of error-correcting dual index sample barcodes identifies the collection of nucleic acid molecules.