

CLAIMS:

1. A method for synthesizing a nucleic acid, comprising:
 - providing a target sequence of a nucleic acid comprising a first end sequence, a second end sequence, and an intermediate sequence therebetween;
 - providing a plurality of overlapping nucleic acid fragments, wherein the plurality of nucleic acid fragments have complementary portions to at least one other fragment of the plurality of nucleic acid fragments, wherein a first fragment of the plurality of nucleic acid fragments comprises a first cleavable adapter and a portion having the first end sequence, wherein an end of the first fragment comprises the first cleavable adapter, and wherein a last fragment of the plurality of nucleic acid fragments comprises a second cleavable adapter, and a portion having the second end sequence, wherein an end of the last fragment comprises the second cleavable adapter, and comprising: generating the first fragment by *de novo* extension of an oligonucleotide immobilized on a synthesis substrate, and selectively harvesting the first fragment from the synthesis substrate;
 - immobilizing the first fragment on an assembly substrate with a first immobilized primer complementary to the first cleavable adapter;
 - assembling the plurality of nucleic acid fragments into an assembled polynucleotide molecule via hybridization of the complementary portions, wherein the assembled polynucleotide molecule is partially double stranded and comprises gaps in both strands, wherein the assembled polynucleotide molecule is immobilized on the assembly substrate via the first immobilized primer;
 - amplifying the assembled polynucleotide molecule on the assembly substrate to generate an amplified cluster comprising amplicons of the assembled polynucleotide molecule on the assembly substrate; and
 - sequencing the amplified cluster.
2. The method of claim 1, wherein the assembling further comprises a step of filling the gaps in a strand of the assembled polynucleotide molecule by polymerase extension.
3. The method of claim 2, wherein an assembled double-stranded polynucleotide is formed by the assembling of the plurality of nucleic acid fragments, and wherein the method

further comprises a step of denaturing the assembled double-stranded polynucleotide molecule to generate a single-stranded polynucleotide molecule that extends from the first immobilized primer.

4. The method of claim 1, wherein the amplifying comprises bridge amplification of the assembled polynucleotide molecule on the assembly substrate.

5. The method of claim 1, wherein the plurality of nucleic acid fragments is single stranded nucleic acids.

6. The method of claim 1, comprising selectively harvesting the amplified cluster, wherein a sequence of the amplified cluster is determined to have a sequence error rate compared to the target sequence or a complement of the target sequence less than or equal to a predetermined threshold.

7. The method of claim 6, wherein the predetermined threshold is zero.

8. The method of claim 6, wherein selectively harvesting the amplified cluster comprises cleaving the second cleavable adapter and/or the first cleavable adapter.

9. The method of claim 6, wherein selectively harvesting the amplified cluster comprises cleaving the second cleavable adapter and/or the first cleavable adapter optically, chemically, magnetically, electrically, electromagnetically, or any combination thereof.

10. The method of claim 1, comprising comparing a sequence of the amplified cluster with the target sequence or a complement of the target sequence to generate a sequence accuracy score or sequence error rate for the amplified cluster.

11. The method of claim 1, wherein each of the plurality of nucleic acid fragments is less than 200 nucleotides in length.

12. The method of claim 1, wherein the overlapping portions of the plurality of nucleic acid fragments are between 20 and 30 nucleotides long.

13. The method of claim 1, wherein the assembling comprises assembling the plurality of nucleic acid fragments in the presence of DNA recombinase, DNA polymerase, DNA ligase, or any combination thereof.

14. The method of claim 1, wherein the substrate comprises a bead, a magnetic bead, a glass slide, a microchip, a nano droplet, an electrowetting cartridge, or any combination thereof.

15. A method for synthesizing a plurality of nucleic acids, comprising carrying out the method of claim 1 to immobilize a plurality of different first fragments on the substrate such that

a plurality of different single-stranded fragments are assembled, a plurality of different amplified clusters are generated and a plurality of different amplified clusters are sequenced.

16. The method of claim 15, comprising selectively harvesting a target amplified cluster compared to other amplified clusters in the plurality of different amplified clusters, wherein the target amplified cluster has highest sequence error rate relative to the other amplified clusters, wherein the sequence error rate is determined by comparing a sequence of each amplified cluster with the target sequence or a complement of the target sequence.

17. The method of claim 15, comprising selectively harvesting a target amplified cluster compared to other amplified clusters in the plurality of different amplified clusters, wherein the target amplified cluster has lowest sequence error rate relative to the other amplified clusters, wherein the sequence error rate is determined by comparing a sequence of each amplified cluster with the target sequence or a complement of the target sequence.

18. The method of claim 15, comprising comparing a sequence of each amplified cluster with the target sequence or a complement of the target sequence to generate a sequence accuracy score or sequence error rate for each of the plurality of amplified clusters.