

CLAIMS

WHAT IS CLAIMED IS:

1. A method for nucleic acid processing, comprising:
 - (a) providing a plurality of partitions, wherein a partition of said plurality of partitions comprises (i) at least two beads of a plurality of beads, (ii) a nucleic acid molecule, and (iii) one or more reagents;
 - (b) in said partition, using said nucleic acid molecule and said one or more reagents to generate one or more amplification products of said nucleic acid molecule, wherein at least a subset of said one or more amplification products are attached to a bead of said at least two beads;
 - (c) recovering said bead from said partition; and
 - (d) assaying an amplification product of said one or more amplification products or derivatives thereof to identify a sequence of said nucleic acid molecule.
2. The method of claim 1, wherein (a) comprises bringing (i) a first solution comprising a plurality of nucleic acid molecules comprising said nucleic acid molecule and (ii) a second solution comprising said plurality of beads comprising said at least two beads in contact with a fluid that is immiscible with said first solution and said second solution, to generate said plurality of partitions.
3. The method of claim 1 or 2, wherein said bead has attached thereto a plurality of primer molecules for performing one or more amplification reactions using said nucleic acid molecule, and (b) comprises using primer molecules of said plurality of primer molecules to conduct said one or more amplification reactions to generate said amplification product of said one or more amplification products.
4. The method of claim 3, wherein said bead has attached thereto a plurality of additional primer molecules for performing one or more additional amplification reactions using said

nucleic acid molecule, which plurality of additional primer molecules are different than said plurality of primer molecules.

5. The method of claim 4, wherein (b) further comprises using additional primer molecules of said plurality of additional primer molecules to conduct said one or more additional amplification reactions to generate additional amplification products of said one or more amplification products, wherein at least a subset of said additional amplification products are attached to said bead, and wherein (d) further comprises assaying said additional amplification products attached to said bead, or derivatives thereof, to identify a sequence of said nucleic acid molecule.
6. The method of claim 5, wherein said nucleic acid molecule is a double-stranded nucleic acid molecule, and wherein amplification products corresponding to a first strand of said nucleic acid molecule are generated using said plurality of primer molecules, and amplification products corresponding to a second strand of said nucleic acid molecule are generated using said plurality of additional primer molecules.
7. The method of any one of claims 3-6, wherein an additional bead of said at least two beads has attached thereto a plurality of additional primer molecules for performing one or more additional amplification reactions using said nucleic acid molecule, which plurality of additional primer molecules are different than said plurality of primer molecules.
8. The method of claim 7, further comprising:
 - (e) using additional primer molecules of said plurality of additional primer molecules to conduct said one or more additional amplification reactions to generate additional amplification products of said one or more amplification products, wherein at least a subset of said additional amplification products are attached to said additional bead of said at least two beads;
 - (f) recovering said additional bead from said partition; and

- (g) assaying said additional amplification products attached to said additional bead, or derivatives thereof, to identify a sequence of said nucleic acid molecule.
9. The method of any one of claims 1-8, wherein each of at least 80% of said plurality of partitions comprises two or more beads of said plurality of beads.
10. The method of any one of claims 1-9, wherein each of at least 80% of said plurality of partitions comprises three or more beads of said plurality of beads.
11. The method of any one of claims 1-10, wherein said at least two beads are attached to one another.
12. The method of any one of claims 1-11, further comprising separating partitions of said plurality of partitions that each comprise at least two beads from other partitions of said plurality of partitions that each comprise at most one bead.
13. The method of claim 12, wherein said separating comprises optically detecting said partitions that each comprise at least two beads or said other partitions that each comprise at most one bead and, based at least in part on said optically detecting, adjusting a direction of flow of a fluid in a fluidic device to provide said partitions that each comprise at least two beads in a first channel of said fluidic device and said other partitions that each comprise at most one bead in a second channel of said fluidic device.
14. The method of any one of claims 1-13, wherein said one or more reagents comprise nucleic acid molecules comprising priming sequences.
15. The method of claim 14, wherein said nucleic acid molecules comprising said priming sequences further comprise unique molecular identifier sequences.

16. The method of claim 14, wherein said nucleic acid molecules comprising said priming sequences further comprise barcode sequences.
17. The method of any one of claims 1-16, wherein (d) comprises using said one or more amplification products or derivatives thereof as a template.
18. The method of any one of claims 1-17, wherein said plurality of partitions is a plurality of droplets.
19. The method of any one of claims 1-18, wherein (d) comprises sequencing said amplification product or derivatives thereof.
20. The method of any one of claims 1-19, wherein, in (a), said nucleic acid molecule is attached to said bead.