CLAIMS

WHAT IS CLAIMED IS:

1. A method of nucleic acid analysis, comprising:

(a) providing a plurality of barcoded nucleic acid molecules comprising a plurality of different barcode sequences;

(b) identifying at least one barcode sequence from said plurality of different barcode sequences, wherein identifying comprises sequencing said plurality of barcoded nucleic acid molecules to generate a plurality of sequencing reads and analyzing said plurality of sequencing reads to identify said at least one barcode sequence; and

(c) enriching nucleic acid molecules comprising said at least one barcode sequence.

2. The method of claim 1, wherein (c) comprises performing a nucleic acid extension reaction using (i) a nucleic acid molecule comprising said at least one barcode sequence and (ii) a primer comprising a sequence specific for said at least one barcode sequence to generate an enriched plurality of nucleic acid molecules comprising said at least one barcode sequence.

3. The method of claim 2, wherein said nucleic acid extension reaction is a polymerase chain reaction (PCR), optionally further comprising performing an additional PCR on said enriched plurality of nucleic acid molecules comprising said at least one barcode sequence, optionally wherein said additional PCR comprises use of an additional primer comprising a sequence specific for said enriched plurality of nucleic acid molecules comprising said at least one barcode sequence, optionally wherein said additional primer comprises one or more functional sequences that facilitate sequencing said enriched plurality of nucleic acid molecules, optionally wherein said one or more functional sequences comprise:

(i) a sequencing primer sequence; and/or

(ii) a sequence configured to attach to a flow cell of a sequencer.

4. The method of claim 2, wherein said primer comprises an affinity group and wherein said enriched plurality of nucleic acid molecules comprises said affinity group, optionally wherein said affinity group comprises biotin.

5. The method of any one of claims 2-4, further comprising, subsequent to said nucleic acid extension reaction, performing a size selection to remove unincorporated primer.

6. The method of claim 4 or claim 5, wherein (c) further comprises coupling said enriched plurality of nucleic acid molecules comprising said affinity group to a solid support specific for said affinity group, optionally:

(i) wherein said solid support is a bead;

(ii) wherein said affinity group comprises biotin and wherein said solid support comprises avidin or streptavidin; and/or

(iii) further comprising performing a polymerase chain reaction (PCR) on said enriched plurality of nucleic acid molecules.

7. The method of any one of claims 2-6, further comprising, prior to said nucleic acid extension reaction, (i) hybridizing (1) a first nucleic acid molecule complementary to a first portion of said at least one barcode sequence and (2) a second nucleic acid molecule complementary to a second portion of said at least one barcode sequence; and (ii) ligating said first nucleic acid molecule to said second nucleic acid molecule to generate said primer comprising said sequence specific for said at least one barcode sequence.

8. The method of any one of claims 1-7, wherein each of said plurality of barcoded nucleic acid molecules further comprise one or more functional sequences selected from the group consisting of a sequencing primer sequence and a sequence configured to attach to a flow cell of a sequencer.

9. The method of any one of claims 1-8, wherein said plurality of barcoded nucleic acid molecules comprise, from 5' to 3', a first adapter sequence, a sequence derived from a template nucleic acid, and a second adapter sequence. ~~,~~

10. The method of claim 9, ~~optionally~~ wherein said first adapter sequence comprises a first sequence configured to attach to a flow cell of a sequencer, a first sequencing primer sequence, and a barcode sequence.~~,~~

11. The method of claims 9 or 10, ~~optionally~~ wherein said second adapter sequence comprises a second sequencing primer sequence and a second sequence configured to attach to a flow cell of a sequencer.~~,~~

12. The method of any of claims claim 9-11, ~~optionally~~ wherein said second adapter sequence further comprises an index sequence.

~~10~~13. The method of any one of claims 1-12~~9~~, wherein each barcode sequence of said plurality of different barcode sequences identifies a nucleic acid molecule as derived from (i) a single cell; and/or (ii) a single partition.

~~11~~14. The method of any one of claims 1-13~~10~~, wherein said enriching of (c) results in at least 10-fold enrichment, at least 20- fold enrichment, at least 50- fold enrichment, at least 100-fold enrichment, at least 200-fold enrichment, at least 500-fold enrichment, or at least 1,000-fold enrichment of nucleic acid molecules comprising said at least one barcode sequence.

~~12~~15. The method of any preceding claim, wherein the plurality of barcoded nucleic acid molecules corresponds to one or more analytes in a sample, wherein the one or more analytes are selected from DNA, RNA, proteins, a region of chromatin, and lipids, or a combination thereof, optionally wherein the plurality of barcoded nucleic acid molecules corresponds to:

(i) one or more mRNA in said sample;

(ii) one or more proteins in said sample, optionally one or more antibodies in said sample or one or more T-cell receptors in said sample;

(iii) one or more regions of genomic DNA in said sample; or

(iv) one or more regions of chromatin in said sample.

~~13~~16. The method of any of the preceding claims, wherein (b) comprises identifying a first barcode sequence and a second barcode sequence, wherein said first barcode sequence is different from said second barcode sequence, and wherein (c) comprises performing a nucleic acid extension reaction using a first oligonucleotide molecule comprising a sequence specific for said first barcode sequence and a second oligonucleotide molecule comprising a sequence specific for said second barcode sequence to generate an enriched plurality of nucleic acid molecules, wherein nucleic acid molecules of said enriched plurality of nucleic acid molecules comprises said first barcode sequence or said second barcode sequence.

~~14~~17. The method of any one of the preceding claims, wherein each barcoded nucleic acid molecule of the plurality of barcoded nucleic acid molecules ~~is associated with~~corresponds to an analyte from a sample.

~~15~~18. The method of any one of the preceding claims, wherein the plurality of barcoded nucleic acid molecules comprises a plurality of subsets of barcoded nucleic acid molecules, wherein a

first subset of said plurality of subsets of barcoded nucleic acid molecules comprises a first common barcode sequence, optionally wherein:

(i) a second subset of the plurality of subsets of barcoded nucleic acid molecules comprises a second common barcode sequence that is different from the first common barcode sequence, optionally wherein the second common barcode sequence corresponds to analytes from a second single cell; or

(ii) the first common barcode sequence corresponds to analytes from a first single cell.