

CLAIMS:

1. A method for labeling nucleic acid targets in a sample, comprising:
 - contacting copies of a nucleic acid target with a first plurality of oligonucleotide barcodes, wherein each oligonucleotide barcode of the first plurality of oligonucleotide barcodes comprises a first universal sequence, a first molecular label, and a first target-binding region capable of hybridizing to the nucleic acid target;
 - extending the first plurality of oligonucleotide barcodes hybridized to the copies of the nucleic acid target to generate a plurality of barcoded nucleic acid molecules each comprising the first universal sequence, the first molecular label, and a sequence complementary to at least a portion of the nucleic acid target;
 - contacting the barcoded nucleic acid molecules with a second plurality of oligonucleotide barcodes for hybridization,
 - wherein each oligonucleotide barcode of the second plurality of oligonucleotide barcodes comprises a second universal sequence, a cleavage domain, and a blocking group,
 - wherein the blocking group is capable of preventing extension of the oligonucleotide barcode, wherein the cleavage domain is positioned 5' of the blocking group, and wherein a cleaving enzyme is capable of cleaving the oligonucleotide barcode at a point within or adjacent to the cleavage domain when the cleavage domain is hybridized to a barcoded nucleic acid molecule;
 - contacting the second plurality of oligonucleotide barcodes hybridized to the barcoded nucleic acid molecules with the cleaving enzyme, thereby removing the blocking group from said oligonucleotide barcodes;
 - extending the 3' ends of oligonucleotide barcodes of the second plurality of oligonucleotide barcodes hybridized to the barcoded nucleic acid molecules to generate a plurality of extended barcoded nucleic acid molecules.
2. The method of claim 1, wherein:
 - a. each extended barcoded nucleic acid molecule of the plurality of extended barcoded nucleic acid molecules comprise a sequence of at least a portion of the nucleic acid target; and/or
 - b. the cleaving enzyme is an RNase H enzyme and/or an RNase H2 enzyme, optionally the RNase H2 enzyme is a *Pyrococcus abyssi* RNase H2 enzyme; and/or

- c. the cleaving enzyme is a hot start cleaving enzyme which is thermostable and has reduced activity at lower temperatures, optionally wherein the hot start cleaving enzyme is *Pyrococcus abyssi* RNase H2 comprising (a) a G12A amino acid substitution; (b) a P13T amino acid substitution; (c) a G169A amino acid substitution; or (d) a combination thereof; and/or
 - d. the cleaving enzyme is chemically modified; and/or
 - e. the cleaving enzyme is a chemically modified hot start cleaving enzyme which is thermostable and has reduced activity at lower temperatures, optionally the cleaving enzyme is reversibly inactivated through interaction with an antibody at lower temperatures.
3. The method of any one of claims 1 or 2, wherein:
- a. the cleavage domain comprises one or more ribonucleotides that are capable of being cleaved by a RNase H enzyme; and/or
 - b. the cleavage domain comprises one or more of the following moieties: a DNA residue, an abasic residue, a modified nucleoside, or a modified phosphate internucleotide linkage; and/or
 - c. the cleavage domain comprises at least one RNA base; and/or
 - d. the cleavage domain comprises one or more 2'-modified nucleosides, optionally the one or more modified nucleosides are 2'- fluoronucleosides.
4. The method of any one of claims 1-3, wherein:
- a. the blocking group is attached to the 3' -terminal nucleotide of the oligonucleotide barcode; and/or
 - b. the blocking group is at or near 3' terminal of the oligonucleotide barcode; and/or
 - c. the blocking group is a 2', 3'-dideoxynucleotide, a ribonucleotide residue, a 2', 3' SH nucleotide, or a 2'-O-PO₃ nucleotide; and/or
 - d. the blocking group comprises a non-nucleotide modification; and/or
 - e. the blocking group further comprises a naphthyl-azo compound, a spacer and/or a biotin.
5. The method of any one of claims 1-4, wherein:
- a. extending the 3' ends of oligonucleotide barcodes of the second plurality of oligonucleotide barcodes comprises extending the 3' ends of oligonucleotide barcodes of the second plurality of oligonucleotide barcodes with a DNA polymerase that has strand displacement activity, optionally wherein extending the 3' ends of oligonucleotide barcodes of the

- second plurality of oligonucleotide barcodes with a DNA polymerase that has strand displacement activity is capable of generating extended barcoded nucleic acid molecules comprising a complement of the first molecular label and a complement of the first universal sequence; and/or
- b. extending the 3' ends of oligonucleotide barcodes of the second plurality of oligonucleotide barcodes comprises extending the 3' ends of oligonucleotide barcodes of the second plurality of oligonucleotide barcodes with a DNA polymerase that does not have strand displacement activity; and/or
 - c. the polymerase is selected from the group comprising Phi29 DNA polymerase, E.coli DNA polymerase I, Bsu DNA polymerase, Bst DNA polymerase, Taq DNA polymerase, VENT™ DNA polymerase, DEEPVENT™ DNA polymerase, LongAmp® Taq DNA polymerase, LongAmp® Hot Start Taq DNA polymerase, Crimson LongAmp® Taq DNA polymerase, Crimson Taq DNA polymerase, OneTaq® DNA polymerase, OneTaq® Quick- Load® DNA polymerase, Hemo KlenTaq® DNA polymerase, REDTaq® DNA polymerase, Phusion® DNA polymerase, Phusion® High-Fidelity DNA polymerase, Platinum Pfx DNA polymerase, AccuPrime Pfx DNA polymerase, Klenow fragment, Pwo DNA polymerase, Pfu DNA polymerase, T4 DNA polymerase, T7 DNA polymerase, derivatives thereof, or any combination thereof; and/or
 - d. extending the 3' ends of oligonucleotide barcodes comprises extending the 3' ends of oligonucleotide barcodes using a mesophilic DNA polymerase, a thermophilic DNA polymerase, a psychrophilic DNA polymerase, or any combination thereof; and/or
 - e. extending the 3' ends of oligonucleotide barcodes comprises extending the 3' ends of oligonucleotide barcodes using a DNA polymerase lacking at least one of 5' to 3' exonuclease activity and 3' to 5' exonuclease activity, and optionally the DNA polymerase comprises a Klenow Fragment; and/or
 - f. extending the first plurality of oligonucleotide barcodes comprises extending the first plurality of oligonucleotide barcodes using a reverse transcriptase, optionally wherein:
 - i. the reverse transcriptase is capable of terminal transferase activity; and/or

- ii. the reverse transcriptase with strand displacement activity is a PrimeScript reverse transcriptase, M-MuLV reverse transcriptase, SmartScribe reverse transcriptase, Maxima H Minus Reverse Transcriptase, and/or Superscript II reverse transcriptase; and/or
 - iii. the reverse transcriptase comprises a viral reverse transcriptase, optionally the viral reverse transcriptase is a murine leukemia virus (MLV) reverse transcriptase or a Moloney murine leukemia virus (MMLV) reverse transcriptase.
- 6. The method of any one of claims 1-5, wherein:
 - a. the each oligonucleotide barcode of the second plurality of oligonucleotide barcodes comprises a second molecular label, wherein at least 10 of the second plurality of oligonucleotide barcodes comprise different second molecular label sequences, optionally each second molecular label comprises at least 6 nucleotides, further optionally the second molecular label sequence is a random sequence; and/or
 - b. the second plurality of oligonucleotide barcodes are hybridized to the barcoded nucleic acid molecules via hybridization between the second molecular label and the sequence complementary to at least a portion of the nucleic acid target; and/or
 - c. the each oligonucleotide barcode of the second plurality of oligonucleotide barcodes comprises a second target-binding region; and/or
 - d. the first target-binding region and/or the second target-binding region comprises a poly(dA) region, a poly(dT) region, a random sequence, a gene-specific sequence, or any combination thereof; and/or
 - e. the each oligonucleotide barcode of the second plurality of oligonucleotide barcodes are hybridized to the barcoded nucleic acid molecules via hybridization between the second target-binding region and the sequence complementary to at least a portion of the nucleic acid target; and/or
 - f. at least 10 of the second plurality of oligonucleotide barcodes comprise different second target-binding regions, optionally at least two of the target-binding regions are capable of binding the complements of different nucleic acid targets, further optionally at least two of the target-binding regions are capable of hybridizing different regions of the complement of the same nucleic acid target; and/or

- g. two or more oligonucleotide barcodes of the second plurality of oligonucleotide barcodes are capable of hybridizing to different regions of the complement of the same nucleic acid target to generate two or more extended barcoded nucleic acid molecules, optionally wherein:
 - i. said two or more extended barcoded nucleic acid molecules are capable of being generated by two or more oligonucleotide barcodes of the second plurality of oligonucleotide barcodes hybridizing to different regions of the complement of the same nucleic acid target; and/or
 - ii. said the two or more extended barcoded nucleic acid molecules collectively comprise the sequence of the entire at least about 50% of the nucleic acid target.
7. The method of any one of claims 1-6, wherein:
- a. the method comprises denaturing the plurality of barcoded nucleic acid molecules; and/or
 - b. the method comprises denaturing the plurality of extended barcoded nucleic acid molecules; and/or
 - c. the method further comprises determining the copy number of the nucleic acid target in the sample based on:

the number of first molecular labels with distinct sequences associated with the plurality of barcoded nucleic acid molecules, or products thereof, optionally wherein determining the copy number of the nucleic acid target comprises determining the copy number of each of a plurality of nucleic acid targets in the sample based on:

 - i. the number of first molecular labels with distinct sequences associated with barcoded nucleic acid molecules of the plurality of barcoded nucleic acid molecules, or products thereof, comprising a sequence of the each of the plurality of nucleic acid targets; and/or
 - ii. the number of first molecular labels with distinct sequences, second molecular labels with distinct sequences, or a combination thereof, associated with extended barcoded nucleic acid molecules of the plurality of extended barcoded nucleic acid molecules comprising a sequence of the each of the plurality of nucleic acid targets; and/or
 - d. the method further comprises determining the copy number of the nucleic acid target in the sample based on:

the number of first molecular labels with distinct sequences, second molecular labels with distinct sequences, or a combination thereof, associated with the plurality of extended barcoded nucleic acid molecules, or products thereof, optionally wherein determining the copy number of the nucleic acid target comprises determining the copy number of each of a plurality of nucleic acid targets in the sample based on:

- i. the number of first molecular labels with distinct sequences associated with barcoded nucleic acid molecules of the plurality of barcoded nucleic acid molecules, or products thereof, comprising a sequence of the each of the plurality of nucleic acid targets; and/or
- ii. the number of first molecular labels with distinct sequences, second molecular labels with distinct sequences, or a combination thereof, associated with extended barcoded nucleic acid molecules of the plurality of extended barcoded nucleic acid molecules comprising a sequence of the each of the plurality of nucleic acid targets.

8. The method of any one of claims 1-7, wherein:
 - a. the sequence of the each of the plurality of nucleic acid targets comprises a subsequence of the each of the plurality of nucleic acid targets; and/or
 - b. the sequence of the nucleic acid target in the plurality of barcoded nucleic acid molecules comprises a subsequence of the nucleic acid target; and/or
 - c. the nucleic acid target comprises mRNA; and/or
 - d. the sample comprises a single cell, optionally an immune cell, and further optionally a B cell or a T cell, optionally wherein single cell comprises a circulating tumor cell; and/or
 - e. the sample comprises a plurality of cells, a plurality of single cells, a tissue, a tumor sample, or any combination thereof, optionally wherein single cell comprises a circulating tumor cell; and/or
 - f. the first universal sequence of each oligonucleotide barcode of the first plurality of oligonucleotide barcodes is 5' of the first molecular label and the first target-binding region; and/or
the second universal sequence of each oligonucleotide barcode of the second plurality of oligonucleotide barcodes is 5' of the second molecular label and/or the second target-binding region.
9. The method of any one of claims 1-8, wherein:

- a. the method comprises amplifying the plurality of barcoded nucleic acid molecules using an amplification primer and a primer comprising the first universal sequence, or a portion thereof, thereby generating a first plurality of single-labeled nucleic acid molecules comprising the sequence of the nucleic acid target, or a portion thereof,
wherein determining the copy number of the nucleic acid target in the sample comprises: determining the copy number of the nucleic acid target in the sample based on the number of first molecular labels with distinct sequences associated with the first plurality of single-labeled nucleic acid molecules, or products thereof, optionally wherein:
- i. the amplification primer comprises a fourth universal sequence;
and/or
 - ii. the amplification primer is a target-specific primer, optionally wherein the target-specific primer specifically hybridizes to an immune receptor, a constant region of an immune receptor, a variable region of an immune receptor, a diversity region of an immune receptor, and/or the junction of a variable region and diversity region of an immune receptor, further optionally wherein the immune receptor is a T cell receptor (TCR) and/or a B cell receptor (BCR) receptor, and optionally
the TCR comprises TCR alpha chain, TCR beta chain, TCR gamma chain, TCR delta chain, or any combination thereof; and
the BCR receptor comprises BCR heavy chain and/or BCR light chain; and/or
- b. the method comprises amplifying the plurality of extended barcoded nucleic acid molecules using an amplification primer and a primer comprising the second universal sequence, or a portion thereof, thereby generating a second plurality of single-labeled nucleic acid molecules comprising the sequence of the nucleic acid target, or a portion thereof,
wherein determining the copy number of the nucleic acid target in the sample comprises: determining the copy number of the nucleic acid target in the sample based on the number of second molecular labels with distinct sequences associated with the second plurality of single-labeled nucleic acid molecules, or products thereof, optionally wherein:

- i. the amplification primer comprises a fourth universal sequence; and/or
- ii. the amplification primer is a target-specific primer, optionally wherein the target-specific primer specifically hybridizes to an immune receptor, a constant region of an immune receptor, a variable region of an immune receptor, a diversity region of an immune receptor, and/or the junction of a variable region and diversity region of an immune receptor, further optionally wherein the immune receptor is a T cell receptor (TCR) and/or a B cell receptor (BCR) receptor, and optionally
 - the TCR comprises TCR alpha chain, TCR beta chain, TCR gamma chain, TCR delta chain, or any combination thereof; and
 - the BCR receptor comprises BCR heavy chain and/or BCR light chain; and/or
- c. the method comprises hybridizing random primers to the plurality of barcoded nucleic acid molecules and extending the random primers to generate a first plurality of extension products, wherein the random primers comprise a third universal sequence, or a complement thereof; and amplifying the first plurality of extension products using a primer capable of hybridizing to the third universal sequence, or a complement thereof, and a primer capable of hybridizing to the first universal sequence, or a complement thereof, thereby generating a third plurality of single-labeled nucleic acid molecules, or products thereof; and/or
- d. determining the copy number of the nucleic acid target in the sample comprises: determining the copy number of the nucleic acid target in the sample based on the number of first molecular labels with distinct sequences associated with the third plurality of single-labeled nucleic acid molecules, or products thereof and/or
- e. the method comprises hybridizing random primers to the plurality of extended barcoded nucleic acid molecules and extending the random primers to generate a second plurality of extension products, wherein the random primers comprise a third universal sequence, or a complement thereof; and amplifying the second plurality of extension products using a primer capable of hybridizing to the third universal sequence, or a complement

- thereof, and a primer capable of hybridizing to the second universal sequence, or a complement thereof, thereby generating a fourth plurality of single-labeled nucleic acid molecules, or products thereof; and/or
- f. determining the copy number of the nucleic acid target in the sample comprises: determining the copy number of the nucleic acid target in the sample based on the number of second molecular labels with distinct sequences associated with the fourth plurality of single-labeled nucleic acid molecules, or products thereof.
10. The method of any one of claims 1-9, wherein:
 - a. the first universal sequence, the second universal sequence, third universal sequence, and/or the fourth universal sequence are the same; and/or
 - b. the first universal sequence, the second universal sequence, third universal sequence, and/or the fourth universal sequence are different; and/or
 - c. the first universal sequence, the second universal sequence, third universal sequence, and/or the fourth universal sequence comprise the binding sites of sequencing primers and/or sequencing adaptors, complementary sequences thereof, and/or portions thereof, optionally wherein:
 - i. the sequencing adaptors comprise a P5 sequence, a P7 sequence, complementary sequences thereof, and/or portions thereof; and/or
 - ii. the sequencing primers comprise a Read 1 sequencing primer, a Read 2 sequencing primer, complementary sequences thereof, and/or portions thereof.
 11. The method of any one of claims 1-10, comprising:
 - a. obtaining sequence information of the plurality of barcoded nucleic acid molecules, or products thereof, optionally wherein obtaining the sequence information comprises attaching sequencing adaptors to the plurality of extended barcoded nucleic acid molecules, or products thereof; and/or
 - b. obtaining sequence information of the plurality of extended barcoded nucleic acid molecules, or products thereof, optionally wherein obtaining the sequence information comprises attaching sequencing adaptors to the extended barcoded nucleic acid molecules, barcoded nucleic acid molecules, products thereof, or any combination thereof; and/or
 - c. obtaining sequence information of one or more of the first, second, third, and fourth pluralities of single-labeled nucleic acid molecules, or products thereof, optionally wherein:

- i. obtaining the sequence information comprises attaching sequencing adaptors to one or more of the first, second, third, and fourth pluralities of single-labeled nucleic acid molecules, or products thereof; and/or
- ii. obtaining sequence information of one or more of the first, second, third, and fourth pluralities of single-labeled nucleic acid molecules, or products thereof, comprises:

obtaining sequencing data comprising a plurality of sequencing reads of one or more of the first, second, third, and fourth pluralities of single-labeled nucleic acid molecules, or products thereof,

wherein each of the plurality of sequencing reads comprise (1) a cell label sequence, (2) a molecular label sequence, and/or (3) a subsequence of the nucleic acid target, optionally wherein: the method comprises for each unique cell label sequence, which indicates a single cell of the sample:

aligning each of the plurality of sequencing reads of the nucleic acid target to generate an aligned sequence of the nucleic acid target, further optionally wherein

- (1) the aligned sequence of the nucleic acid target comprises at least 50% of the cDNA sequence of the nucleic acid target, at least 70% of the cDNA sequence of the nucleic acid target, at least 90% of the cDNA sequence of the nucleic acid target, or the full length of the cDNA sequence of the nucleic acid target; and/or
- (2) the aligned sequence of the nucleic acid target comprises the complementarity determining region 1 (CDR1), the complementarity determining region 2 (CDR2), the complementarity determining region 3 (CDR3), the variable region, the full length of the variable region, or a combination thereof; and/or
- (3) the aligned sequence of the nucleic acid target comprises the variable region, the diversity region, the junction of a variable region diversity region and/or the constant region, or any combination thereof.

12. The method of any one of claims 1-11, wherein the nucleic acid target is an immune receptor, optionally the immune receptor comprises BCR light chain, BCR heavy chain, TCR alpha chain, TCR beta chain, TCR gamma chain, TCR delta chain, or any combination thereof, optionally wherein:
- a. the aligned sequence of the nucleic acid target comprises the complementarity determining region 1 (CDR1), the complementarity determining region 2 (CDR2), the complementarity determining region 3 (CDR3), the variable region, the full length of the variable region, or a combination thereof; and/or
 - b. the aligned sequence of the nucleic acid target comprises the variable region, the diversity region, the junction of a variable region diversity region and/or the constant region, or any combination thereof.
13. The method of any one of claims 11 or 12, wherein:
- a. obtaining the sequence information comprises obtaining the sequence information of the BCR light chain and the BCR heavy chain of a single cell;
the sequence information of the BCR light chain and the BCR heavy chain comprises the sequence of the complementarity determining region 1 (CDR1), the CDR2, the CDR3, or any combination thereof, of the BCR light chain and/or the BCR heavy chain;
the method comprises pairing the BCR light chain and the BCR heavy chain of the single cell based on the obtained sequence information; and/or
the sample comprises a plurality of single cells, the method comprising pairing the BCR light chain and the BCR heavy chain of at least 50% of said single cells based on the obtained sequence information; and/or
 - b. obtaining the sequence information comprises obtaining the sequence information of the TCR alpha chain and the TCR beta chain of a single cell;
the sequence information of the TCR alpha chain and the TCR beta chain comprises the sequence of the complementarity determining region 1 (CDR1), the CDR2, the CDR3, or any combination thereof, of the TCR alpha chain and/or the TCR beta chain;
the method comprises pairing the TCR alpha chain and the TCR beta chain of the single cell based on the obtained sequence information; and/or

the sample comprises a plurality of single cells, the method comprising pairing the TCR alpha chain and the TCR beta chain of at least 50% of said single cells based on the obtained sequence information; and/or

- c. obtaining the sequence information comprises obtaining the sequence information of the TCR gamma chain and the TCR delta chain of a single cell;

the sequence information of the TCR gamma chain and the TCR delta chain comprises the sequence of the complementarity determining region 1 (CDR1), the CDR2, the CDR3, or any combination thereof, of the TCR gamma chain and/or the TCR delta chain;

the method comprises pairing the TCR gamma chain and the TCR delta chain of the single cell based on the obtained sequence information; and/or
the sample comprises a plurality of single cells, the method comprising pairing the TCR gamma chain and the TCR delta chain of at least 50% of said single cells based on the obtained sequence information.

14. The method of any one of claims 1-13, wherein:

- a. the complement of the molecular label comprises a reverse complementary sequence of the molecular label or a complementary sequence of the molecular label; and/or
- b. the plurality of barcoded nucleic acid molecules comprises barcoded deoxyribonucleic acid (DNA) molecules, barcoded ribonucleic acid (RNA) molecules, or a combination thereof; and/or
- c. the nucleic acid target comprises a nucleic acid molecule, optionally the nucleic acid molecule comprises ribonucleic acid (RNA), messenger RNA (mRNA), microRNA, small interfering RNA (siRNA), RNA degradation product, RNA comprising a poly(A) tail, or any combination thereof, and further optionally the mRNA encodes an immune receptor; and/or
- d. the nucleic acid target comprises a cellular component binding reagent, and/or the nucleic acid molecule is associated with the cellular component binding reagent, optionally the method further comprising dissociating the nucleic acid molecule and the cellular component binding reagent; and/or
- e. at least 10 of the first and/or second pluralities of oligonucleotide barcodes comprise different molecular label sequences; and/or
- f. each molecular label of the first and/or second pluralities of oligonucleotide barcodes comprises at least 6 nucleotides; and/or

- g. the first and/or second pluralities of oligonucleotide barcodes are associated with a solid support, optionally wherein:
 - i. the first and/or second pluralities of oligonucleotide barcodes associated with the same solid support each comprise an identical sample label, optionally wherein each sample label of the first and/or second pluralities of oligonucleotide barcodes comprises at least 6 nucleotides; and/or
 - ii. the first and/or second pluralities of oligonucleotide barcodes each comprise a cell label, optionally wherein each cell label of the first and/or second pluralities of oligonucleotide barcodes comprises at least 6 nucleotides; and/or
 - iii. oligonucleotide barcodes of the first and/or second pluralities of oligonucleotide barcodes associated with the same solid support comprise the same cell label; and/or
 - iv. oligonucleotide barcodes of the first and/or second pluralities of oligonucleotide barcodes associated with different solid supports comprise different cell labels; and/or
 - v. the solid support comprises a synthetic particle, a planar surface, or a combination thereof.
15. The method of any one of claims 1-14, wherein:
- a. the method comprises extending the oligonucleotide barcodes in the presence of one or more of ethylene glycol, polyethylene glycol, 1,2-propanediol, dimethyl sulfoxide (DMSO), glycerol, formamide, 7-deaza-GTP, acetamide, tetramethylammonium chloride salt, betaine, or any combination thereof; and/or
 - b. the sample comprises a single cell, the method comprising associating a synthetic particle comprising the first and second pluralities of oligonucleotide barcodes with the single cell in the sample, optionally wherein:
 - i. the method comprises lysing the single cell after associating the synthetic particle with the single cell, optionally lysing the single cell comprises heating the sample, contacting the sample with a detergent, changing the pH of the sample, or any combination thereof; and/or

- ii. the synthetic particle and the single cell are in the same partition, and optionally the partition is a well or a droplet; and/or
- iii. at least one oligonucleotide barcode of the first and/or second pluralities of oligonucleotide barcodes is immobilized or partially immobilized on the synthetic particle, or at least one oligonucleotide barcode of the first and/or second pluralities of oligonucleotide barcodes is enclosed or partially enclosed in the synthetic particle; and/or
- iv. the synthetic particle is disruptable, optionally a disruptable hydrogel particle;
the synthetic particle comprises a bead, optionally the bead is a sepharose bead, a streptavidin bead, an agarose bead, a magnetic bead, a conjugated bead, a protein A conjugated bead, a protein G conjugated bead, a protein A/G conjugated bead, a protein L conjugated bead, an oligo(dT) conjugated bead, a silica bead, a silica-like bead, an anti-biotin microbead, an anti-fluorochrome microbead, or any combination thereof; and/or
the synthetic particle comprises a material selected from the group consisting of polydimethylsiloxane (PDMS), polystyrene, glass, polypropylene, agarose, gelatin, hydrogel, paramagnetic, ceramic, plastic, glass, methylstyrene, acrylic polymer, titanium, latex, Sepharose, cellulose, nylon, silicone, and any combination thereof; and/or
- v. each oligonucleotide barcode of the first and/or second pluralities of oligonucleotide barcodes comprises a linker functional group, wherein the synthetic particle comprises a solid support functional group, and
wherein the support functional group and the linker functional group are associated with each other, and optionally the linker functional group and the support functional group are individually selected from the group consisting of C6, biotin, streptavidin, primary amine(s), aldehyde(s), ketone(s), and any combination thereof.