WHAT IS CLAIMED IS:

1. A method of preparing a plurality of combinatorially indexed beads, comprising:

(a) obtaining a population of primary indexed beads comprising a first polynucleotide comprising a first index, wherein the population of primary indexed beads comprises a plurality of first subpopulations of indexed beads, wherein the first subpopulations of indexed beads comprise a different first index from one another;

(b) splitting the population of primary indexed beads into a plurality of second subpopulations of beads;

(c) obtaining a population of secondary indexed beads, comprising:

(i) extending the first polynucleotide of the plurality of second subpopulations of beads with a second polynucleotide comprising a second index by chemical ligation to obtain second subpopulations of indexed beads, wherein the second subpopulations of indexed beads comprise a different second index from one another, and

(ii) combining the second subpopulations of indexed beads to obtain the population of secondary indexed beads; and optionally, further comprising:

(d) splitting the population of secondary indexed beads into a plurality of third subpopulations of beads; and

(e) obtaining a population of tertiary indexed beads, comprising:

(i) extending the second polynucleotide of the plurality of third subpopulations of beads with a third polynucleotide comprising a third index to obtain third subpopulations of indexed beads, wherein the third subpopulations of indexed beads comprise a different third index from one another, and

(ii) combining the third subpopulations of indexed beads to obtain the population of tertiary indexed beads.

2. The method of claim 1, wherein:

the first polynucleotide comprises a terminal 3′ modified deoxynucleotide (dNTP) comprising a 3′ functional moiety capable of participating in a click chemistry reaction;

the second polynucleotide comprises a terminal 5′ modified dNTP comprising a compatible 5′ functional moiety capable of participating in a click chemistry reaction with the 3′-functional moiety; and

the 3′ functional moiety and the 5′ functional moiety are capable of reacting with one another to form a modified backbone linkage.

3. The method of claim 2, wherein the extending the first polynucleotide with the second polynucleotide obtains a secondary indexed polynucleotide, and the method further comprises modifying the secondary indexed polynucleotide to obtain a modified polynucleotide comprising a terminal 3′ modified deoxynucleotide (dNTP) comprising a 3′ functional moiety capable of participating in a click chemistry reaction.

4. The method of claim 3, wherein the modifying comprises contacting the secondary indexed polynucleotide with a template independent polymerase.

5. The method of claim 4, wherein the template independent polymerase is selected from a terminal deoxynucleotidyl transferase (TdT), PolyA polymerase, or CCA-adding RNA polymerase.

6. The method of claim 5, wherein the template independent polymerase is TdT.

7. The method of any one of claims 1-6, further comprising extending the modified polynucleotide with the third polynucleotide by a chemical ligation reaction, wherein the third polynucleotide comprises a terminal 5′ modified dNTP comprising a compatible 5′ functional moiety capable of participating in a click chemistry reaction with the 3′ functional moiety.

8. The method of any one of claims 2-7, wherein the 3′ functional moiety is selected from the group consisting of an azide, an alkynyl, an alkenyl, a thiol, and a nitrone.

9. The method of any one of claims 2-8, wherein the 5′ functional moiety is different from and compatible with the 3′ functional moiety and is selected from the group consisting of an azide, an alkynyl, an alkenyl, a thiol, and a nitrone

10. The method of any one of claims 2-9, wherein the 3′ functional moiety and the 5′ functional moiety are selected from the following pairs: (i) 3′-azido/5′-alkynyl; (ii) 3′-alkynyl/5′ azido; (iii) 3′-thiol/5′-alkynyl; (iv) 3′-thiol/5′-alkenyl; (v) 3′-alkynyl/5′-thiol; (vi) 3′-alkenyl/5′-thiol; (vii) 3′-azido/5′-cyclooctynyl; (viii) 3′-cyclooctyne/5′-azido; (ix) 3′-nitrone/5′-cyclooctynyl; and (x) 3′-cyclooctynyl/5′-nitrone.

11. The method of any one of claims 2-10, wherein the 3′ functional moiety is a 3′-azido and the 5′ functional moiety is a 5′-alkynyl.

12. The method of any one of claims 2-11, wherein the click chemistry reaction comprises copper catalyzed azide-alkyne cycloaddition (CuAAC) to form a modified backbone linkage comprising a triazolyl.

13. The method of any one of claims 1-12, wherein (a) comprises:

(i) attaching the first polynucleotide to a plurality of first subpopulations of beads to obtain the first subpopulations of indexed beads, wherein the first polynucleotide comprises a different first index for each first subpopulation of beads; and

(ii) combining the first subpopulations of indexed beads to obtain the population of primary indexed beads.

14. The method of claim 13, wherein the first polynucleotide is attached to a bead via a first binding partner and a second binding partner.

15. The method of claim 14, wherein the first binding partner or the second binding partner is selected from the group consisting of biotin, streptavidin, a biotin derivative, a streptavidin derivative, an antibody, and an antigen binding fragment of an antibody.

16. The method of any one of claims 1-15, further comprising repeating (d) and (e) and adding additional indexes to indexed subpopulations of beads.

17. The method of any one of claims 1-16, wherein the first polynucleotide comprises a primer binding site selected from the group consisting of a P5 sequence, a P5′ sequence, P7 sequence, and P7′ sequence.

18. The method of any one of claims 1-17, wherein the first index, the second index, and/or the third index has a length less than 20 consecutive nucleotides.

19. The method of any one of claims 1-18, wherein the first index, the second index, and/or the third index has a length less than 10 consecutive nucleotides.

20. The method of any one of claims 1-19, wherein (b) comprises randomly distributing the population of primary indexed beads into a plurality of compartments.

21. The method of any one of claims 1-20, wherein (d) comprises randomly distributing the population of secondary indexed beads into a plurality of compartments.

22. The method of claim 20 or 21, wherein the plurality of compartments comprise a compartment selected from a well, a channel, or a droplet.

23. The method of any one of claims 1-22, wherein the plurality of combinatorially indexed beads comprise magnetic beads.

24. The method of any one of claims 1-23, further comprising distributing the plurality of combinatorially indexed beads on an array.

25. The method of any one of claims 1-24, further comprising sequencing the combinatorially indexed beads on an array.

26. The method of claim 25, further comprising decoding the location of a bead of the plurality of combinatorially indexed beads on an array based on the combinatorial indexes.

27. The method of any one of claims 1-26, wherein each bead of the plurality of combinatorially indexed beads comprises a capture probe.

28. The method of claim 27, wherein the first polynucleotide, the second polynucleotide or the third polynucleotide comprises the capture probe.

29. The method of any one of claims 1-28, further comprising hybridizing a plurality of target nucleic acid to the capture probes.

30. The method of claim 29, further comprising extending the capture probes.