

WHAT IS CLAIMED IS:

1. A method of determining the source of target nucleic acids from different sources on an array, comprising:

(a) obtaining a first and a second population of beads, wherein:

the first population of beads comprise oligonucleotides comprising first capture probes, first barcodes, and barcode primer binding sites adjacent to the first barcodes, and

the second population of beads comprise oligonucleotides comprising second capture probes, second barcodes, and barcode primer binding sites adjacent to the second barcodes, wherein the barcode primer binding sites comprise the same sequence;

(b) obtaining a first and a second plurality of polynucleotides, wherein:

the first plurality of polynucleotides comprises first target nucleic acids, wherein the first plurality of polynucleotides is in solution, and

the second plurality of polynucleotides comprises second target nucleic acids, wherein the second plurality of polynucleotides is in solution;

(c) hybridizing in a first volume the first target nucleic acids to the first capture probes to obtain hybridized first beads comprising the first indexes, and hybridizing in a second volume the second target nucleic acids to the second capture probes to obtain hybridized second beads comprising second indexes,

wherein the first indexes are the same as one another and are indicative of a source of the first target nucleic acids, the second indexes are the same as one another and are indicative of a source of the second target nucleic acids, and wherein the first indexes are different from the second indexes;

(d) randomly distributing the hybridized first beads and hybridized second beads on an array;

(e) decoding the locations of the first and second beads on the array by sequencing on the array the first and second barcodes;

(f) extending the first and second capture probes to obtain nucleic acid sequence data for the first and second target nucleic acids; and

- (g) determining a source for the nucleic acid sequences of the first and second target nucleic acids by sequencing the first and second indexes.
2. The method of claim 1, wherein:
the first plurality of polynucleotides comprises the first indexes and index primer binding sites adjacent to the first indexes; and
the second plurality of polynucleotides comprises the second indexes and index primer binding sites adjacent to the second indexes.
 3. The method of claim 2, wherein the first or second plurality of polynucleotides is obtained by tagmenting a nucleic acid sample with a plurality of transposomes.
 4. The method of claims 3, wherein the plurality of transposomes comprise the first or second indexes.
 5. The method of claims 4, further comprising adding adaptors to the tagmented nucleic acid sample, wherein the adaptors comprise the first or second indexes.
 6. The method of claims 5, further comprising amplifying the tagmented nucleic acid sample with primers comprising the first or second indexes.
 7. The method of any one of claims 2-6, wherein extending the first and second capture probes incorporates sequences complementary to the first and second indexes and to the first and second index primer binding sites into the extended capture probes.
 8. The method of claim 1, wherein:
the first population of beads comprise first indexes, and index primer binding sites adjacent to the first indexes, and
the second population of beads comprise second indexes, and index primer binding sites adjacent to the second indexes.
 9. The method of claim 8, wherein the oligonucleotides of the first population of beads comprise the first indexes; and the oligonucleotides of the second population of beads comprise the second indexes.
 10. The method of any one of claims 2-9, wherein sequencing the first and second indexes comprises extending primers hybridized to the index primer binding sites.
 11. The method of any one of claims 2-10, wherein the index binding primer sites are the same.

12. The method of any one of claims 1-11, wherein the first and second target nucleic acids are obtained from different nucleic acid samples.
13. The method of any one of claims 1-12, wherein the first and second target nucleic acids are obtained from genomic DNA.
14. The method of any one of claims 1-13, wherein the first and second barcodes are indicative of a nucleic acid sequence of the first or second capture probes.
15. The method of any one of claims 1-14, wherein the first barcodes are different from one another, and the second barcodes are different from one another.
16. The method of any one of claims 1-15, wherein sequencing the first and second barcodes comprises extending primers hybridized to the barcode primer binding sites.
17. The method of any one of claims 1-16, wherein extending the first and second capture probes comprises polymerase extension.
18. The method of claim 17, wherein extending the first and second capture probes comprises addition of a single nucleotide to a capture probe.
19. The method of claim 17 or 18, further comprising ligating locus specific oligonucleotides to the extended capture probes.
20. The method of any one of claims 1-16, wherein extending the first and second capture probes comprises ligating locus specific oligonucleotides to the capture probes.
21. The method of any one of claims 1-20, wherein step (c) is performed in solution.
22. The method of any one of claims 1-21, wherein the array is located on the surface of a flowcell.
23. The method of any one of claims 1-22, wherein the first and second beads are adapted to be attached to the array.
24. The method of claim 23, wherein the first and second beads comprise biotin, streptavidin, or a derivative thereof; and the array comprises biotin, streptavidin, or a derivative thereof.
25. The method of claim 23, wherein the first and second beads are magnetic.
26. The method of claim 1, wherein step (a) further comprises:
 - (i) obtaining a plurality of index polynucleotides, wherein each index polynucleotide comprises the first index or the second index, and the index primer binding site; and

- (ii) attaching the plurality of index polynucleotides to the first or second population of beads via an adaptor.
27. The method of claim 26, wherein step (ii) comprises extending the adaptors by polymerase extension.
28. The method of claim 27, wherein each index polynucleotide comprises an adaptor binding site, and the attaching comprises hybridizing the adaptor binding sites to the adaptors.
29. The method of claim 26, wherein step (ii) comprises ligating the index polynucleotides to the adaptors.
30. The method of claim 29, wherein the attaching comprises hybridizing a splint polynucleotide to the adaptor and to the index polynucleotide.
31. The method of claim 26, wherein step (ii) comprises attaching the plurality of index polynucleotides to the adaptors of the population of beads via a chemically reactive moiety.
32. The method of claim 31, wherein the attaching comprises a click chemistry reaction.
33. The method of any one of claims 26-32, wherein the first polynucleotides of the population of beads comprise capture probes different from one another.
34. The method of any one of claims 26-33, wherein the index of each index polynucleotide is the same.
35. The method of any one of claims 26-34, wherein the first polynucleotide comprises the capture probe.
36. The method of any one of claims 26-35, further comprising contacting the indexed population of beads with a plurality of nucleic acids comprising a target nucleic acid.
37. The method of claim 36, further comprising mixing the indexed population of beads contacted with a plurality of nucleic acids comprising a target nucleic acid with an additional indexed population of beads, wherein the additional indexed population of beads comprises an index polynucleotide comprising an index different from the index of the indexed population of beads contacted with a plurality of nucleic acids.
38. The method of any one of claims 26-34, wherein the capture probe comprises a protein.

39. The method of any one of claims 26-38, performed on a flow cell.