

restriction endonuclease. In some aspects, cleaving the nucleic acid molecule comprises contacting to a nonspecific endonuclease. In some aspects, cleaving the nucleic acid molecule comprises contacting to a tagmentation enzyme. In some aspects, cleaving the nucleic acid molecule comprises contacting to a transposase. In some aspects, cleaving the nucleic acid molecule comprises shearing the first molecule. In some aspects, partitioning comprises separating said nucleic acid molecule from other nucleic acid molecules of a sample. In some aspects, partitioning comprises diluting said nucleic acid sample. In some aspects, partitioning comprises distributing said nucleic acid molecule into a microdroplet of an emulsion.

[0020] Disclosed herein are nucleic acid molecules representative of genomic phase information of an organism's genome, said nucleic acid molecule comprising at least 20 kb of nucleic acid sequence information that maps to a single genomic molecule, wherein said sequence information comprises segments rearranged relative to their position in the genomic molecule, and wherein at least 70% of sequence information that uniquely maps to said organism's genome maps to a single genomic molecule. In some aspects, the nucleic acid molecule comprises at least 20 segments. In some aspects, said segments are not adjacent in said organism's genome.

[0021] Disclosed herein are nucleic acid libraries comprising at least 100 nucleic acid molecule constituents of at least 20 kb, wherein constituents comprise rearranged segments of an organism's genome; wherein at least 70% of uniquely mapping segments from a library constituent map to a common genomic molecule; and wherein constituents are not bound to nucleic acid binding moieties.

[0022] Disclosed herein are nucleic acid datasets comprising sequences corresponding to at least 100 nucleic acid molecule constituents of at least 20 kb, wherein constituents comprise at least 5 rearranged segments of an organism's genome, and wherein constituents for which less than 70% of said rearranged segments map to a common scaffold are excluded from a downstream analysis.

[0023] Disclosed herein are nucleic acid datasets comprising sequences corresponding to at least 100 nucleic acid molecule constituents of at least 20 kb, wherein constituents comprise at least 5 rearranged segments of an organism's genome, and wherein constituents for which less than 70% of said sequence uniquely maps to a common scaffold are excluded from a downstream analysis.

[0023a] Disclosed herein are methods of generating long-distance phase information from a first DNA molecule, comprising:

- (a) providing a first DNA molecule having a first segment, a second segment, and a third segment, wherein none of the first segment, the second segment, and the third segment are adjacent on the first DNA molecule, and wherein the first segment, the second segment, and the third segment are bound to a DNA binding moiety independent of a common phosphodiester backbone of the first DNA molecule;
- (b) cleaving the first DNA molecule such that the first segment, the second segment, and the third segment are not joined by a common phosphodiester backbone;
- (c) attaching the first segment to the second segment via a phosphodiester bond and attaching the second segment to the third segment via a phosphodiester bond to form a reassembled first DNA molecule; and
- (d) sequencing a first portion of the reassembled first DNA molecule comprising a junction between the first segment and the second segment and a junction between the second segment and the third segment in a single sequencing read, wherein first segment sequence, second segment sequence, and third segment sequence represent long-distance phase information from the first DNA molecule.

CLAIMS

1. A method of generating long-distance phase information from a first DNA molecule, comprising:
 - (a) providing a first DNA molecule having a first segment, a second segment, and a third segment, wherein none of the first segment, the second segment, and the third segment are adjacent on the first DNA molecule, and wherein the first segment, the second segment, and the third segment are bound to a DNA binding moiety independent of a common phosphodiester backbone of the first DNA molecule;
 - (b) cleaving the first DNA molecule such that the first segment, the second segment, and the third segment are not joined by a common phosphodiester backbone;
 - (c) attaching the first segment to the second segment via a phosphodiester bond and attaching the second segment to the third segment via a phosphodiester bond to form a reassembled first DNA molecule; and
 - (d) sequencing a first portion of the reassembled first DNA molecule comprising a junction between the first segment and the second segment and a junction between the second segment and the third segment in a single sequencing read,
wherein first segment sequence, second segment sequence, and third segment sequence represent long-distance phase information from the first DNA molecule.
2. The method of claim 1, wherein the DNA binding moiety comprises a plurality of DNA-binding molecules.
3. The method of claim 2, wherein the plurality of DNA-binding molecules comprises a population of DNA-binding proteins.
4. The method of claim 3, wherein the population of DNA-binding proteins comprises nuclear proteins.
5. The method of claim 3, wherein the population of DNA-binding proteins comprises nucleosomes.
6. The method of claim 3, wherein the population of DNA-binding proteins comprises histones.
7. The method of claim 2, wherein the plurality of DNA-binding moieties comprises a population of DNA-binding nanoparticles.
8. The method of any one of claims 1-7, comprising contacting the first DNA molecule to a cross-linking agent.
9. The method of claim 8, wherein the cross-linking agent is formaldehyde.

10. The method of claim 1, wherein the DNA binding moiety is bound to a surface comprising a plurality of DNA binding moieties.
11. The method of claim 1, wherein the DNA binding moiety is bound to a solid framework comprising a bead.
12. The method of claim 1, wherein cleaving the first DNA molecule comprises contacting to a restriction endonuclease.
13. The method of claim 1, wherein cleaving the first DNA molecule comprises contacting to a nonspecific endonuclease.
14. The method of claim 1, wherein cleaving the first DNA molecule comprises contacting to a tagmentation enzyme.
15. The method of claim 1, wherein cleaving the first DNA molecule comprises contacting to a transposase.
16. The method of claim 1, wherein cleaving the first DNA molecule comprises shearing the first molecule.
17. The method of claim 1, comprising adding a tag to at least one exposed end.
18. The method of claim 17, wherein the tag comprises a labeled base.
19. The method of claim 17, wherein the tag comprises a methylated base.
20. The method of claim 17, wherein the tag comprises a biotinylated base.
21. The method of claim 17, wherein the tag comprises uridine.
22. The method of claim 17, wherein the tag comprises a noncanonical base.
23. The method of claim 17, wherein the tag generates a blunt ended exposed end.
24. The method of claim 1, comprising adding at least one base to a recessed strand of a sticky end of the first segment.
25. The method of any one of claims 1-17, comprising adding a linker oligo comprising an overhang that anneals to a sticky end of the first segment.
26. The method of claim 25, wherein the linker oligo comprises an overhang that anneals to the sticky end of the first segment and an overhang that anneals to a sticky end of the second segment.
27. The method of claim 25 or claim 26, wherein the linker oligo does not comprise two 5' phosphate moieties.
28. The method of claim 1, wherein attaching comprises ligating.
29. The method of claim 1, wherein attaching comprises DNA single strand nick repair.

30. The method of claim 1, wherein the first segment and the second segment are separated by at least 10kb on the first DNA molecule prior to cleaving the first DNA molecule.
31. The method of claim 1, wherein the first segment and the second segment are separated by at least 15kb on the first DNA molecule prior to cleaving the first DNA molecule.
32. The method of claim 1, wherein the first segment and the second segment are separated by at least 30kb on the first DNA molecule prior to cleaving the first DNA molecule.
33. The method of claim 1, wherein the first segment and the second segment are separated by at least 50kb on the first DNA molecule prior to cleaving the first DNA molecule.
34. The method of claim 1, wherein the first segment and the second segment are separated by at least 100kb on the first DNA molecule prior to cleaving the first DNA molecule.
35. The method of claim 1, wherein the sequencing comprises single molecule long-read sequencing.
36. The method of claim 35, wherein the long-read sequencing comprises a read of at least 5 kb.
37. The method of claim 35, wherein the long-read sequencing comprises a read of at least 10 kb.
38. The method of claim 1, wherein the reassembled first DNA molecule comprises a hairpin moiety linking a 5' end to a 3' end at one end of the first DNA molecule.
39. The method of claim 1, comprising sequencing a second reassembled version of the first DNA molecule.
40. The method of claim 1, wherein the first segment and the second segment are each at least 500 bp.
41. The method of claim 1, wherein the first segment, the second segment, and the third segment are each at least 500 bp.