

METHODS AND COMPOSITIONS FOR SEQUENCING LIBRARY PREPARATION**CROSS-REFERENCE**

[0001] This application claims the benefit of U.S. Provisional Application No. 63/340,734, filed May 11, 2022, and U.S. Provisional Application No. 63/490,192, filed March 14, 2023, each of which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] Obtaining high-quality, contiguous genome sequences is often difficult, especially in cases when limited source material is available for sequence analysis. While obtaining raw sequence data has become faster and available at a lower cost, suitable methods for analyzing and assembling the data efficiently and accurately remains a challenge.

SUMMARY

[0003] In an aspect, provided herein are methods of nucleic acid processing. In some cases, the method comprises obtaining a stabilized sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein. In some cases, the method comprises cleaving the nucleic acid molecule into a plurality of segments comprising at least a first segment and a second segment, wherein the cleaving is effected by a transposase. In some cases, the method comprises ligating the first segment to the second segment, thereby creating a linked nucleic acid comprising a first sequence from the first segment and a second sequence from the second segment. In some cases, the transposase is a Tn5 transposase. In some cases, the method further comprises circularizing the linked nucleic acid by ligating a 5' end of the linked nucleic acid to a 3' end of the linked nucleic acid. In some cases, the method further comprises sequencing at least a portion of the linked nucleic acid. In some cases, the sequencing comprises sequencing at least a portion of the first sequence and at least a portion of the second sequence. In some cases, the method further comprises mapping at least a portion of the first sequence and at least a portion of the second sequence to a genome. In some cases, the method further comprises conducting three-dimensional genomic analysis using information from the sequencing. In some cases, the stabilized sample is a cross-linked sample. In some cases, obtaining the stabilized sample comprises obtaining a sample and stabilizing the sample. In some cases, obtaining the stabilized sample comprises obtaining a sample that was previously stabilized. In some cases, the nucleic acid binding protein comprises chromatin or a constituent thereof. In some cases, a linker sequence is ligated between the first segment and the second segment. In some cases, the linker sequence comprises a barcode sequence. In some cases, the barcode sequence is indicative of a partition of origin. In some cases, the barcode sequence is indicative of a cell of origin. In some cases, the barcode sequence is indicative of a cell population of origin. In some cases, the barcode sequence is indicative of an organism of origin. In some cases, the cleaving occurs in open and closed chromatin compartments. In some cases, at least 10% of the cleaving occurs in closed chromatin compartments. In some cases, at least 20% of the cleaving occurs in closed chromatin compartments. In some cases, at least 30% of the cleaving occurs in closed chromatin

compartments. In some cases, the stabilized sample comprises no more than 50,000 cells. In some cases, the stabilized sample comprises at least 10,000 cells. In some cases, the stabilized sample comprises stabilized nuclei. In some cases, the stabilized sample comprises no more than 50,000 nuclei. In some cases, the stabilized sample comprises at least 10,000 nuclei. In some cases, the linked nucleic acid does not comprise an affinity tag. In some cases, the linked nucleic acid does not comprise biotin. In some cases, the circularized linked nucleic acid does not comprise an affinity tag. In some cases, the circularized linked nucleic acid does not comprise biotin. In some cases, the linked nucleic acid and/or the circularized linked nucleic acid is isolated without the use of an affinity tag. In some cases, the linked nucleic acid and/or the circularized linked nucleic acid is isolated without use of streptavidin.

INCORPORATION BY REFERENCE

[0004] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0005] An understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0006] **FIG. 1** illustrates various components of an exemplary computer system according to various embodiments of the present disclosure.

[0007] **FIG. 2** is a block diagram illustrating the architecture of an exemplary computer system that can be used in connection with various embodiments of the present disclosure.

[0008] **FIG. 3** is a diagram illustrating an exemplary computer network that can be used in connection with various embodiments of the present disclosure.

[0009] **FIG. 4** is a block diagram illustrating the architecture of another exemplary computer system that can be used in connection with various embodiments of the present disclosure.

[0010] **FIG. 5** depicts a method of identifying long non-coding RNA (lncRNA) binding sites.

[0011] **FIG. 6** depicts an example workflow of a method of tagmentation and proximity ligation.

[0012] **FIG. 7** depicts an example method of tagmentation and proximity ligation.

[0013] **FIG. 8** depicts two examples of proximity ligation methods.

[0014] **FIG. 9A** depicts coverage uniformity achieved using different methods of chromatin fragmentation.

[0015] **FIG. 9B** depicts library characteristics achieved using different methods of chromatin fragmentation.

[0016] **FIG. 10** is a table showing long range sequence information achieved using different library preparation methods.

[0017] **FIG. 11** depicts chromatin contacts captured using different library preparation methods.

[0018] **FIG. 12** depicts results of exonuclease treatment in library preparation methods.

[0019] **FIG. 13** depicts results of exonuclease treatment in library preparation methods.

[0020] **FIG. 14** depicts results of exonuclease treatment in library preparation methods.

DETAILED DESCRIPTION

[0021] In one aspect, provided herein are compositions, systems, and methods related to the determination of genomic sequence including long-range and structural genomic information, the determination of nucleic acid physical conformation in a cell, and for generating extremely long-range read pairs for nucleic acids with improved results over some other methods. Methods herein can utilize techniques including, but not limited to, transposase fragmentation of crosslinked nucleic acids and ligation based linking of transposase fragmented nucleic acids.

Transposase Fragmented Chromatin

[0022] In an aspect, provided herein are methods of nucleic acid processing. Such methods can comprise obtaining a stabilized sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein and cleaving the nucleic acid molecule into a plurality of segments comprising at least a first segment and a second segment, wherein the cleaving is effected by a transposase. Methods herein can further comprise ligating the first segment and the second segment, thereby creating a linked nucleic acid. In some cases, the linked nucleic acid is further ligated to produce a circularized linked nucleic acid.

[0023] In various aspects of methods herein, cleaving stabilized nucleic acids is conducted using a transposase. In some cases, cleaving is conducted in permeabilized cells. In some cases, cleaving is conducted in permeabilized nuclei. In some cases, the transposase is a Tn5, a Tn3, a Tn7, a sleeping beauty transposase, or a combination thereof. In some cases, the transposase is a Tn5 transposase.

[0024] In various aspects of methods herein, cleaving occurs in both open chromatin and closed chromatin. In some cases, at least about 10% to at least about 50% of the cleaving occurs in closed chromatin. For example, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 35%, at least about 40%, at least about 45%, at least about 50%, or more of the cleavage occurs in closed chromatin. In some embodiments, closed chromatin is transcriptionally inactive and bound to one or more nucleosomes or other chromatin proteins. In some embodiments, open chromatin is transcriptionally active and is bound to fewer or no nucleosomes or other chromatin proteins.

[0025] In various aspects of methods herein, a linker comprising recombinase sites can be contacted to the cleaved nucleic acids in the presence of a recombinase, wherein the recombinase sites comprise two recombinase sites oriented as direct repeats. In some cases, the presence of recombinase sites oriented as direct repeats can prevent a resulting product from forming a stable hairpin structure. In some cases, the linked nucleic acid does not form a hairpin loop. In some cases, the resulting product is more easily sequenced than a product where recombinase sites are oriented as inverse repeats.

[0026] In various aspects of methods herein, a first segment and a second segment of a cleaved nucleic acid is contacted to a linker comprising integrase site in the presence of a recombinase. In some cases, the recombinase is an integrase. In some cases, the integrase is a PhiC31 integrase, a Bxb1 integrase, or a combination thereof.

[0027] In various aspects, there are provided methods of processing nucleic acids where the linked nucleic acid is circularized. In some cases, the ends of the are removed to expose the first segment and the second segment prior to ligation. In some embodiments, the circularized product is amplified using PCR to create a sequencing library. An example of this method is illustrated in FIG. 6 and FIG. 7.

[0028] In an example embodiment, a sample can be prepared and crosslinked before subjecting the sample to in situ tagmentation which fragments the chromatin and leaves a mosaic end on each end of the fragmented chromatin. The tagmented chromatin can then be joined using an adapter and a ligase. Ends can be removed and crosslinks reversed. Nucleic acids can be captured and then resulting fragments circularized via ligation resulting in a circular nucleic acid having two genomic DNA fragments joined with mosaic ends on each side joined all together by the adapter. Genomic DNA for analysis can be amplified using adapter PCR and purification/size selection suitable for sequence analysis (FIG. 6 and FIG. 7).

[0029] Circularization-based approaches can provide several advantages. As discussed above, circularization can produce nucleic acid molecules where adapter sites are located surrounding the genomic sequences of interest, allowing straightforward production of nucleic acid molecules for sequencing with a higher proportion of the sequence being genomic (e.g., by excluding linker sequences). Additionally, circularization-based approaches can obviate the need for affinity tag enrichment approaches. Existing proximity ligation approaches generally use affinity tag enrichment (e.g., incorporating biotinylated nucleic acids at proximity ligation sites which can then be enriched with surface-bound streptavidin) to ensure that the nucleic acids that are eventually sequenced are representative of proximity ligation events and not general genomic DNA, for example; alternatively, as presented herein, circularization can be conducted to enrich for nucleic acids that have undergone proximity ligation, as circularization can require nucleic acids of at least a certain length. For example, nucleic acids less than about 250 base pairs may fail to circularize, such as mono-nucleosome size fragments that did not ligate to a partner during proximity ligation. In some cases, enrichment for circularized molecules can be performed, such as by clean up, bead binding, or size selection. In other cases, no enrichment for circularized molecules need be performed, and instead primer-based amplification (e.g., adapter PCR) produces amplification product suitable for sequencing only from circularized molecules.

[0030] In various aspects of methods herein, the linker comprises the mosaic end, sequencing adaptors, and the attB sequences. Alternatively, the linker comprises the mosaic end and sequencing adaptors and attB sequences are added to the transposase product prior to recombination, for example using a ligase.

[0031] In certain aspects of methods herein, the method can further comprise sequencing at least a portion of the linked nucleic acid via any suitable method such as a method provided herein. In some cases, sequencing may comprise sequencing at least a portion of the first sequence and at least a portion of the second sequence. In certain cases, the method may further comprise mapping at least a portion of the first sequence and at least a portion of the second sequence to a genome. In various cases, the method may further comprise conducting three-dimensional genomic analysis using information from the sequencing.

[0032] In various aspects of methods herein, the stabilized sample may be a cross-linked sample. In some cases, the stabilized sample may be crosslinked cells. In some cases, the stabilized sample may be crosslinked nuclei. In some cases, the stabilized sample may be crosslinked chromatin. In some cases, obtaining the stabilized sample can comprise obtaining a sample and stabilizing the sample. In some cases, obtaining the stabilized sample can comprise obtaining a sample that was previously stabilized. In some cases, the nucleic acid binding protein can comprise chromatin or a constituent thereof.

[0033] In various aspects of methods herein, recombinase sites can comprise attP and attB integrase sites. In some cases, the first recombinase sites may be different than the second recombinase sites. In some cases, the first recombinase sites may be attP or attB integrase sites. In some cases, the second recombinase sites may be attP or attB integrase sites. In various cases, the first recombinase sites are attP integrase sites and the second recombinase sites are attB integrase sites. In various cases, the first recombinase sites are attB integrase sites and the second recombinase sites are attP integrase sites. In some cases, the first recombinase sites and the second recombinase sites can comprise transposase mosaic ends.

[0034] In various aspects of methods herein, the linker can comprise additional sequences. In some cases, the linker sequence can comprise a barcode sequence. In some cases, the barcode sequence may be indicative of a partition of origin. In some cases, the barcode sequence may be indicative of a cell of origin. In some cases, the barcode sequence may be indicative of a cell population of origin. In some cases, the barcode sequence may be indicative of an organism of origin. In some cases, the barcode sequence may be indicative of a species of origin. In some cases, the linker can comprise an adapter. In some cases, the adapter can comprise a P5 sequence. In some cases, the adapter can comprise a P7 sequence.

[0035] In various aspects of methods herein, the method may be completed in less than one day. In some cases, the method may be completed in less than 8 hours. In some cases, the method may be completed in less than 6 hours. In some cases, the method may be completed in no more than 4 hours. In some cases, the method may be completed in 4-6 hours. In some cases, the method may be completed in 4-8 hours. In some cases, the method may be completed in 3-4 hours.

[0036] In various aspects of methods herein, the method may require very low input of sample material. In some cases, the stabilized sample can comprise no more than 50,000 cells. In some cases, the sample can comprise no more than 40,000 cells. In some cases, the sample can comprise no more than 30,000 cells. In some cases, the sample can comprise no more than 20,000 cells. In some cases, the sample can comprise at least 10,000 cells. In some cases, the sample can comprise at least 20,000 cells. In some cases, the sample can comprise at least 30,000 cells. In some cases, the sample can comprise at least 40,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 40,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 40,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 30,000

cells. In some cases, the sample can comprise from about 10,000 cells to about 20,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 40,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 30,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 40,000 cells.

[0037] In various aspects of methods herein, the stabilized sample may comprise nuclei. In some cases, the stabilized sample may comprise no more than 50,000 nuclei. In some cases, the sample may comprise no more than 40,000 nuclei. In some cases, the sample may comprise no more than 30,000 nuclei. In some cases, the sample may comprise no more than 20,000 nuclei. In some cases, the sample may comprise at least 10,000 nuclei. In some cases, the sample may comprise at least 20,000 nuclei. In some cases, the sample may comprise at least 30,000 nuclei. In some cases, the sample may comprise at least 40,000 nuclei. In some cases, the sample may comprise from about 10,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 40,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 10,000 nuclei to about 40,000 nuclei. In some cases, the sample may comprise from about 10,000 nuclei to about 30,000 nuclei. In some cases, the sample may comprise from about 10,000 nuclei to about 20,000 nuclei. In some cases, the sample may comprise from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 20,000 nuclei to about 40,000 nuclei. In some cases, the sample may comprise from about 20,000 nuclei to about 30,000 nuclei. In some cases, the sample may comprise from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample may comprise from about 30,000 nuclei to about 40,000 nuclei.

Recombinase Sites Oriented as Direct Repeats

[0038] In another aspect, there are provided methods of nucleic acid processing comprising obtaining a stabilized sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein. Next, the method can comprise cleaving the nucleic acid molecule into a plurality of segments comprising at least a first segment and a second segment and attaching first recombinase sites to the first segment and the second segment. Then the method can comprise contacting the first segment and the second segment with a linker comprising second recombinase sites in the presence of a recombinase, thereby generating a proximity-linked nucleic acid comprising a first sequence from the first segment, a linker sequence from the linker, and a second sequence from the second segment, wherein the second recombinase sites comprise two recombinase sites oriented as direct repeats. In some cases, the stabilized sample may not be sonicated.

[0039] In various aspects of methods herein, cleaving stabilized nucleic acids may be conducted using a transposase. In some cases, cleaving may be conducted in permeabilized cells. In some cases, cleaving may be conducted in permeabilized nuclei. In some cases, the transposase may be a Tn5, a Tn3, a Tn7, a

sleeping beauty transposase, or a combination thereof. In some cases, transposase may be a Tn5 transposase.

[0040] In various aspects of methods herein, a linker comprising recombinase sites may be contacted to the cleaved nucleic acids in the presence of a recombinase, wherein the recombinase sites comprise two recombinase sites oriented as direct repeats. In some cases, the presence of recombinase sites oriented as direct repeats can prevent a resulting product from forming a stable hairpin structure. In some cases, the proximity-linked nucleic acid does not form a hairpin loop. In some cases, the resulting product may be more easily sequenced than a product where recombinase sites are oriented as inverse repeats.

[0041] In various aspects of methods herein, a first segment and a second segment of a cleaved nucleic acid may be contacted to a linker comprising an integrase site in the presence of a recombinase. In some cases, the recombinase may be an integrase. In some cases, the integrase may be a PhiC31 integrase, a Bxb1 integrase, or a combination thereof.

[0042] In various aspects of methods herein, the method can further comprise sequencing at least a portion of the proximity-linked nucleic acid via any suitable method such as a method provided herein. In some cases, sequencing can comprise sequencing at least a portion of the first sequence and at least a portion of the second sequence. In some cases, the method further comprises mapping at least a portion of the first sequence and at least a portion of the second sequence to a genome. In some cases, the method further comprises conducting three-dimensional genomic analysis using information from the sequencing.

[0043] In various aspects of methods herein, the stabilized sample may be a cross-linked sample. In some cases, the stabilized sample may be crosslinked cells. In some cases, the stabilized sample may be crosslinked nuclei. In some cases, the stabilized sample may be crosslinked chromatin. In some cases, obtaining the stabilized sample comprises obtaining a sample and stabilizing the sample. In some cases, obtaining the stabilized sample comprises obtaining a sample that was previously stabilized. In some cases, the nucleic acid binding protein comprises chromatin or a constituent thereof.

[0044] In various aspects of methods herein, recombinase sites can comprise attP and attB integrase sites. In some cases, the first recombinase sites may be different than the second recombinase sites. In some cases, the first recombinase sites may be attP or attB integrase sites. In some cases, the second recombinase sites may be attP or attB integrase sites. In various cases, the first recombinase sites are attP integrase sites and the second recombinase sites are attB integrase sites. In various cases, the first recombinase sites are attB integrase sites and the second recombinase sites are attP integrase sites. In some cases, the first recombinase sites and the second recombinase sites may comprise transposase mosaic ends.

[0045] In various aspects of methods herein, the linker may comprise additional sequences. In some cases, the linker sequence may comprise a barcode sequence. In some cases, the barcode sequence may be indicative of a partition of origin. In some cases, the barcode sequence may be indicative of a cell of origin. In some cases, the barcode sequence may be indicative of a cell population of origin. In some cases, the barcode sequence may be indicative of an organism of origin. In some cases, the barcode sequence may be indicative of a species of origin. In some cases, the linker can comprise an adapter. In

some cases, the adapter can comprise a P5 sequence. In some cases, the adapter can comprise a P7 sequence.

[0046] In various aspects of methods herein, the method may be completed in less than one day. In some cases, the method may be completed in less than 8 hours. In some cases, the method may be completed in less than 6 hours. In some cases, the method may be completed in no more than 4 hours. In some cases, the method may be completed in 4-6 hours. In some cases, the method can be completed in 4-8 hours. In some cases, the method can be completed in 3-4 hours.

[0047] In various aspects of methods herein, the method can require very low input of sample material. In some cases, the stabilized sample may comprise no more than 50,000 cells. In some cases, the sample may comprise no more than 40,000 cells. In some cases, the sample may comprise no more than 30,000 cells. In some cases, the sample may comprise no more than 20,000 cells. In some cases, the sample can comprise at least 10,000 cells. In some cases, the sample can comprise at least 20,000 cells. In some cases, the sample can comprise at least 30,000 cells. In some cases, the sample can comprise at least about 40,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 40,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 40,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 30,000 cells. In some cases, the sample can comprise from about 10,000 cells to about 20,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 40,000 cells. In some cases, the sample can comprise from about 20,000 cells to about 30,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 50,000 cells. In some cases, the sample can comprise from about 30,000 cells to about 40,000 cells.

[0048] In various aspects of methods herein, the stabilized sample may comprise nuclei. In some cases, the stabilized sample may comprise no more than 50,000 nuclei. In some cases, the sample may comprise no more than 40,000 nuclei. In some cases, the sample may comprise no more than 30,000 nuclei. In some cases, the sample may comprise no more than 20,000 nuclei. In some cases, the sample may comprise at least 10,000 nuclei. In some cases, the sample may comprise at least 20,000 nuclei. In some cases, the sample may comprise at least 30,000 nuclei. In some cases, the sample may comprise at least 40,000 nuclei. In some cases, the sample can comprise from about 10,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 40,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 10,000 nuclei to about 40,000 nuclei. In some cases, the sample can comprise from about 10,000 nuclei to about 30,000 nuclei. In some cases, the sample comprises about 10,000 nuclei to about 20,000 nuclei. In some cases, the sample can comprise from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 20,000 nuclei to about 40,000 nuclei. In some cases, the

sample can comprise from about 20,000 nuclei to about 30,000 nuclei. In some cases, the sample can comprise from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample can comprise from about 30,000 nuclei to about 40,000 nuclei.

Proximity Ligation to Create Concatemers

[0049] Provided herein are compositions, systems, and methods which allow concatemer formation using proximity ligation. For example, a biological sample, such as a stabilized biological sample having a nucleic acid molecule complexed to a nucleic acid binding protein, can be contacted with a dendrimer to form a complex. In another example, a biological sample is stabilized by being contacted with dendrimers to form a complex. Next, the nucleic acid molecule can be cleaved into a plurality of segments, for example at least a first segment and a second segment. Then, the plurality segments can be attached at a plurality of junctions, for example, the first segment and the second segment can be attached at a junction.

[0050] In certain aspects of methods herein, a biological sample, such as a stabilized biological sample having a nucleic acid molecule complexed with a nucleic acid binding protein and a dendrimer. In some cases, the dendrimer is conjugated with psoralen. In some cases, the dendrimer is conjugated with Azido-Peg4-N-hydroxysuccinimide (NHS) ester. In some cases, the NHS ester of the Azido-Peg4-NHS ester reacts with the primary amine on the dendrimer to result in a dendrimer having a reactive azide group. In some cases, carboxylated beads (e.g., magnetic beads) are prepared by conjugating using 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC)/Sulpho-NHC chemistry with a dibenzocyclooctyne-amine (DBCO)-Peg4-amine building block. These prepared beads can be used to isolate the dendrimers, for example via magnetic separation methods prior to proximity ligation.

[0051] In some cases, the dendrimer is modified with a compound or contacted with a compound. For example, in some cases, the dendrimer is modified with psoralen. In some cases, the psoralen comprises an N-hydroxysuccinimide (NHS) ester-conjugated psoralen. In some cases, the dendrimer comprises a polyamidoamine (PAMAM) dendrimer. In some cases, the dendrimer is modified with a crosslinking agent such as, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cicycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the dendrimer is modified with an intercalating agent, an antibiotic, or a minor groove binding agent.

[0052] Methods herein can comprise uncoupling the compound from the dendrimer. For example, the compound, such as psoralen, can be uncoupled from the dendrimer using heat. In some cases, the compound, such as psoralen, is uncoupled from the dendrimer using alkali conditions or high pH. Alternatively, the compound, such as psoralen, is uncoupled from the dendrimer using heat and alkali conditions. The compound (e.g., psoralen) can also be uncoupled from the dendrimer using UV radiation.

[0053] Any suitable dendrimer can be used in methods herein. A dendrimer can have a molecular weight of about 5 kilodaltons (kDa) to about 125 kDa. In some cases, the dendrimer has a molecular weight of

from 6 kDa to 8 kDa. In some cases, the dendrimer has a molecular weight of from 25 kDa to 35 kDa. In some cases, the dendrimer has a molecular weight of from 110 kDa to 125 kDa. In some cases, the dendrimer comprises from 32 to 512 reactive groups. In some cases, the dendrimer comprises about 32 reactive groups. In some cases, the dendrimer comprises about 128 reactive groups. In some cases, the dendrimer comprises about 512 reactive groups. In some cases, the dendrimer is a Gen3 dendrimer. In some cases, the dendrimer is a Gen5 dendrimer. In some cases, the dendrimer is a Gen7 dendrimer.

[0054] Methods herein can result in at least a portion of segments being joined into concatemers. For example, at least two segments, at least three segments, at least four segments, at least five segments, at least six segments, at least seven segments, at least eight segments, at least nine segments, at least ten segments, or more can be attached to form a concatemer. In some cases, an oligonucleotide is attached between each segment. In some cases, the oligonucleotide is a bridge oligonucleotide. In some cases, the oligonucleotide is an adapter oligonucleotide. In some cases, the oligonucleotide is a punctuation oligonucleotide. In some cases, the bridge oligonucleotide, the adapter oligonucleotide, and/or the punctuation oligonucleotide comprises a barcode sequence. In some cases, the bridge oligonucleotide, the adapter oligonucleotide, and/or the punctuation oligonucleotide is modified with a dibenzo-cyclooctyne (DBCO) moiety. In some cases, the DBCO moiety facilitates a copper free click chemistry. In some cases, a plurality of oligonucleotides are attached in series between each segment. The attaching can result in samples, cells, nuclei, chromosomes, or nucleic acid molecules of the stabilized biological sample receiving a unique sequence of oligonucleotides (e.g., bridge oligonucleotides).

[0055] In some cases, after the dendrimer is contacted with the stabilized biological sample to form a complex, the complex is photoactivated, for example by exposing the complex to UV radiation having a wavelength of about 360 nm, thereby creating a crosslinked complex. In some cases, the crosslinking is reversible without leaving an adduct on the nucleic acids.

[0056] Methods herein can further comprise subjecting the plurality of segments to size selection to obtain a plurality of selected segments. The size selection herein can include any suitable range of segment sizes.

[0057] Cleaving in methods provided herein can be done using any suitable method, for example by using a nuclease or a deoxyribonuclease (DNase). In some cases, the DNase comprises DNase I, DNaseII, micrococcal nuclease, a restriction endonuclease, or a combination thereof.

[0058] Stabilized biological samples in methods herein can be stabilized by being treated with a stabilizing agent or a crosslinking reagent. In some cases, the crosslinking agent is a chemical fixative, such as formaldehyde, psoralen, disuccinimidyl glutarate (DSG), ethylene glycol bis(succinimidyl succinate) (EGS), ultraviolet light, or a combination thereof. In some cases, the crosslinking agent comprises chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin,

daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. The stabilized biological sample can be a crosslinked paraffin-embedded tissue sample. In some cases, the stabilized biological sample comprises a stabilized intact cell or a stabilized intact nucleus. In some cases, the method comprises lysing cells and/or nuclei in the stabilized biological sample. The cleaving step of methods herein can be conducted prior to lysis of the intact cell or the intact nucleus.

[0059] Methods herein can be conducted on stabilized biological samples comprising small numbers of cells. For example, in some cases, the stabilized biological sample comprises fewer than about 3,000,000 cells. The stabilized biological sample can comprise fewer than about 1,000,000 cells, fewer than about 500,000 cells, fewer than about 400,000 cells, fewer than about 300,000 cells, fewer than about 200,000 cells, fewer than about 100,000 cells, or fewer.

[0060] In aspects of methods herein, the method can further comprise obtaining at least some sequence on each side of the junction to generate a first read pair. In addition, the method can further comprise mapping the first read pair to a set of contigs; and determining a path through the set of contigs that represents an order and/or orientation to a genome. Alternatively or in combination, the method can comprise mapping the first read pair to a set of contigs; and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample. Alternatively or in combination, the method can further comprise mapping the first read pair to a set of contigs; and assigning a variant in the set of contigs to a phase. Alternatively or in combination, the method can further comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs; and conducting a step selected from one or more of: identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; selecting a drug based on the presence of the variant; or identifying a drug efficacy for the stabilized biological sample.

[0061] In aspects of methods herein, proximity ligation can be conducted with click chemistry, including copper-free click chemistry, such as with a DBCO modified bridge oligonucleotide attached between each segment of the concatemer. Then concatemers can be joined, for example via the dendrimers. To enrich for the ligated molecules, a feature of the bridge oligonucleotide can be targeted. In an example, a DBCO containing oligonucleotide can be reacted with an azide-biotin moiety which can be isolated with a streptavidin substrate, such as beads. In another example, a DBCO containing oligonucleotide can be reacted with an azide-modified NHS-S-S-dPEG4-biotin which comprises a disulfide bond; azide can be added to the NHS-S-S-dPEG4-biotin using an azido-PEG3-amine, and in order to isolate the nucleic acids for library preparation, this disulfide bond can be reduced, for example by using DTT and heating, for example heating at 70°C for about 10 minutes.

[0062] In aspects of methods herein, dendrimers with nucleic acid fragments contacted to them can be separated or isolated from the rest of the nucleic acids in the sample prior to proximity ligation of the nucleic acid fragments. This step can ensure that the concatemers formed by the proximity ligation comprise fragments that were contacted to the same dendrimer. This can mean that all the segments of a given concatemer were in proximity to each other in the original stabilized sample. Therefore, rather than

just pairwise information about which nucleic acid regions were proximate to which other regions, such an approach can yield much more complex proximity information – e.g., that 3, 4, 5, 6, 7, 8, 9, 10, or more nucleic acid regions were all proximate to each other.

[0063] In some cases, dendrimers with nucleic acid fragments contacted to them can be separated or isolated from the rest of the nucleic acids to enable barcoding or tagging of those fragments, instead of proximity ligation. The fragments associated with a given dendrimer can be barcoded or tagged – for example, in a droplet or a well. After sequencing, sequences can be associated based on their barcodes and proximity information can be derived based on the barcodes, rather than from presence in the same concatemer as above. This proximity information can then be used as discussed herein. In one example, dendrimers are complexed to nucleic acids in a sample, thereby stabilizing them; the nucleic acids are then fragmented; dendrimers are then isolated with their complexed nucleic acid fragments and encapsulated in droplets; nucleic acids in droplets are labeled with a droplet-specific barcode or label; and nucleic acids are then sequenced, with barcode or label information used to associate fragments that were proximate to each other in the sample.

Long Non-Coding RNA Analysis

[0064] Provided herein are methods of analyzing long non-coding RNA binding sites. In some cases, such methods comprise obtaining a stabilized biological sample comprising a DNA molecule complexed to at least one nucleic acid binding protein and at least one non-coding RNA. Next, the method can comprise contacting the DNA molecule to a Tn5 transposase and an oligonucleotide comprising a mosaic end and a detectable label thereby fragmenting the DNA molecule and attaching the oligonucleotide to the ends of the fragmented DNA molecule. The fragment can then be contacted to a T4 RNA ligase thereby ligating the non-coding RNA to the oligonucleotide and reversing the cross-links. Then, the ligated RNA can be extended with a reverse transcriptase to create a double stranded DNA fragment. Then, the double stranded DNA fragment can then be contacted to an endonuclease linked to an agent that binds to the detectable label thereby digesting DNA near the detectable label. Sequencing adaptors can then be attached in order to create a sequencing library. In some cases, the oligonucleotide is adenylated on one end to facilitate ligation to the non-coding RNA. In some cases, the oligonucleotide further comprises a barcode. In some cases, the sample stabilized biological sample is contacted to an RNase H prior to transposase treatment.

[0065] In aspects of methods herein, in some cases the non-coding RNA is a long non-coding RNA. In some cases, the non-coding RNA is an enhancer RNA. In some cases, the non-coding RNA is a miRNA. In some cases, the non-coding RNA is a Y RNA. In some cases, the non-coding RNA is an RNase P. In some cases, the non-coding RNA is a piRNA. In some cases, the non-coding RNA is Xist.

[0066] In aspects of methods herein, in some cases, the detectable label comprises a modified nucleotide capable of click chemistry reactions. In some cases, the detectable label comprises biotin. In some cases, the agent comprises an antibody, a protein A, a protein G, or streptavidin. In some cases, the DNA joined to non-coding RNA is enriched prior to further analysis.

[0067] In aspects of methods herein, an endonuclease is used to cleave extraneous sample DNA prior to analysis. In some cases, the endonuclease comprises DNase I, DNase II, micrococcal nuclease, a restriction endonuclease, or a combination thereof.

[0068] In aspects of methods herein, sequence is obtained of the double stranded DNA fragment containing the non-coding RNA. Any suitable sequencing method, including methods further described herein can be used.

[0069] Various suitable stabilized biological samples are contemplated for use in methods herein. Stabilized biological samples, described in more detail elsewhere herein, have been crosslinked with a crosslinking agent such as a fixative or with UV light. For example, in some cases, the stabilized biological sample is a crosslinked paraffin-embedded tissue sample. In some cases, the stabilized biological sample comprises a stabilized cell lysate. In some cases, the stabilized biological sample comprises a stabilized intact cell. In some cases, the stabilized biological sample comprises a stabilized intact nucleus.

Nucleic Acid Conformation Assessment

[0070] Disclosed herein are compositions, systems and methods related to the determination of nucleic acid physical conformation in a cell, such as a single cell or a population of cells, distinguishable from a physical conformation of a second cell or population of cells. Through practice of the disclosure herein, nucleic acid molecules indicative of three-dimensional nucleic acid relative position can be generated and optionally provided with a tag (e.g., nucleic acid barcode) to discern a common cell or population of origin for a plurality of molecules.

[0071] Through practice of the disclosed methods herein, nucleic acids can be obtained so as to preserve all or at least some of their three-dimensional configuration in a cell. Exposed nucleic acid loops of such nucleic acids can be cleaved to expose internal segment ends that are randomly reattached to one another such that exposed ends in physical proximity are more likely to become attached to one another (proximity attachment). Accordingly, by determining which exposed ends become attached to one another, one may obtain data informative of the physical proximity of the end-adjacent nucleic acids in a native cell configuration.

[0072] Related approaches are disclosed in, for example US9434985B2 to Dekker et al. published September 6, 2016, which is hereby incorporated by reference in its entirety.

[0073] Through practice of the disclosed methods herein, paired-end library constituents can be further tagged or otherwise provided with sequence information indicative of cell of origin, such that conformational differences among individual cells of a population are readily discerned for a population of cells, or such that conformational differences between a first population of cells and a second population of cells are readily discerned, even when they are concurrently analyzed. Tags can comprise, for example, nucleic acid barcodes. In some cases, tags can comprise a junction between two nucleic acid segments that are not contiguous in the genome. Nucleic acid molecules can be generated such that when sequenced in full or in part, one often obtains at least some genomic sequence sufficient to map each genomic end to its genomic locus and further obtains a tagging or linking sequence sufficient to identify a

precise or likely cell or cell population of origin. Accordingly, one obtains sequence information informative of two regions of a genome being in physical proximity to one another, while also obtaining information informative of the cell or cell population in which this physical conformation occurs, such that it can be assessed in the context of other physical conformation information co-occurring in that cell or cell population.

[0074] Genomic or other nucleic acids in cells can be stabilized and, for eukaryotic cells, nuclei are optionally isolated according to known methods such as those incorporated herein or otherwise known.

[0075] Nucleic acids consistent with the disclosure herein include any number of cellular nucleic acids, such as prokaryotic primary genome or plasmid nucleic acids, eukaryotic nuclear, mitochondrial or plastid nucleic acids, or in some cases cytoplasmic nucleic acids such as rRNA, mRNA, or exogenous nucleic acids in a sample such as viral or other pathogen or other exogenous nucleic acids of a sample.

[0076] Stabilized nucleic acids can be distributed in some cases such that at least some nucleic acids are distributed into individual partitions. Exemplary partitions include wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[0077] Stabilized nucleic acids can be fragmented so as to expose internal breaks for later reconnection so as to obtain nucleic acid configuration information for a particular cell. A number of fragmentation approaches are known and are consistent with the disclosure herein. Nucleic acids can be fragmented using one or more populations of restriction endonucleases, programmable endonucleases such as CRISPR/Cas molecules coupled to guide RNA, non-specific endonucleases (e.g., DNase), tagmentation, shearing, sonication, heating, or other mechanism. In some cases, the DNase is non-sequence specific. In some cases, the DNase is active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase is specific for double-stranded DNA. In some cases, the DNase is preferential to double-stranded DNA. In some cases, the DNase is specific for single-stranded DNA. In some cases, the DNase is preferential to single-stranded DNA. In some cases, the DNase is DNase I. In some cases, the DNase is DNase II. In some cases, the DNase is selected from one or more of DNase I and DNase II. In some cases, the DNase is micrococcal nuclease. In some cases, the DNase is selected from one or more of DNase I, DNase II, and micrococcal nuclease. Other suitable nucleases are also within the scope of this disclosure.

[0078] In particular, the disclosure of WO2014121091A1 to Green et al. published August 7, 2014 (later published as US20150363550A1 on December 17, 2015 and issued as US10089437B2 on October 2, 2018) is incorporated herein in its entirety. Similarly, the disclosure of WO2016019360A1 to Fields et al. published on February 4, 2016 (later published as US20170335369A1 on November 23, 2017) is incorporated herein in its entirety. Similarly, the disclosure of WO2017147279A1 to Green et al. published August 31, 2017 is incorporated herein in its entirety.

[0079] Nucleic acids can be bound to a surface prior to or after attachment. Exemplary surfaces include, but are not limited to, beads, arrays, and wells. In some cases, the surface is a solid phase reversible immobilization (SPRI) surface, such as a SPRI bead. Binding nucleic acids to a surface prior to

attachment can improve performance of downstream steps, such as reducing inter-chromosomal ligations or attachments and increasing intra-chromosomal ligations or attachments.

[0080] Nucleic acids may be immunoprecipitated prior to or after attachment. Such methods can involve fragmenting chromatin and then contacting the fragments with an antibody that specifically recognizes and binds to acetylated histones, particularly H3. Examples of such antibodies include, but are not limited to, Anti Acetylated Histone H3, available from Upstate Biotechnology, Lake Placid, N.Y. The polynucleotides from the immunoprecipitate can subsequently be collected from the immunoprecipitate. Similar targeted enrichment methods also can be employed with target-specific compounds including but not limited to aptamers, oligonucleotides or other nucleic acid probes, and nucleic-acid guided nucleases (e.g., Cas-family enzymes such as Cas9, including catalytically-inactive or “dead” nucleases).

[0081] Linking nucleic acids, such as linking nucleic acids having barcodes, partition-specific sequences, or partition-identifying sequences, can be attached to exposed internal ends so as to generate nucleic acid segments having a left genomic segment, a linking region often having partition-specific or partition-identifying sequence (e.g., nucleic acid barcode), and a right genomic segment, wherein the left genomic segment and the right genomic segment map to genomic segments in physical proximity in the source cell.

[0082] Prior to attachment of exposed nucleic acid ends, the ends can be processed. Such processing can include end polishing or blunt ending. Blunt ended exposed nucleic acid ends can be ligated, for example directly to other blunt ended exposed nucleic acid ends, or to adapters or linkers. Such processing can include generating overhangs, for example, by tailing (e.g., A-tailing or adenylation). In one example, the overhang is one nucleotide in size. In one example, the overhang is a single A nucleotide. Tailed exposed nucleic acid ends can be ligated, for example, directly to other tailed exposed nucleic acid ends, or to adapters or linkers. In some cases, blunt ending or tailing can incorporate affinity tagged nucleic acids, such as biotinylated nucleic acids. Affinity tags can be used, for example, in downstream capture or enrichment steps. In other cases, blunt ending or tailing can be performed without incorporating affinity tagged nucleic acids (e.g., without biotinylated nucleic acids). Affinity tags, if desired, can be added subsequently, for example, in an adapter or a linker (e.g., a bridge). In one example, exposed nucleic acids are end polished, overhangs are generated, and exposed ends are attached via a bridge oligo.

[0083] Attachment can be direct, such as via ligation.

[0084] Attachment can be via a linker or bridge, such as by ligation of one or more linker or bridge nucleic acids connecting one exposed nucleic acid end to another.

[0085] Attachment can be through the use of capping nucleic acid adapter segments such as those consistent with recombinase incorporation, such as integrase or transposase incorporation. Adapters with recombinase sites can be added to exposed nucleic acid ends, and those ends can then be connected, for example, by recombination.

[0086] Taking phiC31 integrase barcode delivery as an example, linkers such as cell-identifying or cell-specific linkers (e.g., nucleic acid barcodes) can be enzymatically added as follows.

[0087] Subsequent to exposure of internal nucleic acid ends, integrase sites can be ligated to exposed nucleic acid ends such as internal ends or exposed linear chromosome ends, such as those from which telomeres have been removed. Exemplary integration sites are attP phiC31 integrase integration sites or nucleic acids comprising attP integration sites, although other integration sites are consistent with the disclosure herein. Ligation results in a population of nucleic acid fragments, at least some of which individually comprise a cellular nucleic acid segment bordered at each end by an integration site, such as a segment comprising an attP segment. In various embodiments, either one or both of fragmentation and integration site attachment occur prior to partitioning, or either one or both of fragmentation and integration site attachment occur subsequent to partitioning.

[0088] Alternatively, a transposase, such as Tn3, Tn5, Tn7, or sleeping beauty transposase can be used for barcode delivery. Subsequent to exposure of internal nucleic acid ends, mosaic ends can be ligated to exposed nucleic acid ends such as internal ends or exposed linear chromosome ends, such as those from which telomeres have been removed. Exemplary mosaic ends are Tn5 mosaic ends or nucleic acids comprising Tn5 mosaic ends, although other mosaic ends are consistent with the disclosure herein. Ligation results in a population of nucleic acid fragments, at least some of which individually comprise a cellular nucleic acid segment bordered at each end by a mosaic end, such as a Tn5 mosaic end.

[0089] In various embodiments, either one or both of fragmentation and mosaic end attachment occur prior to partitioning, or either one or both of fragmentation and mosaic end attachment occur subsequent to partitioning. In an exemplary system for single-cell HiC (or other proximity ligation techniques) integrase mediated intra-aggregate ligation is used. Single cell nuclei are encapsulated in a first set of partitions in combination with an integrase. The partitions are in this case, droplets in an emulsion. Nuclei are subjected to strand breakage so as to generate internal exposed ends and to preserve local three-dimensional information. Adapters are ligated onto exposed internal ends. The adapters optionally comprise exonuclease-resistant ends. In this embodiment, the adapters do not convey partition-distinguishing information. In a second set of partitions, linkers having partition distinguishing sequence such as unique molecular identifiers (UMIs) are encapsulated and optionally subjected to amplification and cleavage-directed linearization. The first and second sets of partitions are merged in an approximately 1:1 ratio, or under conditions such that nucleic acids from two cells are unlikely to be combined into a single resultant partition.

[0090] Recombinase sites, such as integrase sites or mosaic ends can be in some cases carried on unmodified single or double stranded fragments to be ligated onto internal nucleic acid ends. Alternately, so as to facilitate subsequent sequencing library clean-up, some single or double stranded fragments harboring integration sites such as attP sequences or mosaic ends such as Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic ends can comprise at least one modification, such as a modification that interferes with exonuclease or other nucleic acid degrading activity. Examples include thiosulphate modification so as to preclude exonuclease degradation of fragments to which a double stranded fragment harboring an integration site has been added to each end.

[0091] Often, recombinase sites, such as integration sites or mosaic ends are nonspecific, in that the sequence in such integration sites or mosaic ends, such as attP sequence or Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic end, is not used to designate a cell source of the adjacent nucleic acid.

Alternately, often subsequent to nucleic acid partitioning, partitions can be provided with adapters having distinct, specific or cell-distinguishing sequence (e.g., nucleic acid barcode) adjacent to integration sites or mosaic ends, or can be provided with distinct integration sites or mosaic ends, such that nucleic acids of a first partition receive integration segments or mosaic ends having a first identifying segment while nucleic acid segments of a second partition receive integration segments having a second identifying segment.

[0092] Fragments having recombinase borders, such as borders comprising integrase attP segments, can be then contacted to integration sites, such as attB phiC31 integration sites, in a common solution. In an example, the integration enzyme can comprise a phi31 integrase, integration borders can comprise attP segments, and integration sites can comprise attB integration sites. Alternatively, fragments have mosaic end borders, such as Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic end borders.

[0093] When recombinase sites such as attB integration sites or Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic ends flank a linking segment having a sequence that identifies a partition or cell, such as one that is specific to a segment or cell source (e.g., nucleic acid barcode), that sequence identifies the adjacent cellular nucleic acid as arising from a particular or a common cell source or partition, such that multiple exposed ends from a common cell joined by a common cell-distinguishing or partition distinguishing segment can be readily identified as arising from a common cell even if they are bulked with fragments of a second partition prior to or concurrent with sequence determination.

[0094] When cell-distinguishing sequence is delivered via a recombinase site-bordered fragment, the integration or transposition is preferably performed subsequent to partitioning. Nucleic acid contents of at least some partitions can be thereby distinguished by the cell-distinguishing sequence of its linkers, such that even after nucleic acids from multiple cell sources are bulked for sequencing, one is able to assign internal end pairs, and the proximity information assigned to the vicinity to which they map in a contig set up to and including a largely or completely sequenced genome, to a common cell distinguished from at least one other cell of a sample, such that differences in predicted nucleic acid three dimensional conformation can be established.

[0095] A recombination site-bordered fragment variously comprises a left border fragment and a right border fragment (attB sites or Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic ends, for example) linked by a linker region optionally comprising cell or partition designating sequence (e.g., nucleic acid barcode). The linker region optionally further comprises a moiety to facilitate subsequent isolation. A number of affinity tags or modified bases are consistent with the disclosure herein. Exemplary moieties facilitate physical or chemical isolation of linkers subsequent to integrase or transposase treatment. Any number of affinity tags are consistent with the disclosure herein, such as one or a plurality of biotin tags that may facilitate avidin- or streptavidin-based isolation. Alternately, any antigen, receptor or ligand that facilitates isolation without interfering with integrase or transposase activity is suitable for some embodiments herein.

[0096] As mentioned above, some library generation approaches comprise a clean-up step, such as a step to selectively remove unincorporated reagents. Exonuclease treatment, for example, is often used to selectively remove unattached linker molecules, genomic fragments to which no integration site has been attached, or both unattached linker molecules and genomic fragments to which no integration site has been attached. A genomic fragment ligated to an integration site fragment having an exonuclease resistant modification such as a thiosulphate backbone is resistant to exonuclease degradation from that end, and a nucleic acid molecule bounded on both ends by an integration site fragment having an exonuclease resistant modification such as a thiosulphate backbone is resistant to degradation at both ends and can survive exonuclease treatment.

[0097] Alternately or in combination, some linker molecules comprise a counter-affinity tag on an opposite side of a recombination site such as an attP integration site or a Tn3, Tn5, Tn7, or sleeping beauty transposase mosaic end, such that the counter-affinity tag is removed pursuant to a successful recombination reaction. In such cases, unwanted reagents can be removed by contacting to a binding partner of the counter-affinity tag.

[0098] Integrase activity partially destroys both integration sites, such as attB and attP sites, as part of the integration event. Accordingly, by designing primers to anneal to ligated adapter sites such as attP integration sites, alone or in combination with linker-based isolation, one may generate clonal amplicons spanning at least one linker such that cell or aliquot-distinguishing information and internal end adjacent information is amplified, in some cases facilitating sequencing or other downstream analysis.

[0099] Following library generation and optionally library clean-up, nucleic acids can be sequenced completely or partially, so as to obtain information sufficient for the cell-distinguished or cell-specific three-dimensional nucleic acid position assessment. As mentioned above, sequencing is preferably performed such that one obtains at least some genomic sequence sufficient to map each genomic end of a library constituent to its genomic locus and further obtains a linking sequence sufficient to identify a precise or likely cell of origin. Accordingly, one obtains sequence information informative of two regions of a genome being in physical proximity to one another, while also obtaining information informative of the cell in which this physical conformation occurs, such that it can be assessed in the context of other physical conformation information co-occurring in that cell. Often this information is obtained through paired-end sequencing rather than through full length sequencing, although both approaches and others are consistent with the disclosure herein.

[00100] The compositions and methods related to the determination of nucleic acid physical conformation in a cell such as a single cell distinguishable from a physical conformation on a second cell can be implemented on a number of systems consistent with the disclosure herein. Some systems comprise distribution of fixed cellular nucleic acid material into first droplets of an emulsion or in wells, e.g. on a well plate. These droplets further comprise recombinase sites, such as integrase sites or mosaic ends, optionally modified to be exonuclease resistant as described herein, as well as integrase or transposase enzymes and ligase enzymes. Separately, linker nucleic acid molecules can be configured for delivery to the first droplets of the emulsion. The linker nucleic acids can be optionally distributed into droplets of a

second emulsion or second wells and optionally amplified, for example using rolling circle amplification, and processed to generate multiple copies of a given linker molecule per second emulsion droplet.

[00101] Second emulsion droplets and first emulsion droplets can be then merged pairwise so as to assemble integrase or transposase-ligates nucleic acid fragments with integrase or transposase compatible linkers, often exhibiting a uniform label per droplet. However, droplets having two or more identifiers per nucleic acid sample can be still capable of yielding meaningful data, particularly when data analysis indicates the presence of more than one type of tag in a droplet.

[00102] As an alternative to pairwise merger, in some cases integrase or transposase-compatible linkers can be delivered as colonies of solid particles in a reagent stream that is contacted to first emulsion droplet via droplet to stream merger, such as that described in US20170335369A1, published November 23, 2017, which is hereby incorporated by reference in its entirety. Linker nucleic acids can be optionally amplified on solid particles or in gels. First emulsion droplets can be merged to the stream and second emulsion droplets can be recovered by segmenting or partitioning the stream so that a desired proportion of nucleic acid clusters to linker particles, such as 1:1 greater than 1:1 or less than 1:1 is obtained.

[00103] Alternately, some systems and methods comprise distribution of fixed cellular nucleic acid material into wells of a chip or plate, followed by delivery of linker nucleic acids into the partitions, either unamplified or amplified as discussed above.

[00104] Alternately, in some cases delivery of linker nucleic acids is not temporally separated from partitioning. Rather, linker nucleic acids or an enzymatic activity or factor necessary for enzymatic activity is sequestered until a particular treatment, such as heat, electromagnetic activation, or other administration so as to temporally activate the enzymatic activity leading to covalent binding of the linker to the nucleic acid sample exposed ends, such as via the linker.

[00105] A number of integration enzymes are consistent with the disclosure herein. PhiC31 integrase, such as that commercially available by ThermoFisher, exhibits a number of benefits for the practice of the methods, operation of the systems and for use in the compositions herein. Some benefits of this integrase are as follows. It uses the small integration sites (attB / attP). The enzyme itself is a small single polypeptide. Integration is irreversible without use of a separate enzyme to excise integration events. Activity is high, and the enzyme is readily engineered to alter activity. Nonetheless, its use is not required to the exclusion of other enzymes, as a number of integration systems are consistent with the disclosure herein. Aspects of the present disclosure may be described with respect to PhiC31 integrase, though use of any compatible enzymes is contemplated.

[00106] A number of transposase enzymes are consistent with the disclosure herein. Tn5 transposase, such as that commercially available by Lucigen, exhibits a number of benefits for the practice of the methods, operation of the systems, and for use in the compositions herein. Some benefits of this transposase are as follows: Tn5 uses a 19 bp mosaic end recognition sequence, insertions have little bias and are stable, and Tn5 can be delivered to cells for in vivo transposition or isolated nucleic acids for in vitro reactions. Nonetheless, its use is not required to the exclusion of other enzymes, as a number of transposase systems, such as Tn3, Tn7, or sleeping beauty transposase are consistent with the disclosure herein. Aspects of the

present disclosure may be described with respect to Tn3, Tn5, Tn7, or sleeping beauty transposase, though use of any compatible enzyme is contemplated.

[00107] Sequence information obtained from library constituents is assessed through a number of approaches, such as those in the context of Hi-C, Chicago® *in vitro* proximity ligation or other three-dimensional conformational analysis. Importantly, cell-specific read pair frequencies can be obtained, such that the frequency of end adjacent sequence mapping to particular regions of a genome or particular contig can be assessed on a cell-specific basis. That is, one is able to assess the cell-specific occurrence of a likely three-dimensional conformation. In some cases, one is also able to assess the cell-specific strength of signal, correlating to cell-specific distance in the three dimensional conformation, such that one is able to conclude that certain regions of a nucleic acid are in relatively close proximity in one cell relative to a second cell where they are in comparable but ‘weaker’ or more distant proximity, while in a third cell there is no signal indicative of proximity. That is, both qualitative and quantitative assessments of three-dimensional configuration are consistent with the disclosure herein. In some cases, the proximity of one region to a second region is assessed at least in part by counting the number of cluster constituents of a first cluster that co-occur in paired end reads with cluster constituents of a second cluster, particularly in library constituents sharing a common partition-distinguishing sequence such as a unique partition tag.

[00108] Configuration information need not be made through multiple occurrence of identical end-adjacent sequence in multiple library constituents. Rather, in some cases end adjacent sequence that maps to near a second end adjacent sequence mapping site (to a common ‘cluster’) can re-enforce three-dimensional conformation assessments when both members of the cluster map to non-identical regions of a second cluster on a second region of an nucleic acid reference such as a genome.

[00109] In some cases, the methods disclosed herein are used to label and/or associate polynucleotides or sequence segments thereof, and to utilize that data for various applications. In some cases, the disclosure provides methods that produce a highly contiguous and accurate human genomic assembly with less than about 10,000, about 20,000, about 50,000, about 100,000, about 200,000, about 500,000, about 1 million, about 2 million, about 5 million, about 10 million, about 20 million, about 30 million, about 40 million, about 50 million, about 60 million, about 70 million, about 80 million, about 90 million, about 100 million, about 200 million, about 300 million, about 400 million, about 500 million, about 600 million, about 700 million, about 800 million, about 900 million, or about 1 billion read pairs. In some cases, the disclosure provides methods that phase, or assign physical linkage information to, about 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more of heterozygous variants in a human genome with about 50%, 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater accuracy.

[00110] In some embodiments, the compositions and methods described herein allow for the investigation of meta-genomes, for example those found in the human gut. Accordingly, the partial or whole genomic sequences of some or all organisms that inhabit a given ecological environment can be investigated. Examples include random sequencing of all gut microbes, the microbes found on certain areas of skin, and the microbes that live in toxic waste sites. The composition of the microbe population in these

environments can be determined using the compositions and methods described herein and as well as the aspects of interrelated biochemistries encoded by their respective genomes. The methods described herein can enable metagenomic studies from complex biological environments, for example, those that comprise more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 5000, 10000 or more organisms and/or variants of organisms.

[00111] Accordingly, methods disclosed herein may be applied to intact human genomic DNA samples but may also be applied to a broad diversity of nucleic acid samples, such as reverse-transcribed RNA samples, circulating free DNA samples, cancer tissue samples, crime scene samples, archaeological samples, nonhuman genomic samples, or environmental samples such as environmental samples comprising genetic information from more than one organism, such as an organism that is not easily cultured under laboratory conditions.

[00112] High degrees of accuracy required by cancer genome sequencing can be achieved using the methods and systems described herein. Inaccurate reference genomes can make base-calling challenges when sequencing cancer genomes. Heterogeneous samples and small starting materials, for example a sample obtained by biopsy introduce additional challenges. Further, detection of large-scale structural variants and/or losses of heterozygosity is often crucial for cancer genome sequencing, as well as the ability to differentiate between somatic variants and errors in base-calling.

[00113] Systems and methods described herein may generate accurate long sequences from complex samples containing 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20 or more varying genomes. Mixed samples of normal, benign, and/or tumor origin may be analyzed, optionally without the need for a normal control. In some embodiments, starting samples as little as 100ng or even as little as hundreds of genome equivalents are utilized to generate accurate long sequences. Systems and methods described herein may allow for detection of large scale structural variants and rearrangements. Phased variant calls may be obtained over long sequences spanning about 1 kbp, about 2 kbp, about 5 kbp, about 10 kbp, about 20 kbp, about 50 kbp, about 100 kbp, about 200 kbp, about 500 kbp, about 1 Mbp, about 2 Mbp, about 5 Mbp, about 10 Mbp, about 20 Mbp, about 50 Mbp, or about 100 Mbp or more nucleotides. For example, phase variant call may be obtained over long sequences spanning about 1 Mbp or about 2 Mbp.

[00114] In certain aspects, the methods disclosed herein are used to assemble a plurality of contigs originating from a single DNA molecule. In some cases, the method comprises generating a plurality of read-pairs from the single DNA molecule that is cross-linked to a plurality of nanoparticles and assembling the contigs using the read-pairs. In certain cases, single DNA molecule is cross-linked outside of a cell. In some cases, at least 0.1%, 0.2%, 0.3%, 0.4%, 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, or 50% of the read-pairs span a distance greater than 1kB, 2kB, 3kB, 4kB, 5kB, 6kB, 7kB, 8kB, 9kB, 10kB, 15kB, 20kB, 30kB, 40kB, 50kB, 60kB, 70kB, 80kB, 90kB, 100kB, 150kB, 200kB, 250kB, 300kB, 400kB, 500kB, 600kB, 700kB, 800kB, 900kB, or 1MB on the single DNA molecule. In certain cases, at least 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, or 20% of the read-pairs span a distance greater than 5kB,

6kB, 7kB, 8kB, 9kB, 10kB, 15kB, 20kB, 30kB, 40kB, 50kB, 60kB, 70kB, 80kB, 90kB, 100kB, 150kB, or 200kB on the single DNA molecule. In further cases, at least 0.5%, 0.6%, 0.7%, 0.8%, 0.9%, 1%, 2%, 3%, 4%, or 5% of the read-pairs span a distance greater than 20kB, 30kB, 40kB, 50kB, 60kB, 70kB, 80kB, 90kB, or 100kB on the single DNA molecule. In particular cases, at least 1% or 5% of the read pairs span a distance greater than 50kB or 100kB on the single DNA molecule. In some cases, the read-pairs are generated within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 30, 40, 50 or 60 days. In certain cases, the read-pairs are generated within 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 or 18 days. In further cases, the read-pairs are generated within 7, 8, 9, 10, 11, 12, 13, or 14 days. In particular cases, the read-pairs are generated within 7 or 14 days.

[00115] Haplotypes determined using the methods and systems described herein may be assigned to computational resources, for example computational resources over a network, such as a cloud system. Short variant calls can be corrected, if necessary, using relevant information that is stored in the computational resources. Structural variants can be detected based on the combined information from short variant calls and the information stored in the computational resources. Problematic parts of the genome, such as segmental duplications, regions prone to structural variation, the highly variable and medically relevant MHC region, centromeric and telomeric regions, and other heterochromatic regions including those with repeat regions, low sequence accuracy, high variant rates, ALU repeats, segmental duplications, or any other relevant problematic parts, can be reassembled for increased accuracy.

[00116] A sample type can be assigned to the sequence information either locally or in a networked computational resource, such as a cloud. In cases where the source of the information is known, for example when the source of the information is from a cancer or normal tissue, the source can be assigned to the sample as part of a sample type. Other sample type examples generally include, but are not limited to, tissue type, sample collection method, presence of infection, type of infection, processing method, size of the sample, etc. In cases where a complete or partial comparison genome sequence is available, such as a normal genome in comparison to a cancer genome, the differences between the sample data and the comparison genome sequence can be determined and optionally output.

[00117] The methods of the present disclosure can be used in the analysis of genetic information of selective genomic regions of interest as well as genomic regions which may interact with the selective region of interest. Amplification methods as disclosed herein can be used in the devices, kits, and methods for genetic analysis, such as, but not limited to those found in U.S. Pat. Nos. 6,449,562, 6,287,766, 7,361,468, 7,414,117, 6,225,109, and 6,110,709. In some cases, amplification methods of the present disclosure can be used to amplify target nucleic acid for DNA hybridization studies to determine the presence or absence of polymorphisms. The polymorphisms, or alleles, can be associated with diseases or conditions such as genetic disease. In some other cases, the polymorphisms can be associated with susceptibility to diseases or conditions, for example, polymorphisms associated with addiction, degenerative and age related conditions, cancer, and the like. In other cases, the polymorphisms can be associated with beneficial traits such as increased coronary health, or resistance to diseases such as HIV or malaria, or resistance to degenerative diseases such as osteoporosis, Alzheimer's, or dementia.

[00118] The compositions and methods of the disclosure can be used for diagnostic, prognostic, therapeutic, patient stratification, drug development, treatment selection, and screening purposes. The present disclosure provides the advantage that many different target molecules can be analyzed at one time from a single biomolecular sample using the methods of the disclosure. This allows, for example, for several diagnostic tests to be performed on one sample.

[00119] The methods provided herein can greatly advance the field of genomics by overcoming the substantial barriers posed by these repetitive regions and can thereby enable important advances in many domains of genomic analysis. To perform a *de novo* assembly with previous technologies, one must either settle for an assembly fragmented into many small scaffolds or commit substantial time and resources to producing a large-insert library or using other approaches to generate a more contiguous assembly. Such approaches may include acquiring very deep sequencing coverage, constructing BAC or fosmid libraries, optical mapping, or, most likely, some combination of these and other techniques. The intense resource and time requirements put such approaches out of reach for most small labs and prevents studying non-model organisms. Since the methods described herein can produce very long-range read-sets, *de novo* assembly may be achieved with a single sequencing run. This cuts assembly costs by orders of magnitude and shorten the time required from months or years to weeks. In some cases, the methods disclosed herein allow for generating a plurality of read-sets in less than 14 days, less than 13 days, less than 12 days, less than 11 days, less than 10 days, less than 9 days, less than 8 days, less than 7 days, less than 6 days, less than 5 days, less than 4 days, less than 3 days, less than 2 days, less than 1 day or in a range between any two of foregoing specified time periods. In some cases, the methods allow for generating a plurality of read-sets in about 10 days to 14 days. Building genomes for even the most niche of organisms would become routine, phylogenetic analyses would suffer no lack of comparisons, and projects such as Genome 10k could be realized.

[00120] The methods described herein allow for assignment of previously provided, previously generated, or *de novo* synthesized contig information into physical linkage groups such as chromosomes or shorter contiguous nucleic acid molecules. Similarly, the methods disclosed herein allow said contigs to be positioned relative to one another in linear order along a physical nucleic acid molecule. Similarly, the methods disclosed herein allow said contigs to be oriented relative to one another in linear order along a physical nucleic acid molecule.

[00121] Similarly, the methods disclosed herein can provide advances in structural and phasing analyses for medical purposes. There is astounding heterogeneity among cancers, individuals with the same type of cancer, or even within the same tumor. Teasing out the causative from consequential effects requires very high precision and throughput at a low per-sample cost. In the domain of personalized medicine, one of the gold standards of genomic care is a sequenced genome with all variants thoroughly characterized and phased, including large and small structural rearrangements and novel mutations. To achieve this with previous technologies demands effort akin to that required for a *de novo* assembly, which is currently too expensive and laborious to be a routine medical procedure. In some cases, the methods disclosed herein

rapidly produce complete, accurate genomes at low cost and thereby yield many highly sought capabilities in the study and treatment of human disease.

[00122] Further, applying the methods disclosed herein to phasing can combine the convenience of statistical approaches with the accuracy of familial analysis, providing savings – money, labor, and samples – greater than those using either method alone. De novo variant phasing, a highly desirable phasing analysis that is prohibitive with previous technologies, can be performed readily using the methods disclosed herein. This is particularly important as the vast majority of human variation is rare (less than 5% minor allele frequency). Phasing information is valuable for population genetic studies that gain significant advantages from networks of highly connected haplotypes (collections of variants assigned to a single chromosome), relative to unlinked genotypes. Haplotype information may enable higher resolution studies of historical changes in population size, migrations, and exchange between subpopulations, and allows us to trace specific variants back to particular parents and grandparents. This in turn clarifies the genetic transmission of variants associated with disease, and the interplay between variants when brought together in a single individual. In further cases, the methods of the disclosure enable the preparation, sequencing, and analysis of extremely long range read-set (XLRS) or extremely long range read-pair (XLRP) libraries.

[00123] In some embodiments of the disclosure, a tissue or a DNA sample from a subject is provided and the method returns an assembled genome, alignments with called variants (including large structural variants), phased variant calls, or any additional analyses. In other embodiments, the methods disclosed herein provide XLRP libraries directly for the individual.

[00124] In various embodiments, the methods disclosed herein generate extremely long-range read pairs separated by large distances. The upper limit of this distance may be improved by the ability to collect DNA samples of large size. In some cases, the read pairs span up to 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 4000, 5000 kbp or more in genomic distance. In some cases, the read pairs span up to 500 kbp in genomic distance. In other cases, the read pairs span up to 2000 kbp in genomic distance. The methods disclosed herein can integrate and build upon standard techniques in molecular biology, and are further well-suited for increases in efficiency, specificity, and genomic coverage. In some cases, the read pairs are generated in less than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 60, or 90 days. In some cases, the read pairs are generated in less than about 14 days. In further cases, the read pairs are generated in less about 10 days. In some cases, the methods of the present disclosure provide greater than about 5%, about 10%, about 15 %, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, or about 100% of the read pairs with at least about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, or about 100% accuracy in correctly ordering and/or orientating the plurality of contigs. In some cases, the methods provide about 90 to 100% accuracy in correctly ordering and/or orientating the plurality of contigs.

[00125] In other embodiments, the methods disclosed herein are used with currently employed sequencing technology. In some cases, the methods are used in combination with well-tested and/or widely deployed sequencing instruments. In further embodiments, the methods disclosed herein are used with technologies and approaches derived from currently employed sequencing technology.

[00126] The methods disclosed herein can dramatically simplify de novo genomic assembly for a wide range of organisms. Using previous technologies, such assemblies are currently limited by the short inserts of economical mate-pair libraries. While it may be possible to generate read pairs at genomic distances up to the 40-50 kbp accessible with fosmids, these are expensive, cumbersome, and too short to span the longest repetitive stretches, including those within centromeres, which in humans range in size from 300 kbp to 5 Mbp. In some cases, the methods disclosed herein provide read pairs capable of spanning large distances (e.g., megabases or longer) and thereby overcome these scaffold integrity challenges. Accordingly, producing chromosome-level assemblies may be routine by utilizing the methods disclosed herein. Similarly, the acquisition of long-range phasing information can provide tremendous additional power to population genomic, phylogenetic, and disease studies. In certain cases, the methods disclosed herein enable accurate phasing for large numbers of individuals, thus extending the breadth and depth of our ability to probe genomes at the population and deep-time levels.

[00127] In the realm of personalized medicine, the XLRs read-sets generated from the methods disclosed herein represents a meaningful advance toward accurate, low-cost, phased, and rapidly produced personal genomes. Previous methods are insufficient in their ability to phase variants at long distances, thereby preventing the characterization of the phenotypic impact of compound heterozygous genotypes. Additionally, structural variants of substantial interest for genomic diseases are difficult to accurately identify and characterize with previous techniques due to their large size in comparison to the reads and read inserts used to study them. Read-sets spanning tens of kilobases to megabases or longer can help alleviate this difficulty, thereby allowing for highly parallel and personalized analyses of structural variation.

[00128] Basic evolutionary and biomedical research can be driven by technological advances in high-throughput sequencing. It is now relatively inexpensive to generate massive quantities of DNA sequence data. However, it is difficult in theory and in practice to produce high-quality, highly contiguous genome sequences with previous technologies. Further, many organisms, including humans, are diploid, wherein each individual has two haploid copies of the genome. At sites of heterozygosity (e.g., where the allele given by the mother differs from the allele given by the father), it is difficult to know which sets of alleles came from which parent (known as haplotype phasing). This information can be critically important for performing a number of evolutionary and biomedical studies such as disease and trait association studies.

[00129] The present disclosure provides methods for genome assembly that combine technologies for DNA preparation with tagged sequence reads for high-throughput discovery of short, intermediate, and long-term connections corresponding to sequence reads from a single physical nucleic acid molecule bound to a complex such as a chromatin complex within a given genome. The disclosure further provides methods using these connections to assist in genome assembly, for haplotype phasing, and/or for

metagenomic studies. While the methods presented herein can be used to determine the assembly of a subject's genome, it should also be understood that in certain cases the methods presented herein are used to determine the assembly of portions of the subject's genome such as chromosomes, or the assembly of the subject's chromatin of varying lengths. It should also be understood that, in certain cases, the methods presented herein are used to determine or direct the assembly of non-chromosomal nucleic acid molecules. Indeed, any nucleic acid the sequencing of which is complicated by the presence of repetitive regions separating non-repetitive contigs may be facilitated using the methods disclosed herein.

[00130]In further cases, the methods disclosed herein allow for accurate and predictive results for genotype assembly, haplotype phasing, and metagenomics with small amounts of materials. In some cases, less than about 100 picograms (pg), about 200 pg, about 300 pg, about 400 pg, about 500 pg, about 600 pg, about 700 pg, about 800 pg, about 900 pg, about 1.0 nanograms (ng), about 2.0 ng, about 3.0 ng, about 4.0 ng, about 5.0 ng, about 6.0 ng, about 7.0 ng, about 8.0 ng, about 9.0 ng, about 10 ng, about 15 ng, about 20 ng, about 30 ng, about 40 ng, about 50 ng, about 60 ng, about 70 ng, about 80 ng, about 90 ng, about 100 ng, about 200 ng, about 300 ng, about 400 ng, about 500 ng, about 600 ng, about 700 ng, about 800 ng, about 900 ng, about 1.0 micrograms (μg), about 1.2 μg, about 1.4 μg, about 1.6 μg, about 1.8 μg, about 2.0 μg, about 2.5 μg, about 3.0 μg, about 3.5 μg, about 4.0 μg, about 4.5 μg, about 5.0 μg, about 6.0 μg, about 7.0 μg, about 8.0 μg, about 9.0 μg, about 10 μg, about 15 μg, about 20 μg, about 30 μg, about 40 μg, about 50 μg, about 60 μg, about 70 μg, about 80 μg, about 90 μg, about 100 μg, about 150 μg, about 200 μg, about 300 μg, about 400 μg, about 500 μg, about 600 μg, about 700 μg, about 800 μg, about 900 μg, or about 1000 μg of DNA is used with the methods disclosed herein. In some cases, the DNA used in the methods disclosed herein is extracted from less than about 10,000,000, about 5,000,000, about 4,000,000, about 3,000,000, about 2,000,000, about 1,000,000, about 500,000, about 200,000, about 100,000, about 50,000, about 20,000, about 10,000, about 5,000, about 2,000, about 1,000, about 500, about 200, about 100, about 50, about 20, or about 10 cells.

[00131]In diploid genomes, it often important to know which allelic variants are physically linked on the same chromosome rather than mapping to the homologous position on a chromosome pair. Mapping an allele or other sequence to a specific physical chromosome of a diploid chromosome pair is known as the haplotype phasing. Short reads from high-throughput sequence data rarely allow one to directly observe which allelic variants are linked, particularly, as is most often the case, if the allelic variants are separated by a greater distance than the longest single read. Computational inference of haplotype phasing can be unreliable at long distances. Methods disclosed herein allow for determining which allelic variants are physically linked using allelic variants on read pairs.

[00132]In various cases, the methods and compositions of the disclosure enable the haplotype phasing of diploid or polyploid genomes with regard to a plurality of allelic variants. Methods described herein thus provide for the determination of linked allelic variants based on variant information from labeled sequence segments and/or assembled contigs using the same. Cases of allelic variants include, but are not limited to, those that are known from the 1000genomes, UK10K, HapMap and other projects for discovering genetic variation among humans. In some cases, disease association to a specific gene are

revealed more easily by having haplotype phasing data as demonstrated, for example, by the finding of unlinked, inactivating mutations in both copies of SH3TC2 leading to Charcot-Marie-Tooth neuropathy (Lupski JR, Reid JG, Gonzaga-Jauregui C, et al. N. Engl. J. Med. 362:1181–91, 2010) and unlinked, inactivating mutations in both copies of ABCG5 leading to hypercholesterolemia 9 (Rios J, Stein E, Shendure J, et al. Hum. Mol. Genet. 19:4313–18, 2010).

[00133] Humans are heterozygous at an average of 1 site in 1,000. In some cases, a single lane of data using high throughput sequencing methods generates at least about 150,000,000 reads. In further cases, individual reads are about 100 base pairs long. If we assume input DNA fragments average 150 kbp in size and we get 100 paired-end reads per fragment, then we expect to observe 30 heterozygous sites per set, i.e., per 100 read-pairs. Every read-pair containing a heterozygous site within a set is in phase (i.e., molecularly linked) with respect to all other read-pairs within the same set. This property enables greater power for phasing with sets as opposed to singular pairs of reads in some cases. With approximately 3 billion bases in the human genome, and one in one-thousand being heterozygous, there are approximately 3 million heterozygous sites in an average human genome. With about 45,000,000 read pairs that contain heterozygous sites, the average coverage of each heterozygous site to be phased using a single lane of a high throughput sequence method is about (15X), using a typical high throughput sequencing machine. A diploid human genome can therefore be reliably and completely phased with one lane of a high-throughput sequence data relating sequence variants from a sample that is prepared using the methods disclosed herein. In some cases, a lane of data is a set of DNA sequence read data. In further cases, a lane of data is a set of DNA sequence read data from a single run of a high throughput sequencing instrument.

[00134] As the human genome consists of two homologous sets of chromosomes, understanding the true genetic makeup of an individual requires delineation of the maternal and paternal copies or haplotypes of the genetic material. Obtaining a haplotype in an individual is useful in several ways. For example, haplotypes are useful clinically in predicting outcomes for donor-host matching in organ transplantation. Haplotypes are increasingly used to detect disease associations. In genes that show compound heterozygosity, haplotypes provide information as to whether two deleterious variants are located on the same allele (that is, ‘in cis’, to use genetics terminology) or on two different alleles (‘in trans’), greatly affecting the prediction of whether inheritance of these variants is harmful, and impacting conclusions as to whether an individual carries a functional allele and a single nonfunctional allele having two deleterious variant positions, or whether that individual carries two nonfunctional alleles, each with a different defect. Haplotypes from groups of individuals have provided information on population structure of interest to both epidemiologists and anthropologists and informative of the evolutionary history of the human race. In addition, widespread allelic imbalances in gene expression have been reported, and suggest that genetic or epigenetic differences between allele phase may contribute to quantitative differences in expression. An understanding of haplotype structure will delineate the mechanisms of variants that contribute to allelic imbalances.

[00135] In certain embodiments, the methods disclosed herein comprise an in vitro technique to fix and capture associations among distant regions of a genome as needed for long-range linkage and phasing. In

some cases, the method comprises constructing and sequencing one or more read-sets to deliver very genomically distant read pairs. In further cases, each read-set comprises two or more reads that are labeled by a common barcode, which may represent two or more sequence segments from a common polynucleotide. In some cases, the interactions primarily arise from the random associations within a single polynucleotide. In some cases, the genomic distance between sequence segments are inferred because sequence segments near to each other in a polynucleotide interact more often and with higher probability, while interactions between distant portions of the molecule are less frequent. Consequently, there is a systematic relationship between the number of pairs connecting two loci and their proximity on the input DNA.

[00136] In some aspects, the disclosure provides methods and compositions that produce data to achieve extremely high phasing accuracy. In comparison to previous methods, the methods described herein can phase a higher proportion of the variants. In some cases, phasing is achieved while maintaining high levels of accuracy. In further cases, this phase information is extended to longer ranges, for example greater than about 200 kbp, about 300 kbp, about 400 kbp, about 500 kbp, about 600 kbp, about 700 kbp, about 800 kbp, about 900 kbp, about 1 Mbp, about 2 Mbp, about 3 Mbp, about 4 Mbp, about 5 Mbp, or about 10 Mbp, or longer than about 10 Mbp, up to and including the entire length of a chromosome. In some embodiments, more than 90% of the heterozygous SNPs for a human sample is phased at an accuracy greater than 99% using less than about 250 million reads, e.g., by using only 1 lane of Illumina HiSeq data. In other cases, more than about 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of the heterozygous SNPs for a human sample is phased at an accuracy greater than about 70%, 80%, 90%, 95%, or 99% using less than about 250 million or about 500 million reads, e.g., by using only 1 or 2 lanes of Illumina HiSeq data. In some cases, more than 95% or 99% of the heterozygous SNPs for a human sample are phased at an accuracy greater than about 95% or 99% using less about 250 million or about 500 million reads. In further cases, additional variants are captured by increasing the read length to about 200 bp, 250 bp, 300 bp, 350 bp, 400 bp, 450 bp, 500 bp, 600 bp, 800 bp, 1000 bp, 1500 bp, 2 kbp, 3 kbp, 4 kbp, 5 kbp, 10 kbp, 20 kbp, 50 kbp, or 100 kbp.

[00137] The composition and methods of the disclosure can be used in gene expression analysis. The methods described herein discriminate between nucleotide sequences. The difference between the target nucleotide sequences can be, for example, a single nucleic acid base difference, a nucleic acid deletion, a nucleic acid insertion, or rearrangement. Such sequence differences involving more than one base can also be detected. The process of the present disclosure is able to detect infectious diseases, genetic diseases, and cancer. It is also useful in environmental monitoring, forensics, and food science. Examples of genetic analyses that can be performed on nucleic acids include, e.g., SNP detection, STR detection, RNA expression analysis, promoter methylation, gene expression, virus detection, viral subtyping, and drug resistance.

[00138] The present methods can be applied to the analysis of biomolecular samples obtained or derived from a patient so as to determine whether a diseased cell type is present in the sample, the stage of the disease, the prognosis for the patient, the ability to the patient to respond to a particular treatment, or the

best treatment for the patient. The present methods can also be applied to identify biomarkers for a particular disease.

[00139]In some embodiments, the methods described herein are used in the diagnosis of a condition. As used herein the term “diagnose” or “diagnosis” of a condition may include predicting or diagnosing the condition, determining predisposition to the condition, monitoring treatment of the condition, diagnosing a therapeutic response of the disease, or prognosis of the condition, condition progression, or response to particular treatment of the condition. For example, a blood sample can be assayed according to any of the methods described herein to determine the presence and/or quantity of markers of a disease or malignant cell type in the sample, thereby diagnosing or staging a disease or a cancer.

[00140]In some embodiments, the methods and composition described herein are used for the diagnosis and prognosis of a condition.

[00141]Numerous immunologic, proliferative, and malignant diseases and disorders are especially amenable to the methods described herein. Immunologic diseases and disorders include allergic diseases and disorders, disorders of immune function, and autoimmune diseases and conditions. Allergic diseases and disorders include but are not limited to allergic rhinitis, allergic conjunctivitis, allergic asthma, atopic eczema, atopic dermatitis, and food allergy. Immunodeficiencies include but are not limited to severe combined immunodeficiency (SCID), hypereosinophilic syndrome, chronic granulomatous disease, leukocyte adhesion deficiency I and II, hyper IgE syndrome, Chediak Higashi, neutrophilias, neutropenias, aplasias, Agammaglobulinemia, hyper-IgM syndromes, DiGeorge/Velocardial-facial syndromes and Interferon gamma-TH1 pathway defects. Autoimmune and immune dysregulation disorders include but are not limited to rheumatoid arthritis, diabetes, systemic lupus erythematosus, Graves' disease, Graves ophthalmopathy, Crohn's disease, multiple sclerosis, psoriasis, systemic sclerosis, goiter and struma lymphomatosa (Hashimoto's thyroiditis, lymphadenoid goiter), alopecia aerata, autoimmune myocarditis, lichen sclerosis, autoimmune uveitis, Addison's disease, atrophic gastritis, myasthenia gravis, idiopathic thrombocytopenic purpura, hemolytic anemia, primary biliary cirrhosis, Wegener's granulomatosis, polyarteritis nodosa, and inflammatory bowel disease, allograft rejection and tissue destructive from allergic reactions to infectious microorganisms or to environmental antigens.

[00142]Proliferative diseases and disorders that may be evaluated by the methods of the disclosure include, but are not limited to, hemangiomatosis in newborns; secondary progressive multiple sclerosis; chronic progressive myelodegenerative disease; neurofibromatosis; ganglioneuromatosis; keloid formation; Paget's Disease of the bone; fibrocystic disease (e.g., of the breast or uterus); sarcoidosis; Peronies and Duputren's fibrosis, cirrhosis, atherosclerosis, and vascular restenosis.

[00143]Malignant diseases and disorders that may be evaluated by the methods of the disclosure include both hematologic malignancies and solid tumors.

[00144]Hematologic malignancies are especially amenable to the methods of the disclosure when the sample is a blood sample, because such malignancies involve changes in blood-borne cells. Such malignancies include non-Hodgkin's lymphoma, Hodgkin's lymphoma, non-B cell lymphomas, and other lymphomas, acute or chronic leukemias, polycythemia, thrombocythemia, multiple myeloma,

myelodysplastic disorders, myeloproliferative disorders, myelofibroses, atypical immune lymphoproliferations and plasma cell disorders.

[00145] Plasma cell disorders that may be evaluated by the methods of the disclosure include multiple myeloma, amyloidosis and Waldenstrom's macroglobulinemia.

[00146] Examples of solid tumors include, but are not limited to, colon cancer, breast cancer, lung cancer, prostate cancer, brain tumors, central nervous system tumors, bladder tumors, melanomas, liver cancer, osteosarcoma and other bone cancers, testicular and ovarian carcinomas, head and neck tumors, and cervical neoplasms.

[00147] Genetic diseases can also be detected by the process of the present disclosure. This can be carried out by prenatal or post-natal screening for chromosomal and genetic aberrations or for genetic diseases. Examples of detectable genetic diseases include: 21 hydroxylase deficiency, cystic fibrosis, Fragile X Syndrome, Turner Syndrome, Duchenne Muscular Dystrophy, Down Syndrome or other trisomies, heart disease, single gene diseases, HLA typing, phenylketonuria, sickle cell anemia, Tay-Sachs Disease, thalassemia, Klinefelter Syndrome, Huntington Disease, autoimmune diseases, lipidosis, obesity defects, hemophilia, inborn errors of metabolism, and diabetes.

[00148] The methods described herein can be used to diagnose pathogen infections, for example infections by intracellular bacteria and viruses, by determining the presence and/or quantity of markers of bacterium or virus, respectively, in the sample.

[00149] A wide variety of infectious diseases can be detected by the process of the present disclosure. The infectious diseases can be caused by bacterial, viral, parasite, and fungal infectious agents. The resistance of various infectious agents to drugs can also be determined using the present disclosure.

[00150] Bacterial infectious agents which can be detected by the present disclosure include *Escherichia coli*, *Salmonella*, *Shigella*, *Klebsiella*, *Pseudomonas*, *Listeria monocytogenes*, *Mycobacterium tuberculosis*, *Mycobacterium aviumintracellulare*, *Yersinia*, *Francisella*, *Pasteurella*, *Brucella*, *Clostridia*, *Bordetella pertussis*, *Bacteroides*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, B-Hemolytic strep., *Corynebacteria*, *Legionella*, *Mycoplasma*, *Ureaplasma*, *Chlamydia*, *Neisseria gonorrhea*, *Neisseria meningitidis*, *Hemophilus influenza*, *Enterococcus faecalis*, *Proteus vulgaris*, *Proteus mirabilis*, *Helicobacter pylori*, *Treponema palladium*, *Borrelia burgdorferi*, *Borrelia recurrentis*, Rickettsial pathogens, *Nocardia*, and *Acitnomyces*.

[00151] Fungal infectious agents which can be detected by the present disclosure include *Cryptococcus neoformans*, *Blastomyces dermatitidis*, *Histoplasma capsulatum*, *Coccidioides immitis*, *Paracoccidioides brasiliensis*, *Candida albicans*, *Aspergillus fumigatus*, *Phycomycetes* (*Rhizopus*), *Sporothrix schenckii*, *Chromomycosis*, and *Maduromycosis*.

[00152] Viral infectious agents which can be detected by the present disclosure include human immunodeficiency virus, human T-cell lymphocytotropic virus, hepatitis viruses (e.g., Hepatitis B Virus and Hepatitis C Virus), Epstein-Barr virus, cytomegalovirus, human papillomaviruses, orthomyxo viruses, paramyxo viruses, adenoviruses, corona viruses, rhabdo viruses, polio viruses, toga viruses, bunya viruses, arena viruses, rubella viruses, and reo viruses.

[00153] Parasitic agents which can be detected by the present disclosure include *Plasmodium falciparum*, *Plasmodium malaria*, *Plasmodium vivax*, *Plasmodium ovale*, *Onchocerca volvulus*, *Leishmania*, *Trypanosoma* spp., *Schistosoma* spp., *Entamoeba histolytica*, *Cryptosporidium*, *Giardia* spp., *Trichomonas* spp., *Balantidium coli*, *Wuchereria bancrofti*, *Toxoplasma* spp., *Enterobius vermicularis*, *Ascaris lumbricoides*, *Trichuris trichiura*, *Dracunculus medinensis*, trematodes, *Diphyllobothrium latum*, *Taenia* spp., *Pneumocystis carinii*, and *Necator americanus*.

[00154] The present disclosure is also useful for detection of drug resistance by infectious agents. For example, vancomycin-resistant *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus*, penicillin-resistant *Streptococcus pneumoniae*, multi-drug resistant *Mycobacterium tuberculosis*, and AZT-resistant human immunodeficiency virus can all be identified with the present disclosure.

[00155] Thus, the target molecules detected using the compositions and methods of the disclosure can be either patient markers (such as a cancer marker) or markers of infection with a foreign agent, such as bacterial or viral markers.

[00156] The compositions and methods of the disclosure can be used to identify and/or quantify a target molecule whose abundance is indicative of a biological state or disease condition, for example, blood markers that are upregulated or downregulated as a result of a disease state.

[00157] In some embodiments, the methods and compositions of the present disclosure can be used for cytokine expression. The low sensitivity of the methods described herein would be helpful for early detection of cytokines, e.g., as biomarkers of a condition, diagnosis, or prognosis of a disease such as cancer, and the identification of subclinical conditions.

[00158] The different samples from which the target polynucleotides are derived can comprise multiple samples from the same individual, samples from different individuals, or combinations thereof. In some embodiments, a sample comprises a plurality of polynucleotides from a single individual. In some embodiments, a sample comprises a plurality of polynucleotides from two or more individuals. An individual is any organism or portion thereof from which target polynucleotides can be derived, non-limiting examples of which include plants, animals, fungi, protists, monerans, viruses, mitochondria, and chloroplasts. Sample polynucleotides can be isolated from a subject, such as a cell sample, tissue sample, or organ sample derived therefrom, including, for example, cultured cell lines, biopsy, blood sample, or fluid sample containing a cell. The subject may be an animal, including but not limited to, an animal such as a cow, a pig, a mouse, a rat, a chicken, a cat, a dog, etc., and is usually a mammal, such as a human. Samples can also be artificially derived, such as by chemical synthesis. In some embodiments, the samples comprise DNA. In some embodiments, the samples comprise genomic DNA. In some embodiments, the samples comprise mitochondrial DNA, chloroplast DNA, plasmid DNA, bacterial artificial chromosomes, yeast artificial chromosomes, oligonucleotide tags, or combinations thereof. In some embodiments, the samples comprise DNA generated by primer extension reactions using any suitable combination of primers and a DNA polymerase, including but not limited to polymerase chain reaction (PCR), reverse transcription, and combinations thereof. Where the template for the primer extension reaction is RNA, the product of reverse transcription is referred to as complementary DNA

(cDNA). Primers useful in primer extension reactions can comprise sequences specific to one or more targets, random sequences, partially random sequences, and combinations thereof. Reaction conditions suitable for primer extension reactions are known. In general, sample polynucleotides comprise any polynucleotide present in a sample, which may or may not include target polynucleotides.

[00159]In some embodiments, nucleic acid template molecules (e.g., DNA or RNA) are isolated from a biological sample containing a variety of other components, such as proteins, lipids, and non-template nucleic acids. Nucleic acid template molecules can be obtained from any cellular material, obtained from an animal, plant, bacterium, fungus, or any other cellular organism. Biological samples for use in the present disclosure include viral particles or preparations. Nucleic acid template molecules can be obtained directly from an organism or from a biological sample obtained from an organism, e.g., from blood, urine, cerebrospinal fluid, seminal fluid, saliva, sputum, stool, and tissue. Any tissue or body fluid specimen may be used as a source for nucleic acid for use in the disclosure. Nucleic acid template molecules can also be isolated from cultured cells, such as a primary cell culture or a cell line. The cells or tissues from which template nucleic acids are obtained can be infected with a virus or other intracellular pathogen. A sample can also be total RNA extracted from a biological specimen, a cDNA library, viral, or genomic DNA. A sample may also be isolated DNA from a non-cellular origin, e.g., amplified/isolated DNA from the freezer.

[00160]Methods for the extraction and purification of nucleic acids are known. For example, nucleic acids can be purified by organic extraction with phenol, phenol/chloroform/isoamyl alcohol, or similar formulations, including TRIzol and TriReagent. Other non-limiting examples of extraction techniques include: (1) organic extraction followed by ethanol precipitation, e.g., using a phenol/chloroform organic reagent (Ausubel *et al.*, 1993), with or without the use of an automated nucleic acid extractor, e.g., the Model 341 DNA Extractor available from Applied Biosystems (Foster City, Calif.); (2) stationary phase adsorption methods (U.S. Pat. No. 5,234,809; Walsh *et al.*, 1991); and (3) salt-induced nucleic acid precipitation methods (Miller *et al.*, (1988), such precipitation methods being typically referred to as “salting-out” methods. Another example of nucleic acid isolation and/or purification includes the use of magnetic particles to which nucleic acids can specifically or non-specifically bind, followed by isolation of the beads using a magnet, and washing and eluting the nucleic acids from the beads (see, e.g., U.S. Pat. No. 5,705,628). In some embodiments, the above isolation methods may be preceded by an enzyme digestion step to help eliminate unwanted protein from the sample, e.g., digestion with proteinase K, or other like proteases. See, e.g., U.S. Pat. No. 7,001,724. If desired, RNase inhibitors may be added to the lysis buffer. For certain cell or sample types, it may be desirable to add a protein denaturation/digestion step to the protocol. Purification methods may be directed to isolate DNA, RNA, or both. When both DNA and RNA are isolated together during or subsequent to an extraction procedure, further steps may be employed to purify one or both separately from the other. Sub-fractions of extracted nucleic acids can also be generated, for example, purification by size, sequence, or other physical or chemical characteristic. In addition to an initial nucleic isolation step, purification of nucleic acids can be performed after any step in the methods of the disclosure, such as to remove excess or unwanted reagents, reactants, or products.

[00161] Nucleic acid template molecules can be obtained as described in U.S. Patent Application Publication Number US2002/0190663 A1, published Oct. 9, 2003. Generally, nucleic acid can be extracted from a biological sample by a variety of techniques such as those described by Maniatis, *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, N.Y., pp. 280-281 (1982). In some cases, the nucleic acids can be first extracted from the biological samples and then cross-linked *in vitro*. In some cases, native association proteins (e.g., histones) can be further removed from the nucleic acids.

[00162] In other embodiments, the disclosure can be easily applied to any high molecular weight double stranded DNA including, for example, DNA isolated from tissues, cell culture, bodily fluids, animal tissue, plant, bacteria, fungi, viruses, etc.

[00163]

Hi-C Methods Comprising Size Selection

[00164] Provided herein are methods comprising obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein; contacting the stabilized biological sample to a DNase to cleave the nucleic acid molecule into a plurality of segments; attaching a first segment and a second segment of the plurality of segments at a junction; and subjecting the plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments is about 145 to about 600 bp. In some cases, the plurality of selected segments is about 100 to about 2500 bp. In some cases, the plurality of selected segments is about 100 to about 600 bp. In some cases, the plurality of selected segments is about 600 to about 2500 bp. In some cases, the plurality of selected segments is between about 100 bp and about 600 bp, between about 100 bp and about 700 bp, between about 100 bp and about 800 bp, between about 100 bp and about 900 bp, between about 100 bp and about 1000 bp, between about 100 bp and about 1100 bp, between about 100 bp and about 1200 bp, between about 100 bp and about 1300 bp, between about 100 bp and about 1400 bp, between about 100 bp and about 1500 bp, between about 100 bp and about 1600 bp, between about 100 bp and about 1700 bp, between about 100 bp and about 1800 bp, between about 100 bp and about 1900 bp, between about 100 bp and about 2000 bp, between about 100 bp and about 2100 bp, between about 100 bp and about 2200 bp, between about 100 bp and about 2300 bp, between about 100 bp and about 2400 bp, or between about 100 bp and about 2500 bp.

[00165] In another aspect of methods involving a size selection step provided herein, methods further comprise, prior a size selection step, preparing a sequencing library from the plurality of segments. In some embodiments, the method further comprises subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library is between about 350 bp and about 1000 bp in size. In some cases, the size-selected library is between about 100 bp and about 2500 bp in size, for example, between about 100 bp and about 350 bp, between about 350 bp and about 500 bp, between about 500 bp and about 1000 bp, between about 1000 bp and about 1500 bp and about 2000 bp, between about 2000 bp and about 2500 bp, between about 350 bp and about 1000 bp, between about 350 bp and about 1500 bp, between about 350 bp and about 2000 bp, between about 350 bp and about 2500 bp, between about 500 bp and about 1500 bp, between about 500 bp and about 2000 bp, between about

500 bp and about 3500 bp, between about 1000 bp and about 1500 bp, between about 1000 bp and about 2000 bp, between about 1000 bp and about 2500 bp, between about 1500 bp and about 2000 bp, between about 1500 bp and about 2500 bp, or between about 2000 bp and about 2500 bp.

[00166] Size selection utilized in methods involving a size selection step provided herein can be conducted with gel electrophoresis, capillary electrophoresis, size selection beads, a gel filtration column, other suitable methods, or combinations thereof.

[00167] In another aspect, methods involving a size selection step provided herein can further comprise analyzing the plurality of selected segments to obtain a QC value. In some cases, a QC value is selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE is calculated as the proportion of segments having a desired length. For example, in some cases, the CDE is calculated as the proportion of segments between 100 and 2500 bp in size prior to size selection. In some cases, a sample is selected for further analysis when the CDE value is at least 65%. In some cases, a sample is selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%. A CDI is calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size of 600-2500 bp versus fragments having a size of 100-600 bp. In some cases, a sample is selected for further analysis when the CDI value is greater than -1.5 and less than 1. In some cases, a sample is selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00168] In another aspect, stabilized biological samples used in methods involving a size selection step herein comprise biological material that has been treated with a stabilizing agent. In some cases, the stabilized biological sample comprises a stabilized cell lysate. Alternatively, the stabilized biological sample comprises a stabilized intact cell. Alternatively, the stabilized biological sample comprises a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a DNase is conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei are lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00169]In another aspect, methods involving a size selection step herein are conducted on small samples containing few cells or small amounts of nucleic acid. For example, in some cases, the stabilized biological sample comprises fewer than 3,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 2,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 1,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 500,000 cells. In some cases, the stabilized biological sample comprises fewer than 400,000 cells. In some cases, the stabilized biological sample comprises fewer than 300,000 cells. In some cases, the stabilized biological sample comprises fewer than 200,000 cells. In some cases, the stabilized biological sample comprises fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the stabilized biological sample can comprise about 10,000 cells. In some cases, the stabilized biological sample comprises less than 10 μ g DNA. In some cases, the stabilized biological sample comprises less than 9 μ g DNA. In some cases, the stabilized biological sample comprises less than 8 μ g DNA. In some cases, the stabilized biological sample comprises less than 7 μ g DNA. In some cases, the stabilized biological sample comprises less than 6 μ g DNA. In some cases, the stabilized biological sample comprises less than 5 μ g DNA. In some cases, the stabilized biological sample comprises less than 4 μ g DNA. In some cases, the stabilized biological sample comprises less than 3 μ g DNA. In some cases, the stabilized biological sample comprises less than 2 μ g DNA. In some cases, the stabilized biological sample comprises less than 1 μ g DNA. In some cases, the stabilized biological sample comprises less than 0.5 μ g DNA.

[00170]In another aspect, methods involving a size selection step herein can be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00171]In additional aspects, stabilized biological samples used in methods involving a size selection step herein are treated with a nuclease, such as a DNase to create fragments of DNA. In some cases, the DNase is non-sequence specific. In some cases, the DNase is active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase is specific for double-stranded DNA. In some cases, the DNase preferentially cleaves double-stranded DNA. In some cases, the DNase is specific for single-stranded DNA. In some cases, the DNase preferentially cleaves single-stranded DNA. In some cases, the DNase is DNase I. In some cases, the DNase is DNase II. In some cases, the DNase is selected from one or more of DNase I and DNase II. In some cases, the DNase is micrococcal nuclease. In some cases, the DNase is selected from one or more of DNase I, DNase II, and micrococcal nuclease. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or a fragment thereof. The

immunoglobulin binding protein may be, for example, a Protein A, a Protein G, a Protein A/G, or a Protein L. In some embodiments, the DNase may be coupled to a fusion protein including two or more immunoglobulin binding proteins and/or fragments thereof. Other suitable nucleases are also within the scope of this disclosure.

[00172] In additional aspects, stabilized biological samples as provided herein for use in methods involving a size selection step are treated with one or more crosslinking agents. In some cases, the crosslinking agent is a chemical fixative. In some cases, the chemical fixative comprises formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (Å). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 Å, 4 Å, 5 Å, 6 Å, 7 Å, 8 Å, 9 Å, 10 Å, 11 Å, 12 Å, 13 Å, 14 Å, 15 Å, 16 Å, 17 Å, 18 Å, 19 Å, or 20 Å. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 Å. The chemical fixative can comprise disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 Å. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative comprises psoralen. In some cases, the crosslinking agent is ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample is a crosslinked paraffin-embedded tissue sample.

[00173] In further aspects, methods involving a size selection step provided herein comprise contacting the plurality of selected segments to an antibody.

[00174] In additional aspects, methods involving a size selection step provided herein comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching comprises filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching comprises contacting at least the first segment and the second segment to a bridge

oligonucleotide. In some cases, attaching comprises contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein can be from at least about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein can be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides can be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may comprise a barcode. In some embodiments, bridge oligonucleotides can comprise multiple barcodes. In some embodiments, bridge oligonucleotides comprise multiple bridge oligonucleotides connected together. In some embodiments, bridge oligonucleotides may be coupled or linked to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. In some cases, coupled bridge oligonucleotides may be delivered to a location in the sample nucleic acid where an antibody is bound.

[00175] A splitting and pooling approach can be employed to produce bridge oligonucleotides with unique barcodes. A population of samples can be split into multiple groups, bridge oligonucleotides can be attached to the samples such that the bridge oligonucleotide barcodes are different between groups but the same within a group, the groups of samples can be pooled together again, and this process can be repeated multiple times. Iterating this process can ultimately result in each sample in the population having a unique series of bridge oligonucleotide barcodes, allowing single-sample (e.g., single cell, single nucleus, single chromosome) analysis. In one illustrative example, a sample of crosslinked digested nuclei attached to a solid support of beads is split across 8 tubes, each containing 1 of 8 unique members of a first adaptor group (first iteration) comprising double-stranded DNA (dsDNA) adaptors to be ligated. Each of the 8 adaptors can have the same 5' overhang sequence for ligation to the nucleic acid ends of the cross-linked chromatin aggregates in the nuclei, but otherwise has a unique dsDNA sequence. After the first adaptor group is ligated, the nuclei can be pooled back together and washed to remove the ligation reaction components. The scheme of distributing, ligating, and pooling can be repeated 2 additional times (2 iterations). Following ligation of members from each adaptor group, a cross-linked chromatin aggregate can be attached to multiple barcodes in series. In some cases, the sequential ligation of a plurality of members of a plurality of adaptor groups (iterations) results in barcode combinations. The number of barcode combinations available depends on the number of groups per iteration and the total number of barcode oligonucleotides used. For example, 3 iterations comprising 8 members each can have 83 possible combinations. In some cases, barcode combinations are unique. In some cases, barcode combinations are redundant. The total number of barcode combinations can be adjusted by increasing or decreasing the number of groups receiving unique barcodes and/or increasing or decreasing the number of iterations. When more than one adaptor group is used, a distributing, attaching, and pooling scheme can be used for iterative adaptor attachment. In some cases, the scheme of distributing, attaching, and pooling can be repeated at least 3, 4, 5, 6, 7, 8, 9, or 10 additional times. In some cases, the members of the last adaptor

group include a sequence for subsequent enrichment of adaptor-attached DNA, for example, during sequencing library preparation through PCR amplification.

[00176] In additional aspects, methods involving a size selection step herein do not comprise a shearing step (e.g., the nucleic acid is not sheared).

[00177] In further aspects of methods involving a size selection step herein, methods comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about 150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00178] In additional aspects of methods involving a size selection step herein, methods comprise mapping the first read pair to a set of contigs, and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00179] In further aspects of methods involving a size selection step herein, methods comprise mapping the first read pair to a set of contigs; and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00180] In additional aspects of methods involving a size selection step herein, methods comprise mapping the first read pair to a set of contigs, and assigning a variant in the set of contigs to a phase.

[00181] In further aspects of methods involving a size selection step herein, methods comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs, and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Hi-C Methods Comprising a QC Calculation

[00182] Additionally, provided herein are methods comprising obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein, contacting the stabilized biological sample to a DNase to cleave the nucleic acid molecule into a plurality of segments, attaching a first segment and a second segment of the plurality of segments at a junction, and analyzing the plurality of segments to determine a QC value. In some cases, a QC value is selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE is calculated as the proportion of segments having a desired length. For example, in some cases, the CDE is calculated as the proportion of segments between 100 and 2500 bp in size prior to size selection. In some cases, a sample is selected for further analysis when the CDE value is at least 65%. In some cases, a sample is selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%. A CDI is calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size 600-2500 bp versus fragments having a size 100-600 bp. In some cases, a sample is selected for further analysis when the CDI value is greater than -1.5 and

less than 1. In some cases, a sample is selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00183] In another aspect, methods involving a QC determination step herein may comprise subjecting a plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments is about 145 to about 600 bp. In some cases, the plurality of selected segments is about 100 to about 2500 bp. In some cases, the plurality of selected segments is about 100 to about 600 bp. In some cases, the plurality of selected segments is about 600 to about 2500 bp. In some cases, the plurality of selected segments is between about 100 bp and about 600 bp, between about 100 bp and about 700 bp, between about 100 bp and about 800 bp, between about 100 bp and about 900 bp, between about 100 bp and about 1000 bp, between about 100 bp and about 1100 bp, between about 100 bp and about 1200 bp, between about 100 bp and about 1300 bp, between about 100 bp and about 1400 bp, between about 100 bp and about 1500 bp, between about 100 bp and about 1600 bp, between about 100 bp and about 1700 bp, between about 100 bp and about 1800 bp, between about 100 bp and about 1900 bp, between about 100 bp and about 2000 bp, between about 100 bp and about 2100 bp, between about 100 bp and about 2200 bp, between about 100 bp and about 2300 bp, between about 100 bp and about 2400 bp, or between about 100 bp and about 2500 bp.

[00184] In another aspect of methods involving a QC determination step provided herein, methods can further comprise, prior to a size selection step, preparing a sequencing library from the plurality of segments. In some embodiments, the method further comprises subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library is between about 350 bp and about 1000 bp in size. In some cases, the size-selected library is between about 100 bp and about 2500 bp in size, for example, between about 100 bp and about 350 bp, between about 350 bp and about 500 bp, between about 500 bp and about 1000 bp, between about 1000 and about 1500 bp and about 2000 bp, between about 2000 bp and about 2500 bp, between about 350 bp and about 1000 bp, between about 350 bp and about 1500 bp, between about 350 bp and about 2000 bp, between about 350 bp and about 2500 bp, between about 500 bp and about 1500 bp, between about 500 bp and about 2000 bp, between about 500 bp and about 3500 bp, between about 1000 bp and about 1500 bp, between about 1000 bp and

about 2000 bp, between about 1000 bp and about 2500 bp, between about 1500 bp and about 2000 bp, between about 1500 bp and about 2500 bp, or between about 2000 bp and about 2500 bp.

[00185] Size selection utilized in methods involving a QC determination step herein may be conducted with gel electrophoresis, capillary electrophoresis, size selection beads, a gel filtration column, or combinations thereof. Other suitable methods of size selection are also within the scope of this disclosure.

[00186] In another aspect, stabilized biological samples used in involving a QC determination step herein comprise biological material that has been treated with a stabilizing agent. In some cases, the stabilized biological sample comprises a stabilized cell lysate. Alternatively, the stabilized biological sample comprises a stabilized intact cell. Alternatively, the stabilized biological sample comprises a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a DNase is conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei are lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00187] In another aspect, methods involving a QC determination step herein are conducted on small samples containing few cells or small amounts of nucleic acid. In some cases, the stabilized biological sample comprises fewer than 3,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 2,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 1,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 500,000 cells. In some cases, the stabilized biological sample comprises fewer than 400,000 cells. In some cases, the stabilized biological sample comprises fewer than 300,000 cells. In some cases, the stabilized biological sample comprises fewer than 200,000 cells. In some cases, the stabilized biological sample comprises fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the stabilized biological sample comprises about 10,000 cells. In some cases, the stabilized biological sample comprises less than 10 µg DNA. In some cases, the stabilized biological sample comprises less than 9 µg DNA. In some cases, the stabilized biological sample comprises less than 8 µg DNA. In some cases, the stabilized biological sample comprises less than 7 µg DNA. In some cases, the stabilized biological sample comprises less than 6 µg DNA. In some cases, the stabilized biological sample comprises less than 5 µg DNA. In some cases, the stabilized biological sample comprises less than 4 µg DNA. In some cases, the stabilized biological sample comprises less than 3 µg DNA. In some cases, the stabilized biological sample comprises less than 2 µg DNA. In some cases, the stabilized biological sample comprises less than 1 µg DNA. In some cases, the stabilized biological sample comprises less than 0.5 µg DNA.

[00188] In another aspect, methods involving a QC determination step herein can be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced

linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00189]In additional aspects, stabilized biological samples used in methods involving a QC determination step herein are treated with a nuclease, such as a DNase to create fragments of DNA. In some cases, the DNase is non-sequence specific. In some cases, the DNase is active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase is specific for double-stranded DNA. In some cases, the DNase preferentially cleaves double-stranded DNA. In some cases, the DNase is specific for single-stranded DNA. In some cases, the DNase preferentially cleaves single-stranded DNA. In some cases, the DNase is DNase I. In some cases, the DNase is DNase II. In some cases, the DNase is selected from one or more of DNase I and DNase II. In some cases, the DNase is micrococcal nuclease. In some cases, the DNase is selected from one or more of DNase I, DNase II, and micrococcal nuclease. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. Other suitable nucleases are also within the scope of this disclosure.

[00190]In additional aspects, stabilized biological samples used in methods involving a QC determination step herein are treated with a crosslinking agent. In some cases, the crosslinking agent is a chemical fixative. In some cases, the chemical fixative comprises formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (A). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 A, 4 A, 5 A, 6 A, 7 A, 8 A, 9 A, 10 A, 11 A, 12 A, 13 A, 14 A, 15 A, 16 A, 17 A, 18 A, 19 A, or 20 A. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 A. The chemical fixative can comprise disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 A. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative comprises psoralen. In some cases, the crosslinking agent is ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine,

mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample is a crosslinked paraffin-embedded tissue sample.

[00191] In further aspects, methods involving a QC determination step provided herein comprise contacting the plurality of selected segments to an antibody.

[00192] In additional aspects, methods involving a QC determination step provided herein comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching comprises filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching comprises contacting at least the first segment and the second segment to a bridge oligonucleotide. In some cases, attaching comprises contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein can be from at least about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein can be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides can be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may comprise a barcode. In some embodiments, bridge oligonucleotides can comprise multiple barcodes. In some embodiments, bridge oligonucleotides comprise multiple bridge oligonucleotides connected together. In some embodiments, bridge oligonucleotides may be coupled or linked to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. In some cases, coupled bridge oligonucleotides may be delivered to a location in the sample nucleic acid where an antibody is bound.

[00193] In additional aspects, methods involving a QC determination step herein do not comprise a shearing step.

[00194] In further aspects of methods involving a QC determination step herein, methods comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about 150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00195] In additional aspects of methods involving a QC determination step herein, methods comprise mapping the first read pair to a set of contigs and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00196] In further aspects of methods involving a QC determination step herein, methods may comprise mapping the first read pair to a set of contigs and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00197] In additional aspects of methods involving a QC determination step herein, methods comprise mapping the first read pair to a set of contigs and assigning a variant in the set of contigs to a phase.

[00198] In further aspects of methods involving a QC determination step herein, methods comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs; and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Hi-C Methods Comprising Whole Cell or Whole Nuclei Digestion

[00199] Further provided herein are methods comprising obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein; contacting the stabilized biological sample to a DNase to cleave the nucleic acid molecule into a plurality of segments; and attaching a first segment and a second segment of the plurality of segments at a junction, wherein the stabilized biological sample comprises intact cells and/or intact nuclei. In some cases, the stabilized biological sample comprises a stabilized intact cell. Alternatively, or in combination, the stabilized biological sample comprises a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a DNase is conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei are lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00200] In another aspect, methods involving digestion of whole cells or whole nuclei herein can comprise subjecting a plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments is about 145 to about 600 bp. In some cases, the plurality of selected segments is about 100 to about 2500 bp. In some cases, the plurality of selected segments is about 100 to about 600 bp. In some cases, the plurality of selected segments is about 600 to about 2500 bp. In some cases, the plurality of selected segments is between about 100 bp and about 600 bp, between about 100 bp and about 700 bp, between about 100 bp and about 800 bp, between about 100 bp and about 900 bp, between about 100 bp and about 1000 bp, between about 100 bp and about 1100 bp, between about 100 bp and about 1200 bp, between about 100 bp and about 1300 bp, between about 100 bp and about 1400 bp, between about 100 bp and about 1500 bp, between about 100 bp and about 1600 bp, between about 100 bp and about 1700 bp, between about 100 bp and about 1800 bp, between about 100 bp and about 1900 bp, between about 100 bp and about 2000 bp, between about 100 bp and about 2100 bp, between about 100 bp and about 2200 bp, between about 100 bp and about 2300 bp, between about 100 bp and about 2400 bp, or between about 100 bp and about 2500 bp.

[00201] In another aspect of methods involving digestion of whole cells or whole nuclei provided herein, methods further comprise, prior a size selection step, preparing a sequencing library from the plurality of segments. In some embodiments, the method further comprises subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library is between about 350 bp and about 1000 bp in size. In some cases, the size-selected library is between about 100 bp and about 2500 bp in size, for example, between about 100 bp and about 350 bp, between about 350 bp and about 500 bp, between about 500 bp and about 1000 bp, between about 1000 and about 1500 bp and about 2000 bp, between about 2000 bp and about 2500 bp, between about 350 bp and about 1000 bp, between about

350 bp and about 1500 bp, between about 350 bp and about 2000 bp, between about 350 bp and about 2500 bp, between about 500 bp and about 1500 bp, between about 500 bp and about 2000 bp, between about 500 bp and about 3500 bp, between about 1000 bp and about 1500 bp, between about 1000 bp and about 2000 bp, between about 1000 bp and about 2500 bp, between about 1500 bp and about 2000 bp, between about 1500 bp and about 2500 bp, or between about 2000 bp and about 2500 bp.

[00202] Size selection utilized in methods involving digestion of whole cells or whole nuclei herein can be conducted with gel electrophoresis, capillary electrophoresis, size selection beads, a gel filtration column, or combinations thereof.

[00203] In another aspect, methods involving digestion of whole cells or whole nuclei herein may comprise further analyzing the plurality of selected segments to obtain a QC value. In some cases, a QC value is selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE is calculated as the proportion of segments having a desired length. For example, in some cases, the CDE is calculated as the proportion of segments between 100 and 2500 bp in size prior to size selection. In some cases, a sample is selected for further analysis when the CDE value is at least 65%. In some cases, a sample is selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%. A CDI is calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size 600-2500 bp versus fragments having a size 100-600 bp. In some cases, a sample is selected for further analysis when the CDI value is greater than -1.5 and less than 1. In some cases, a sample is selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00204] In another aspect, methods involving digestion of whole cells or whole nuclei herein are conducted on small samples containing few cells or small amounts of nucleic acid. In some cases, the stabilized biological sample comprises fewer than 3,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 2,000,000 cells. In some cases, the stabilized biological sample comprises

fewer than 1,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 500,000 cells. In some cases, the stabilized biological sample comprises fewer than 400,000 cells. In some cases, the stabilized biological sample comprises fewer than 300,000 cells. In some cases, the stabilized biological sample comprises fewer than 200,000 cells. In some cases, the stabilized biological sample comprises fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the stabilized biological sample comprises about 10,000 cells. In some cases, the stabilized biological sample comprises less than 10 μ g DNA. In some cases, the stabilized biological sample comprises less than 9 μ g DNA. In some cases, the stabilized biological sample comprises less than 8 μ g DNA. In some cases, the stabilized biological sample comprises less than 7 μ g DNA. In some cases, the stabilized biological sample comprises less than 6 μ g DNA. In some cases, the stabilized biological sample comprises less than 5 μ g DNA. In some cases, the stabilized biological sample comprises less than 4 μ g DNA. In some cases, the stabilized biological sample comprises less than 3 μ g DNA. In some cases, the stabilized biological sample comprises less than 2 μ g DNA. In some cases, the stabilized biological sample comprises less than 1 μ g DNA. In some cases, the stabilized biological sample comprises less than 0.5 μ g DNA.

[00205] In another aspect, methods involving a digestion of whole cells or whole nuclei herein may be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00206] In additional aspects, stabilized biological samples used in methods involving digestion of whole cells or whole nuclei herein are treated with a nuclease, such as a DNase to create fragments of DNA. In some cases, the DNase is non-sequence specific. In some cases, the DNase is active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase is specific for double-stranded DNA. In some cases, the DNase preferentially cleaves double-stranded DNA. In some cases, the DNase is specific for single-stranded DNA. In some cases, the DNase preferentially cleaves single-stranded DNA. In some cases, the DNase is DNase I. In some cases, the DNase is DNase II. In some cases, the DNase is selected from one or more of DNase I and DNase II. In some cases, the DNase is micrococcal nuclease. In some cases, the DNase is selected from one or more of DNase I, DNase II, and micrococcal nuclease. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. Other suitable nucleases are also within the scope of this disclosure.

[00207] In additional aspects, stabilized biological samples used in methods involving digestion of whole cells or whole nuclei herein are treated with a crosslinking agent. In some cases, the crosslinking agent is

a chemical fixative. In some cases, the chemical fixative comprises formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (A). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 A, 4 A, 5 A, 6 A, 7 A, 8 A, 9 A, 10 A, 11 A, 12 A, 13 A, 14 A, 15 A, 16 A, 17 A, 18 A, 19 A, or 20 A. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 A. The chemical fixative can comprise disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 A. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative comprises psoralen. In some cases, the crosslinking agent is ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, ciccycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample is a crosslinked paraffin-embedded tissue sample.

[00208] In further aspects, methods involving digestion of whole cells or whole nuclei provided herein comprise contacting the plurality of selected segments to an antibody.

[00209] In additional aspects, methods involving digestion of whole cells or whole nuclei provided herein comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching comprises filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching comprises contacting at least the first segment and the second segment to a bridge oligonucleotide. In some cases, attaching comprises contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein may be from at least about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides may be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about

35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein can comprise a barcode. In some embodiments, bridge oligonucleotides can comprise multiple barcodes. In some embodiments, bridge oligonucleotides comprise multiple bridge oligonucleotides connected together. In some embodiments, bridge oligonucleotides may be coupled or linked to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. In some cases, coupled bridge oligonucleotides may be delivered to a location in the sample nucleic acid where an antibody is bound.

[00210] A splitting and pooling approach can be employed to produce bridge oligonucleotides with unique barcodes. A population of samples can be split into multiple groups, bridge oligonucleotides can be attached to the samples such that the bridge oligonucleotide barcodes are different between groups but the same within a group, the groups of samples can be pooled together again, and this process can be repeated multiple times. Iterating this process can ultimately result in each sample in the population having a unique series of bridge oligonucleotide barcodes, allowing single-sample (e.g., single cell, single nucleus, single chromosome) analysis. In one illustrative example, a sample of crosslinked digested nuclei attached to a solid support of beads is split across 8 tubes, each containing 1 of 8 unique members of a first adaptor group (first iteration) comprising double-stranded DNA (dsDNA) adaptors to be ligated. Each of the 8 adaptors can have the same 5' overhang sequence for ligation to the nucleic acid ends of the cross-linked chromatin aggregates in the nuclei, but otherwise has a unique dsDNA sequence. After the first adaptor group is ligated, the nuclei can be pooled back together and washed to remove the ligation reaction components. The scheme of distributing, ligating, and pooling can be repeated 2 additional times (2 iterations). Following ligation of members from each adaptor group, a cross-linked chromatin aggregate can be attached to multiple barcodes in series. In some cases, the sequential ligation of a plurality of members of a plurality of adaptor groups (iterations) results in barcode combinations. The number of barcode combinations available depends on the number of groups per iteration and the total number of barcode oligonucleotides used. For example, 3 iterations comprising 8 members each can have 83 possible combinations. In some cases, barcode combinations are unique. In some cases, barcode combinations are redundant. The total number of barcode combinations can be adjusted by increasing or decreasing the number of groups receiving unique barcodes and/or increasing or decreasing the number of iterations. When more than one adaptor group is used, a distributing, attaching, and pooling scheme can be used for iterative adaptor attachment. In some cases, the scheme of distributing, attaching, and pooling can be repeated at least 3, 4, 5, 6, 7, 8, 9, or 10 additional times. In some cases, the members of the last adaptor group include a sequence for subsequent enrichment of adaptor-attached DNA, for example, during sequencing library preparation through PCR amplification.

[00211] In additional aspects, methods involving digestion of whole cells or whole nuclei herein do not comprise a shearing step.

[00212] In further aspects of methods involving digestion of whole cells or whole nuclei herein, methods comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about

150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00213] In additional aspects of methods involving digestion of whole cells or whole nuclei herein, methods comprise mapping the first read pair to a set of contigs and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00214] In further aspects of methods involving digestion of whole cells or whole nuclei herein, methods comprise mapping the first read pair to a set of contigs; and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00215] In additional aspects of methods involving digestion of whole cells or whole nuclei herein, methods comprise mapping the first read pair to a set of contigs and assigning a variant in the set of contigs to a phase.

[00216] In further aspects of methods involving digestion of whole cells or whole nuclei herein, methods comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs; and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Hi-C Methods Having Low Nucleic Acid Input Requirements

[00217] Additionally provided herein are methods comprising obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein; contacting the stabilized biological sample to a DNase to cleave the nucleic acid molecule into a plurality of segments; and attaching a first segment and a second segment of the plurality of segments at a junction, wherein the stabilized biological sample comprises fewer than 3,000,000 cells or less than 10 µg DNA. In some cases, the stabilized biological sample comprises fewer than 3,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 2,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 1,000,000 cells. In some cases, the stabilized biological sample comprises fewer than 500,000 cells. In some cases, the stabilized biological sample comprises fewer than 400,000 cells. In some cases, the stabilized biological sample comprises fewer than 300,000 cells. In some cases, the stabilized biological sample comprises fewer than 200,000 cells. In some cases, the stabilized biological sample comprises fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the sample comprises at least 10,000 cells. In some cases, the sample comprises at least 20,000 cells. In some cases, the sample comprises at least 30,000 cells. In some cases, the sample comprises at least 40,000 cells. In some cases, the sample comprises from about 10,000 cells to about 50,000 cells. In some cases, the sample comprises from about 20,000 cells to about 50,000 cells.

In some cases, the sample comprises from about 30,000 cells to about 50,000 cells. In some cases, the sample comprises from about 40,000 cells to about 50,000 cells. In some cases, the sample comprises from about 10,000 cells to about 40,000 cells. In some cases, the sample comprises from about 10,000 cells to about 30,000 cells. In some cases, the sample comprises from about 10,000 cells to about 20,000 cells. In some cases, the sample comprises from about 20,000 cells to about 50,000 cells. In some cases, the sample comprises from about 20,000 cells to about 40,000 cells. In some cases, the sample comprises from about 20,000 cells to about 30,000 cells. In some cases, the sample comprises from about 30,000 cells to about 50,000 cells. In some cases, the sample comprises from about 30,000 cells to about 40,000 cells. In some cases, the stabilized biological sample comprises less than 10 μ g DNA. In some cases, the stabilized biological sample comprises less than 9 μ g DNA. In some cases, the stabilized biological sample comprises less than 8 μ g DNA. In some cases, the stabilized biological sample comprises less than 7 μ g DNA. In some cases, the stabilized biological sample comprises less than 6 μ g DNA. In some cases, the stabilized biological sample comprises less than 5 μ g DNA. In some cases, the stabilized biological sample comprises less than 4 μ g DNA. In some cases, the stabilized biological sample comprises less than 3 μ g DNA. In some cases, the stabilized biological sample comprises less than 2 μ g DNA. In some cases, the stabilized biological sample comprises less than 1 μ g DNA. In some cases, the stabilized biological sample comprises less than 0.5 μ g DNA.

[00218] In various aspects of methods herein, the stabilized sample may comprise nuclei. In some cases, the stabilized sample comprises no more than 50,000 nuclei. In some cases, the sample comprises no more than 40,000 nuclei. In some cases, the sample comprises no more than 30,000 nuclei. In some cases, the sample comprises no more than 20,000 nuclei. In some cases, the sample comprises at least 10,000 nuclei. In some cases, the sample comprises at least 20,000 nuclei. In some cases, the sample comprises at least 30,000 nuclei. In some cases, the sample comprises at least 40,000 nuclei. In some cases, the sample comprises from about 10,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 40,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 10,000 nuclei to about 40,000 nuclei. In some cases, the sample comprises from about 10,000 nuclei to about 30,000 nuclei. In some cases, the sample comprises from about 10,000 nuclei to about 20,000 nuclei. In some cases, the sample comprises from about 20,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 20,000 nuclei to about 40,000 nuclei. In some cases, the sample comprises from about 20,000 nuclei to about 30,000 nuclei. In some cases, the sample comprises from about 30,000 nuclei to about 50,000 nuclei. In some cases, the sample comprises from about 30,000 nuclei to about 40,000 nuclei.

[00219] In another aspect, methods having low nucleic acid input requirements herein may be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced

linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00220]In another aspect, methods having low nucleic acid input requirements herein comprise subjecting a plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments is about 145 to about 600 bp. In some cases, the plurality of selected segments is about 100 to about 2500 bp. In some cases, the plurality of selected segments is about 100 to about 600 bp. In some cases, the plurality of selected segments is about 600 to about 2500 bp. In some cases, the plurality of selected segments is between about 100 bp and about 600 bp, between about 100 bp and about 700 bp, between about 100 bp and about 800 bp, between about 100 bp and about 900 bp, between about 100 bp and about 1000 bp, between about 100 bp and about 1100 bp, between about 100 bp and about 1200 bp, between about 100 bp and about 1300 bp, between about 100 bp and about 1400 bp, between about 100 bp and about 1500 bp, between about 100 bp and about 1600 bp, between about 100 bp and about 1700 bp, between about 100 bp and about 1800 bp, between about 100 bp and about 1900 bp, between about 100 bp and about 2000 bp, between about 100 bp and about 2100 bp, between about 100 bp and about 2200 bp, between about 100 bp and about 2300 bp, between about 100 bp and about 2400 bp, or between about 100 bp and about 2500 bp.

[00221]In another aspect of methods having low nucleic acid input requirements provided herein, methods further comprise, prior a size selection step, preparing a sequencing library from the plurality of segments. In some embodiments, the method further comprises subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library is between about 350 bp and about 1000 bp in size. In some cases, the size-selected library is between about 100 bp and about 2500 bp in size, for example, between about 100 bp and about 350 bp, between about 350 bp and about 500 bp, between about 500 bp and about 1000 bp, between about 1000 and about 1500 bp and about 2000 bp, between about 2000 bp and about 2500 bp, between about 350 bp and about 1000 bp, between about 350 bp and about 1500 bp, between about 350 bp and about 2000 bp, between about 350 bp and about 2500 bp, between about 500 bp and about 1500 bp, between about 500 bp and about 2000 bp, between about 500 bp and about 3500 bp, between about 1000 bp and about 1500 bp, between about 1000 bp and about 2000 bp, between about 1000 bp and about 2500 bp, between about 1500 bp and about 2000 bp, between about 1500 bp and about 2500 bp, or between about 2000 bp and about 2500 bp.

[00222]Size selection utilized in methods having low nucleic acid input requirements herein is often conducted with gel electrophoresis, capillary electrophoresis, size selection beads, a gel filtration column, or combinations thereof.

[00223]In another aspect, methods having low nucleic acid input requirements herein may further comprise analyzing the plurality of selected segments to obtain a QC value. In some cases, a QC value is selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE is calculated as the proportion of segments having a desired length. For example, in some cases, the CDE is calculated as the proportion of segments between 100 and 2500 bp in size prior to size selection. In some cases, a sample is selected for further analysis when the CDE value is at least 65%. In some cases, a

sample is selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%. A CDI is calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size 600-2500 bp versus fragments having a size 100-600 bp. In some cases, a sample is selected for further analysis when the CDI value is greater than -1.5 and less than 1. In some cases, a sample is selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00224] In another aspect, stabilized biological samples used in methods having low nucleic acid input requirements herein comprise biological material that has been treated with a stabilizing agent. In some cases, the stabilized biological sample comprises a stabilized cell lysate. Alternatively, the stabilized biological sample comprises a stabilized intact cell. Alternatively, the stabilized biological sample comprises a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a DNase is conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei are lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00225] In additional aspects, stabilized biological samples used in methods having low nucleic acid input requirements herein are treated with a nuclease, such as a DNase to create fragments of DNA. In some cases, the DNase is non-sequence specific. In some cases, the DNase is active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase is specific for double-stranded DNA. In some cases, the DNase preferentially cleaves double-stranded DNA. In some cases, the DNase is specific for single-stranded DNA. In some cases, the DNase preferentially cleaves single-stranded DNA. In some cases, the DNase is DNase I. In some cases, the DNase is DNase II. In some cases, the DNase is selected from one or more of DNase I and DNase II. In some cases, the DNase is micrococcal nuclease. In some cases, the DNase is selected from one or more of DNase I, DNase II, and micrococcal nuclease. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof,

such as a Protein A, a Protein G, a Protein A/G, or a Protein L. Other suitable nucleases are also within the scope of this disclosure.

[00226]In additional aspects, stabilized biological samples used in methods having low nucleic acid input requirements herein are treated with a crosslinking agent. In some cases, the crosslinking agent is a chemical fixative. In some cases, the chemical fixative comprises formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (A). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 A, 4 A, 5 A, 6 A, 7 A, 8 A, 9 A, 10 A, 11 A, 12 A, 13 A, 14 A, 15 A, 16 A, 17 A, 18 A, 19 A, or 20 A. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 A. The chemical fixative can comprise disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 A. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative comprises psoralen. In some cases, the crosslinking agent is ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample is a crosslinked paraffin-embedded tissue sample.

[00227]In further aspects, methods provided herein comprise contacting the plurality of selected segments to an antibody.

[00228]In additional aspects, methods having low nucleic acid input requirements provided herein comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching comprises filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching comprises contacting at least the first segment and the second segment to a bridge oligonucleotide. In some cases, attaching comprises contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein may be from at least

about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides may be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may comprise a barcode. In some embodiments, bridge oligonucleotides can comprise multiple barcodes. In some embodiments, bridge oligonucleotides comprise multiple bridge oligonucleotides connected together. In some embodiments, bridge oligonucleotides may be coupled or linked to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. In some cases, coupled bridge oligonucleotides may be delivered to a location in the sample nucleic acid where an antibody is bound.

[00229] A splitting and pooling approach can be employed to produce bridge oligonucleotides with unique barcodes. A population of samples can be split into multiple groups, bridge oligonucleotides can be attached to the samples such that the bridge oligonucleotide barcodes are different between groups but the same within a group, the groups of samples can be pooled together again, and this process can be repeated multiple times. Iterating this process can ultimately result in each sample in the population having a unique series of bridge oligonucleotide barcodes, allowing single-sample (e.g., single cell, single nucleus, single chromosome) analysis. In one illustrative example, a sample of crosslinked digested nuclei attached to a solid support of beads is split across 8 tubes, each containing 1 of 8 unique members of a first adaptor group (first iteration) comprising double-stranded DNA (dsDNA) adaptors to be ligated. Each of the 8 adaptors can have the same 5' overhang sequence for ligation to the nucleic acid ends of the cross-linked chromatin aggregates in the nuclei, but otherwise has a unique dsDNA sequence. After the first adaptor group is ligated, the nuclei can be pooled back together and washed to remove the ligation reaction components. The scheme of distributing, ligating, and pooling can be repeated 2 additional times (2 iterations). Following ligation of members from each adaptor group, a cross-linked chromatin aggregate can be attached to multiple barcodes in series. In some cases, the sequential ligation of a plurality of members of a plurality of adaptor groups (iterations) results in barcode combinations. The number of barcode combinations available depends on the number of groups per iteration and the total number of barcode oligonucleotides used. For example, 3 iterations comprising 8 members each can have 83 possible combinations. In some cases, barcode combinations are unique. In some cases, barcode combinations are redundant. The total number of barcode combinations can be adjusted by increasing or decreasing the number of groups receiving unique barcodes and/or increasing or decreasing the number of iterations. When more than one adaptor group is used, a distributing, attaching, and pooling scheme can be used for iterative adaptor attachment. In some cases, the scheme of distributing, attaching, and pooling can be repeated at least 3, 4, 5, 6, 7, 8, 9, or 10 additional times. In some cases, the members of the last adaptor group include a sequence for subsequent enrichment of adaptor-attached DNA, for example, during sequencing library preparation through PCR amplification.

[00230] In additional aspects, methods having low nucleic acid input requirements herein do not comprise a shearing step.

[00231] In further aspects of methods having low nucleic acid input requirements herein, methods comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about 150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00232] In additional aspects of methods having low nucleic acid input requirements herein, methods comprise mapping the first read pair to a set of contigs and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00233] In further aspects of methods having low nucleic acid input requirements herein, methods comprise mapping the first read pair to a set of contigs and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00234] In additional aspects of methods having low nucleic acid input requirements herein, methods comprise mapping the first read pair to a set of contigs and assigning a variant in the set of contigs to a phase.

[00235] In further aspects of methods having low nucleic acid input requirements herein, methods comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs; and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Hi-C Methods Using Micrococcal Nuclease (MNase)

[00236] Additionally, provided herein are methods that may comprise obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein; contacting the stabilized biological sample to a micrococcal nuclease (MNase) to cleave the nucleic acid molecule into a plurality of segments; and attaching a first segment and a second segment of the plurality of segments at a junction. Use of MNase in methods herein may provide specific information about where DNA binding proteins are bound to the chromatin with up to single base pair resolution because, for example, MNase can cleave all base pairs not bound to a DNA binding protein. In addition, use of MNase digestion may allow for creation of contact maps and topologically associated domains to decipher three-dimensional chromatin structural information. In some cases, the MNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L.

[00237] For example, MNase Hi-C methods can provide locations of protein binding or genome contact interactions at a resolution of less than or equal to about 1 bp, 2 bp, 3 bp, 4 bp, 5 bp, 6 bp, 7 bp, 8 bp, 9 bp, 10 bp, 20 bp, 30 bp, 40 bp, 50 bp, 60 bp, 70 bp, 80 bp, 90 bp, 100 bp, 200 bp, 300 bp, 400 bp, 500 bp, 600 bp, 700 bp, 800 bp, 900 bp, 1000 bp, 2000 bp, 3000 bp, 4000 bp, 5000 bp, 6000 bp, 7000 bp, 8000 bp,

9000 bp, 10 kb, 20 kb, 30 kb, 40 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb, or 100 kb. In some cases, protein binding sites, protein footprints, contact interactions, or other features can be mapped to within 1000 bp, within 900 bp, within 800 bp, within 700 bp, within 600 bp, within 500 bp, within 400 bp, within 300 bp, within 200 bp, within 190 bp, within 180 bp, within 170 bp, within 160 bp, within 150 bp, within 140 bp, within 130 bp, within 120 bp, within 110 bp, within 100 bp, within 90 bp, within 80 bp, within 70 bp, within 60 bp, within 50 bp, within 40 bp, within 30 bp, within 20 bp, within 10 bp, within 9 bp, within 8 bp, within 7 bp, within 6 bp, within 5 bp, within 4 bp, within 3 bp, within 2 bp, or within 1 bp.

[00238]In certain aspects, methods involving a MNase digestion step may further comprise subjecting a plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments can be from about 145 to about 600 bp. In some cases, the plurality of selected segments can be from about 100 to about 2500 bp. In some cases, the plurality of selected segments can be from about 100 to about 600 bp. In some cases, the plurality of selected segments can be from about 600 to about 2500 bp. In some cases, the plurality of selected segments can be from about 100 bp to about 600 bp, from about 100 bp to about 700 bp, from about 100 bp to about 800 bp, from about 100 bp to about 900 bp, from about 100 bp to about 1000 bp, from about 100 bp to about 1100 bp, from about 100 bp to about 1200 bp, from about 100 bp to about 1300 bp, from about 100 bp to about 1400 bp, from about 100 bp to about 1500 bp, from about 100 bp to about 1600 bp, from about 100 bp to about 1700 bp, from about 100 bp to about 1800 bp, from about 100 bp to about 1900 bp, from about 100 bp to about 2000 bp, from about 100 bp to about 2100 bp, from about 100 bp to about 2200 bp, from about 100 bp to about 2300 bp, from about 100 bp to about 2400 bp, or from about 100 bp to about 2500 bp.

[00239]In another aspect of methods involving a MNase digestion step as provided herein, the methods may further comprise preparing a sequencing library from the plurality of segments. In some embodiments, the method may further comprise subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library may be from about 350 bp to about 1000 bp in size. In some cases, the size-selected library may be from about 100 bp to about 2500 bp in size, for example, from about 100 bp to about 350 bp, from about 350 bp to about 500 bp, from about 500 bp to about 1000 bp, from about 1000 to about 1500 bp, from about 2000 bp to about 2500 bp, from about 350 bp to about 1000 bp, from about 350 bp to about 1500 bp, from about 350 bp to about 2000 bp, from about 350 bp to about 2500 bp, from about 500 bp to about 1500 bp, from about 500 bp to about 2000 bp, from about 500 bp to about 3500 bp, from about 1000 bp to about 1500 bp, from about 1000 bp to about 2000 bp, from about 1000 bp to about 2500 bp, from about 1500 bp to about 2000 bp, from about 1500 bp to about 2500 bp, or from about 2000 bp to about 2500 bp.

[00240]In another aspect, methods involving a MNase digestion step as provided herein can further comprise analyzing the plurality of segments to obtain a QC value. In some cases, a QC value may be selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE can be calculated as the proportion of segments having a desired length. For example, in some cases, the CDE can be calculated as the proportion of segments from 100 bp to 2500 bp in size prior to size selection. In some cases, a sample may be selected for further analysis when the CDE value is at least 65%. In some

cases, a sample may be selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%.

[00241] A CDI can be calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size of 600-2500 bp versus fragments having a size of 100-600 bp. In some cases, a sample may be selected for further analysis when the CDI value is greater than -1.5 and less than 1. In some cases, a sample may be selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00242] In another aspect, stabilized biological samples used in methods involving a MNase digestion step as provided herein may comprise biological material that has been treated with a stabilizing agent. In some cases, the stabilized biological sample may comprise a stabilized cell lysate. Alternatively, the stabilized biological sample may comprise a stabilized intact cell. Alternatively, the stabilized biological sample may comprise a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a MNase may be conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei may be lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00243] In another aspect, methods involving a MNase digestion step as provided herein may be conducted on small samples containing few cells or small amounts of nucleic acid. For example, in some cases, the stabilized biological sample may comprise fewer than 3,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 2,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 1,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 500,000 cells. In some cases, the stabilized biological sample may comprise fewer than 400,000 cells. In some cases, the stabilized biological sample may comprise fewer than 300,000 cells. In some cases, the stabilized biological sample may comprise fewer than 200,000 cells. In some cases, the stabilized biological sample may comprise fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized

biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the stabilized biological sample comprises about 10,000 cells. In some cases, the stabilized biological sample may comprise less than 10 μ g DNA. In some cases, the stabilized biological sample may comprise less than 9 μ g DNA. In some cases, the stabilized biological sample may comprise less than 8 μ g DNA. In some cases, the stabilized biological sample may comprise less than 7 μ g DNA. In some cases, the stabilized biological sample may comprise less than 6 μ g DNA. In some cases, the stabilized biological sample may comprise less than 5 μ g DNA. In some cases, the stabilized biological sample may comprise less than 4 μ g DNA. In some cases, the stabilized biological sample may comprise less than 3 μ g DNA. In some cases, the stabilized biological sample may comprise less than 2 μ g DNA. In some cases, the stabilized biological sample comprises less than 1 μ g DNA. In some cases, the stabilized biological sample comprises less than 0.5 μ g DNA.

[00244] In another aspect, methods involving a MNase digestion step herein may be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00245] In additional aspects, stabilized biological samples used in methods involving a MNase digestion step herein may be further treated with an additional nuclease, such as a DNase to create fragments of DNA. In some cases, the DNase may be non-sequence specific. In some cases, the DNase may be active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase may be specific for double-stranded DNA. In some cases, the DNase may preferentially cleave double-stranded DNA. In some cases, the DNase may be specific for single-stranded DNA. In some cases, the DNase may preferentially cleave single-stranded DNA. In some cases, the DNase can be DNase I. In some cases, the DNase can be DNase II. In some cases, the DNase may be selected from one or more of DNase I and DNase II. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. Other suitable nucleases are also within the scope of this disclosure.

[00246] In additional aspects, stabilized biological samples as provided herein for use in methods involving a MNase digestion step can be treated with a crosslinking agent. In some cases, the crosslinking agent may be a chemical fixative. In some cases, the chemical fixative comprises formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (A). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 A, 4 A, 5 A, 6 A, 7 A, 8 A, 9 A, 10 A, 11 A, 12 A, 13 A, 14 A, 15 A, 16 A, 17 A, 18 A, 19 A, or 20 A. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 A. The chemical fixative can comprise

disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 Å. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative may comprise psoralen. In some cases, the crosslinking agent may be ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, cicycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample may be a crosslinked paraffin-embedded tissue sample.

[00247] In further aspects, methods involving a MNase digestion step provided herein may comprise contacting the plurality of selected segments to an antibody. In some cases, an immunoglobulin binding protein or fragment thereof tethered to an oligonucleotide adaptor may be targeted to the antibody bound to a plurality of selected segments.

[00248] In additional aspects, methods involving a MNase digestion step provided herein may comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching may comprise filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching may comprise contacting at least the first segment and the second segment to a bridge oligonucleotide. In some cases, attaching may comprise contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein may be from at least about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides may be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may comprise a barcode.

[00249] In further aspects of methods involving a MNase digestion step herein, methods can comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the

methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about 150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00250] In additional aspects of methods involving a MNase digestion step herein, methods can comprise mapping the first read pair to a set of contigs, and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00251] In further aspects of methods involving a MNase digestion step herein, methods can comprise mapping the first read pair to a set of contigs; and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00252] In additional aspects of methods involving a MNase digestion step herein, methods can comprise mapping the first read pair to a set of contigs, and assigning a variant in the set of contigs to a phase.

[00253] In further aspects of methods involving a MNase digestion step herein, methods can comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs, and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Improved Methods for HiChIP, HiChIRP, and Methyl HiC

[00254] HiChIP is an approach combining methods of HiC with methods of chromatin immunoprecipitation, allowing targeted analysis of interactions involving one or more proteins of interest. A proximity ligated nucleic acid can be prepared, and targeted regions can be immunoprecipitated for further analysis. HiChIRP, a related approach, uses chromatin isolation by RNA purification (ChIRP) enrichment in combination with HiC methods, enabling the interrogation of RNAs, such as of the scaffolding function of long non-coding RNAs (lncRNAs). Methyl-HiC combines methylation analysis with HiC methods, allowing simultaneous capture of chromosome conformation and DNA methylome information. Methyl-HiC can reveal coordinated DNA methylation status between distal genomic segments that are in spatial proximity in the nucleus, delineate heterogeneity of both the chromatin architecture and DNA methylome in a mixed population, and enable simultaneous characterization of cell-type-specific chromatin organization and epigenome in complex tissues. These methods and other methods can be improved by use of the techniques of the present disclosure, including but not limited to size selection steps, surface binding steps (e.g., binding to a bead such as a SPRI bead), use of bridge oligonucleotides to conduct proximity ligation, use of recombination to conduct proximity ligation, and others.

[00255] In additional aspects, provided herein are improved methods for HiChIP, HiChIRP, and Methyl HiC that can comprise obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein, for example, by immunoprecipitation of nucleic acids bound to the nucleic acid binding protein or by immunoprecipitation of methylated nucleic acids; contacting the stabilized biological sample to a DNase to cleave the nucleic acid molecule into a plurality of segments; attaching a first segment and a second segment of the plurality of segments at a junction; and

subjecting the plurality of segments to size selection to obtain a plurality of selected segments.

Alternatively, or in combination, methods herein can comprise obtaining a stabilized biological sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein, for example, by immunoprecipitation of nucleic acids bound to the nucleic acid binding protein or by immunoprecipitation of methylated nucleic acids; contacting the stabilized biological sample to a micrococcal nuclease (MNase) to cleave the nucleic acid molecule into a plurality of segments; and attaching a first segment and a second segment of the plurality of segments at a junction.

[00256] In some aspects of improved methods for HiChIP, HiChIRP, and Methyl HiC herein, the stabilized biological sample can comprise intact cells and/or intact nuclei. In some cases, the stabilized biological sample can comprise a stabilized intact cell. Alternatively, or in combination, the stabilized biological sample can comprise a stabilized intact nucleus. In some cases, contacting the stabilized intact cell or intact nucleus sample to a DNase may be conducted prior to lysis of the intact cell or the intact nucleus. In some cases, cells and/or nuclei may be lysed prior to attaching a first segment and a second segment of a plurality of segments at a junction.

[00257] In another aspect, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein can comprise subjecting a plurality of segments to size selection to obtain a plurality of selected segments. In some cases, the plurality of selected segments may be from about 145 to about 600 bp. In some cases, the plurality of selected segments may be from about 100 to about 2500 bp. In some cases, the plurality of selected segments may be from about 100 to about 600 bp. In some cases, the plurality of selected segments may be from about 600 to about 2500 bp. In some cases, the plurality of selected segments may be from about 100 bp to about 600 bp, from about 100 bp to about 700 bp, from about 100 bp to about 800 bp, from about 100 bp to about 900 bp, from about 100 bp to about 1000 bp, from about 100 bp to about 1100 bp, from about 100 bp to about 1200 bp, from about 100 bp to about 1300 bp, from about 100 bp to about 1400 bp, from about 100 bp to about 1500 bp, from about 100 bp to about 1600 bp, from about 100 bp to about 1700 bp, from about 100 bp to about 1800 bp, from about 100 bp to about 1900 bp, from about 100 bp to about 2000 bp, from about 100 bp to about 2100 bp, from about 100 bp to about 2200 bp, from about 100 bp to about 2300 bp, from about 100 bp to about 2400 bp, or from about 100 bp to about 2500 bp.

[00258] In another aspect of methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein, the methods may further comprise, prior to a size selection step, preparing a sequencing library from the plurality of segments. In some embodiments, the method may further comprise subjecting the sequencing library to a size selection to obtain a size-selected library. In some cases, the size-selected library may be from about 350 bp to about 1000 bp in size. In some cases, the size-selected library may be from about 100 bp to about 2500 bp in size, for example, from about 100 bp to about 350 bp, from about 350 bp to about 500 bp, from about 500 bp to about 1000 bp, from about 1000 to about 1500 bp, from about 2000 bp to about 2500 bp, from about 350 bp to about 1000 bp, from about 350 bp to about 1500 bp, from about 350 bp to about 2000 bp, from about 350 bp to about 2500 bp, from about 500 bp to about 1500 bp, from about 500 bp to about 2000 bp, from about 500 bp to about 3500 bp, from about 1000 bp to

about 1500 bp, from about 1000 bp to about 2000 bp, from about 1000 bp to about 2500 bp, from about 1500 bp to about 2000 bp, from about 1500 bp to about 2500 bp, or from about 2000 bp to about 2500 bp.

[00259] Size selection utilized in methods involving improved methods for HiChIP, HiChIRP and Methyl HiC herein can be conducted with gel electrophoresis, capillary electrophoresis, size selection beads, a gel filtration column, combinations thereof, or any other suitable method.

[00260] In another aspect, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein may comprise further analyzing the plurality of selected segments to obtain a QC value. In some cases, a QC value may be selected from a chromatin digest efficiency (CDE) and a chromatin digest index (CDI). A CDE can be calculated as the proportion of segments having a desired length. For example, in some cases, the CDE can be calculated as the proportion of segments from 100 to 2500 bp in size prior to size selection. In some cases, a sample may be selected for further analysis when the CDE value is at least 65%. In some cases, a sample may be selected for further analysis when the CDE value is at least about 50%, at least about 55%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, or at least about 95%.

[00261] A CDI can be calculated as a ratio of a number of mononucleosome-sized segments to a number of dinucleosome-sized segments prior to size selection. For example, a CDI may be calculated as a logarithm of the ratio of fragments having a size 600-2500 bp versus fragments having a size 100-600 bp. In some cases, a sample may be selected for further analysis when the CDI value is greater than -1.5 and less than 1. In some cases, a sample may be selected for further analysis when the CDI value is greater than about -2 and less than about 1.5, greater than about -1.9 and less than about 1.5, greater than about -1.8 and less than about 1.5, greater than about -1.7 and less than about 1.5, greater than about -1.6 and less than about 1.5, greater than about -1.5 and less than about 1.5, greater than about -1.4 and less than about 1.5, greater than about -1.3 and less than about 1.5, greater than about -1.2 and less than about 1.5, greater than about -1.1 and less than about 1.5, greater than about -2 and less than about 1.5, greater than about -1 and less than about 1.5, greater than about -0.9 and less than about 1.5, greater than about -0.8 and less than about 1.5, greater than about -0.7 and less than about 1.5, greater than about -0.6 and less than about 1.5, greater than about -0.5 and less than about 1.5, greater than about -2 and less than about 1.4, greater than about -2 and less than about 1.3, greater than about -2 and less than about 1.2, greater than about -2 and less than about 1.1, greater than about -2 and less than about 1, greater than about -2 and less than about 0.9, greater than about -2 and less than about 0.8, greater than about -2 and less than about 0.7, greater than about -2 and less than about 0.6, or greater than about -2 and less than about 0.5.

[00262] In another aspect, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein can be conducted on small samples containing few cells or small amounts of nucleic acid. In some cases, the stabilized biological sample may comprise fewer than 3,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 2,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 1,000,000 cells. In some cases, the stabilized biological sample may comprise fewer than 500,000 cells. In some cases, the stabilized biological sample may comprise fewer than 400,000 cells. In some cases, the stabilized biological sample may comprise fewer

than 300,000 cells. In some cases, the stabilized biological sample may comprise fewer than 200,000 cells. In some cases, the stabilized biological sample may comprise fewer than 100,000 cells. In some cases, the stabilized biological sample comprises fewer than 50,000 cells. In some cases, the stabilized biological sample comprises fewer than 40,000 cells. In some cases, the stabilized biological sample comprises fewer than 30,000 cells. In some cases, the stabilized biological sample comprises fewer than 20,000 cells. In some cases, the stabilized biological sample comprises fewer than 10,000 cells. In some cases, the stabilized biological sample comprises about 10,000 cells. In some cases, the stabilized biological sample may comprise less than 10 μ g DNA. In some cases, the stabilized biological sample may comprise less than 9 μ g DNA. In some cases, the stabilized biological sample may comprise less than 8 μ g DNA. In some cases, the stabilized biological sample may comprise less than 7 μ g DNA. In some cases, the stabilized biological sample may comprise less than 6 μ g DNA. In some cases, the stabilized biological sample may comprise less than 5 μ g DNA. In some cases, the stabilized biological sample may comprise less than 4 μ g DNA. In some cases, the stabilized biological sample may comprise less than 3 μ g DNA. In some cases, the stabilized biological sample may comprise less than 2 μ g DNA. In some cases, the stabilized biological sample may comprise less than 1 μ g DNA. In some cases, the stabilized biological sample may comprise less than 0.5 μ g DNA.

[00263] In another aspect, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein may be conducted on individual or single cells. For example, methods herein may be conducted on cells distributed into individual partitions. Exemplary partitions include, but are not limited to, wells, droplets in an emulsion, or surface positions (e.g., array spots, beads, etc.) comprising distinct patches of differentially sequenced linker molecules as described elsewhere herein. Additional partitions are also contemplated and consistent with the methods, compositions, and systems disclosed herein.

[00264] In additional aspects, stabilized biological samples used in methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein can be treated with a nuclease, such as a DNase, to create fragments of DNA. In some cases, the DNase may be a non-sequence specific. In some cases, the DNase may be active for both single-stranded DNA and double-stranded DNA. In some cases, the DNase may be specific for double-stranded DNA. In some cases, the DNase may preferentially cleave double-stranded DNA. In some cases, the DNase may be specific for single-stranded DNA. In some cases, the DNase may preferentially cleave single-stranded DNA. In some cases, the DNase may be DNase I. In some cases, the DNase may be DNase II. In some cases, the DNase may be selected from one or more of DNase I and DNase II. In some cases, the DNase may be micrococcal nuclease. In some cases, the DNase may be selected from one or more of DNase I, DNase II, and micrococcal nuclease. In some cases, the DNase may be coupled or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. Other suitable nucleases are also within the scope of this disclosure.

[00265] In additional aspects, stabilized biological samples used in methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein may be treated with a crosslinking agent. In some cases, the crosslinking agent may be a chemical fixative. In some cases, the chemical fixative comprises

formaldehyde, which has a spacer arm length of about 2.3-2.7 angstrom (Å). In some cases, the chemical fixative comprises a crosslinking agent with a long spacer arm length. For example, the crosslinking agent can have a spacer length of at least about 3 Å, 4 Å, 5 Å, 6 Å, 7 Å, 8 Å, 9 Å, 10 Å, 11 Å, 12 Å, 13 Å, 14 Å, 15 Å, 16 Å, 17 Å, 18 Å, 19 Å, or 20 Å. The chemical fixative can comprise ethylene glycol bis(succinimidyl succinate) (EGS), which has a spacer arm with length about 16.1 Å. The chemical fixative can comprise disuccinimidyl glutarate (DSG), which has a spacer arm with length about 7.7 Å. In some cases, the chemical fixative comprises formaldehyde and EGS, formaldehyde and DSG, or formaldehyde, EGS, and DSG. In some cases where multiple chemical fixatives are employed, each chemical fixative is used sequentially; in other cases, some or all of the multiple chemical fixatives are applied to the sample at the same time. The use of crosslinkers with long spacer arms can increase the fraction of read pairs with large (e.g., > 1 kb) read pair separation distances. DSG is membrane-permeable, allowing for intracellular crosslinking. DSG can increase crosslinking efficiency compared to disuccinimidyl suberate (DSS) in some applications. EGS has NHS ester reactive groups at both ends and can be reactive towards amino groups (e.g., primary amines). EGS is membrane-permeable, allowing for intracellular crosslinking. EGS crosslinks can be reversed, for example, by treatment with hydroxylamine for 3 to 6 hours at pH 8.5; in an example, lactose dehydrogenase retained 60% of its activity after reversible crosslinking with EGS. In some cases, the chemical fixative may comprise psoralen. In some cases, the crosslinking agent may be ultraviolet light, chlormethine, cyclophosphamide, chlorambucil, uramustine, melphalan, bendamustine, bis(2-chloroethyl)ethylamine, bis(2-chloroethyl)methylamine, tris(2-chloroethyl)amine, isofamide, carmustine, lomustine, streptozocin, busulfan, cisplatin, carboplatin, ciccycloplatin, eptaplatin, lobaplatin, miriplatin, nedaplatin, oxaliplatin, picoplatin, satraplatin, triplatin tetranitrate, procarbazine, altretamine, dacarbazine, mitozolomide, temozolomide, mitomycin C, nitrous acid, formaldehyde, acetaldehyde, doxorubicin, daunorubicin, epirubicin, or idarubicin. In some cases, the crosslinking agent comprises an intercalating agent, an antibiotic, or a minor groove binding agent. In some cases, the stabilized biological sample may be a crosslinked paraffin-embedded tissue sample.

[00266] In additional aspects, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein may comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching can comprise filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In some cases, attaching can comprise contacting at least the first segment and the second segment to a bridge oligonucleotide. In some cases, attaching can comprise contacting at least the first segment and the second segment to a barcode. In some embodiments, bridge oligonucleotides herein may be from at least about 5 nucleotides in length to about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may be from about 15 to about 18 nucleotides in length. In some embodiments, bridge oligonucleotides may be about 5, about 6, about 7, about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 25, about 30, about 35, about 40, about 45, or about 50 nucleotides in length. In some embodiments, bridge oligonucleotides herein may comprise a barcode.

[00267] In additional aspects, methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein may not comprise a shearing step.

[00268] In further aspects of methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein, methods may comprise obtaining at least some sequence on each side of the junction to generate a first read pair. For example, the methods may comprise obtaining at least about 50 bp, at least about 100 bp, at least about 150 bp, at least about 200 bp, at least about 250 bp, or at least about 300 bp of sequence on each side of the junction to generate a first read pair.

[00269] In additional aspects of methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein, methods may comprise mapping the first read pair to a set of contigs and determining a path through the set of contigs that represents an order and/or orientation to a genome.

[00270] In further aspects of methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein, methods may comprise mapping the first read pair to a set of contigs; and determining, from the set of contigs, a presence of a structural variant or loss of heterozygosity in the stabilized biological sample.

[00271] In additional aspects of methods involving digestion of whole cells or whole nuclei herein, methods may comprise mapping the first read pair to a set of contigs and assigning a variant in the set of contigs to a phase.

[00272] In further aspects of methods involving improved methods for HiChIP, HiChIRP, and Methyl HiC herein, methods may comprise mapping the first read pair to a set of contigs; determining, from the set of contigs, a presence of a variant in the set of contigs; and conducting a step selected from one or more of: (1) identifying a disease stage, a prognosis, or a course of treatment for the stabilized biological sample; (2) selecting a drug based on the presence of the variant; or (3) identifying a drug efficacy for the stabilized biological sample.

Generating Long-Range Read Pairs

[00273] The disclosure provides methods for generating extremely long-range read pairs and to utilize that data for the advancement of all of the aforementioned pursuits. In some embodiments, the disclosure provides methods that produce a highly contiguous and accurate human genomic assembly with only ~300 million read pairs. In other embodiments, the disclosure provides methods that phase 90% or more of heterozygous variants in a human genome with 99% or greater accuracy. Further, the range of the read pairs generated by the disclosure can be extended to span much larger genomic distances. The assembly is produced from a standard shotgun library in addition to an extremely long-range read pair library. In yet other embodiments, the disclosure provides software that is capable of utilizing both of these sets of sequencing data. Phased variants are produced with a single long-range read pair library, the reads from which are mapped to a reference genome and then used to assign variants to one of the individual's two parental chromosomes. Finally, the disclosure provides for the extraction of even larger DNA fragments using known techniques, so as to generate exceptionally long reads.

[00274] The mechanism by which these repeats obstruct assembly and alignment processes is fairly straightforward and is ultimately a consequence of ambiguity. In the case of large repetitive regions, the

difficulty can be one of span. If a read or read pair is not long enough to span a repetitive region, one may not be able to confidently connect regions bordering the repetitive element. In the case of smaller repetitive elements, the problem can be primarily placement. When a region is flanked by two repetitive elements that are common in the genome, determining its exact placement becomes difficult, if not impossible, due to the similarity of the flanking elements to all others of their class. In both cases, it is the lack of distinguishing information in the repeat that makes the identification, and thus placement of a particular repeat, challenging. What is needed is the ability to experimentally establish connection between unique segments hemmed or separated by repetitive regions.

[00275] The methods of the disclosure advance the field of genomics by overcoming the substantial barriers posed by these repetitive regions, and can thereby enable important advances in many domains of genomic analysis. To perform a de novo assembly with previous technologies, one must either settle for an assembly fragmented into many small scaffolds or commit substantial time and resources to producing a large-insert library or using other approaches to generate a more contiguous assembly. Such approaches may include acquiring very deep sequencing coverage, constructing BAC or fosmid libraries, optical mapping, or some combination of these and/or other techniques. The intense resource and time requirements put such approaches out of reach for most small labs and prevents studying non-model organisms. Since the methods described herein can produce very long-range read pairs, de novo assembly can be achieved with a single sequencing run. This would cut assembly costs by orders of magnitude and shorten the time required from months or years to weeks. In some cases, the methods disclosed herein allow for generating a plurality of read-pairs in less than 14 days, less than 13 days, less than 12 days, less than 11 days, less than 10 days, less than 9 days, less than 8 days, less than 7 days, less than 6 days, less than 5 days, less than 4 days, or in a range between any two of foregoing specified time periods. For example, the methods can allow for generating a plurality of read-pairs in about 10 days to 14 days. Building genomes for even the most niche of organisms would become routine, phylogenetic analyses would suffer no lack of comparisons, and projects such as Genome 10k could be realized.

[00276] Similarly, structural and phasing analyses for medical purposes also remain challenging. There is astounding heterogeneity among cancers, individuals with the same type of cancer, or even within the same tumor. Teasing out the causative from consequential effects requires very high precision and throughput at a low per-sample cost. In the domain of personalized medicine, one of the gold standards of genomic care is a sequenced genome with all variants thoroughly characterized and phased, including large and small structural rearrangements and novel mutations. To achieve this with previous technologies demands effort akin to that required for a de novo assembly, which is currently too expensive and laborious to be a routine medical procedure. The disclosed methods can rapidly produce complete, accurate genomes at low cost and can thereby yield many highly sought capabilities in the study and treatment of human disease.

[00277] Applying the methods disclosed herein to phasing can combine the convenience of statistical approaches with the accuracy of familial analysis, providing savings – money, labor, and samples – than using either method alone. De novo variant phasing, a highly desirable phasing analysis that is prohibitive

with previous technologies, can be performed readily using the methods disclosed herein. This is particularly important as the vast majority of human variation is rare (less than 5% minor allele frequency). Phasing information is valuable for population genetic studies that gain significant advantages from networks of highly connected haplotypes (collections of variants assigned to a single chromosome), relative to unlinked genotypes. Haplotype information can enable higher resolution studies of historical changes in population size, migrations, and exchange between subpopulations, and allows us to trace specific variants back to particular parents and grandparents. This in turn clarifies the genetic transmission of variants associated with disease, and the interplay between variants when brought together in a single individual. The methods of the disclosure can eventually enable the preparation, sequencing, and analysis of extremely long range read pair (XLRP) libraries.

[00278] In some embodiments of the disclosure, a tissue or a DNA sample from a subject can be provided and the method can return an assembled genome, alignments with called variants (including large structural variants), phased variant calls, or any additional analyses. In other embodiments, the methods disclosed herein can provide XLRP libraries directly for the individual.

Extremely Long-Range Read Pairs

[00279] In various embodiments of the disclosure, the methods disclosed herein can generate extremely long-range read pairs separated by large distances. The upper limit of this distance may be improved by the ability to collect DNA samples of large size. In some cases, the read pairs can span up to 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 225, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 1500, 2000, 2500, 3000, 4000, 5000 kbp or more in genomic distance. In some examples, the read pairs can span up to 500 kbp in genomic distance. In other examples, the read pairs can span up to 2000 kbp in genomic distance. The methods disclosed herein can integrate and build upon standard techniques in molecular biology, and are further well-suited for increases in efficiency, specificity, and genomic coverage. In some cases, the read pairs can be generated in less than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 60, or 90 days. In some examples, the read pairs can be generated in less than about 14 days. In further examples, the read pairs can be generated in less about 10 days. In some cases, the methods of the present disclosure can provide greater than about 5%, about 10%, about 15 %, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, or about 100% of the read pairs with at least about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, or about 100% accuracy in correctly ordering and/or orientating the plurality of contigs. For example, the methods can provide about 90 to 100% accuracy in correctly ordering and/or orientating the plurality of contigs.

[00280] In other embodiments, the methods disclosed herein can be used with currently employed sequencing technology. For example, the methods can be used in combination with well-tested and/or widely deployed sequencing instruments. In further embodiments, the methods disclosed herein can be used with technologies and approaches derived from currently employed sequencing technology.

[00281] The methods of the disclosure dramatically simplify de novo genomic assembly for a wide range of organisms. Using previous technologies, such assemblies are currently limited by the short inserts of

economical mate-pair libraries. While it may be possible to generate read pairs at genomic distances up to the 40-50 kbp accessible with fosmids, these are expensive, cumbersome, and too short to span the longest repetitive stretches, including those within centromeres, which – in humans – can range in size from 300 kbp to 5 Mbp. The methods disclosed herein can provide read pairs capable of spanning large distances (e.g., megabases or longer) and thereby overcome these scaffold integrity challenges. Accordingly, producing chromosome-level assemblies can be routine by utilizing the methods of the disclosure. More laborious avenues for assembly – currently costing research labs incredible amounts of time and money, and prohibiting expansive genomic catalogs – may become unnecessary, freeing up resources for more meaningful analyses. Similarly, the acquisition of long-range phasing information can provide tremendous additional power to population genomic, phylogenetic, and disease studies. The methods disclosed herein enable accurate phasing for large numbers of individuals, thus extending the breadth and depth of our ability to probe genomes at the population and deep-time levels.

[00282] In the realm of personalized medicine, the XLRP read pairs generated from the methods disclosed herein represent a meaningful advance toward accurate, low-cost, phased, and rapidly produced personal genomes. Current methods are insufficient in their ability to phase variants at long distances, thereby preventing the characterization of the phenotypic impact of compound heterozygous genotypes. Additionally, structural variants of substantial interest for genomic diseases are difficult to accurately identify and characterize with current techniques due to their large size in comparison to reads and read pair inserts used to study them. Read pairs spanning tens of kilobases to megabases or longer can help alleviate this difficulty, thereby allowing for highly parallel and personalized analyses of structural variation.

[00283] Basic evolutionary and biomedical research is being driven by technological advances in high-throughput sequencing. Whereas whole genome sequencing and assembly used to be the provenance of large genome sequencing centers, commercially available sequencers are now inexpensive enough that most research universities have one or several of these machines. It is now relatively inexpensive to generate massive quantities of DNA sequence data. However, it remains difficult in theory and in practice to produce high-quality, highly contiguous genome sequences with current technology. Furthermore, because most organisms that one would care to analyze, including humans, are diploid, each individual has two haploid copies of the genome. At sites of heterozygosity (e.g., where the allele given by the mother differs from the allele given by the father), it is difficult to know which sets of alleles came from which parent (known as haplotype phasing). This information can be used for performing a number of evolutionary and biomedical studies such as disease and trait association studies.

[00284] In various embodiments, the disclosure provides methods for genome assembly that combine technologies for DNA preparation with paired-end sequencing for high-throughput discovery of short, intermediate, and long-term connections within a given genome. The disclosure further provides methods using these connections to assist in genome assembly, for haplotype phasing, and/or for metagenomic studies. While the methods presented herein can be used to determine the assembly of a subject's genome, it should also be understood that the methods presented herein can also be used to determine the assembly

of portions of the subject's genome such as chromosomes, or the assembly of the subject's chromatin of varying lengths.

[00285] In some embodiments, the disclosure provides for one or more methods disclosed herein that comprise the step of generating a plurality of contigs from sequencing fragments of target DNA obtained from a subject. Long stretches of target DNA can be fragmented by cutting the DNA with one or more nucleases (e.g., DNase I, DNase II, micrococcal nuclease, etc.). The resulting fragments can be sequenced using high-throughput sequencing methods to obtain a plurality of sequencing reads. Examples of high-throughput sequencing methods which can be used with the methods of the disclosure include, but are not limited to, 454 pyrosequencing methods developed Roche Diagnostics, "clusters" sequencing methods developed by Illumina, SOLiD and Ion semiconductor sequencing methods developed by Life Technologies, and DNA nanoball sequencing methods developed by Complete Genomics. Overlapping ends of different sequencing reads can then be assembled to form a contig. Alternatively, fragmented target DNA can be cloned into vectors. Cells or organisms are then transfected with the DNA vectors to form a library. After replicating the transfected cells or organisms, the vectors are isolated and sequenced to generate a plurality of sequencing reads. The overlapping ends of different sequencing reads can then be assembled to form a contig.

[00286] Genome assembly, especially with high-throughput sequencing technology, can be problematic. Often, the assembly consists of thousands or tens of thousands of short contigs. The order and orientation of these contigs is generally unknown, limiting the usefulness of the genome assembly. Technologies exist to order and orient these scaffolds, but they are generally expensive, labor intensive, and often fail in discovering very long-range interactions.

[00287] Samples comprising target DNA used to generate contigs can be obtained from a subject by any number of means, including by taking bodily fluids (e.g., blood, urine, serum, lymph, saliva, buccal swab, anal and vaginal secretions, perspiration, and semen, etc.), taking tissue, or by collecting cells/organisms. The sample obtained may be comprised of a single type of cell/organism, or may be comprised multiple types of cells/organisms. The DNA can be extracted and prepared from the subject's sample. For example, the sample may be treated to lyse a cell comprising the polynucleotide, using known lysis buffers, sonication techniques, electroporation, and the like. The target DNA may be further purified to remove contaminants, such as proteins, by using alcohol extractions, cesium gradients, and/or column chromatography.

[00288] In other embodiments of the disclosure, a method to extract very high molecular weight DNA is provided. In some cases, the data from an XLRP library can be improved by increasing the fragment size of the input DNA. In some examples, extracting megabase-sized fragments of DNA from a cell can produce read pairs separated by megabases in the genome. In some cases, the produced read-pairs can provide sequence information over a span of greater than about 10 kB, about 50 kB, about 100 kB, about 200 kB, about 500 kB, about 1 Mb, about 2 Mb, about 5 Mb, about 10 Mb, or about 100 Mb. In some examples, the read-pairs can provide sequence information over a span of greater than about 500 kB. In further examples, the read-pairs can provide sequence information over a span of greater than about 2 Mb.

In some cases, the very high molecular weight DNA can be extracted by very gentle cell lysis (Teague, B. et al. (2010) Proc. Nat. Acad. Sci. USA 107(24), 10848–53) and agarose plugs (Schwartz, D. C., & Cantor, C. R. (1984) Cell, 37(1), 67–75). In other cases, commercially available machines that can purify DNA molecules up to megabases in length can be used to extract very high molecular weight DNA.

Probing Physical Layout of Chromosomes

[00289] In various embodiments, the disclosure provides for one or more methods disclosed herein that comprise the step of probing the physical layout of chromosomes within living cells. Examples of techniques to probe the physical layout of chromosomes through sequencing include the “C” family of techniques, such as chromosome conformation capture (“3C”), circularized chromosome conformation capture (“4C”), carbon-copy chromosome capture (“5C”), and Hi-C based methods; and ChIP based methods, such as ChIP-loop, ChIA-PET, and HiChIP. These techniques utilize the fixation of chromatin in live cells to cement spatial relationships in the nucleus. Subsequent processing and sequencing of the products allows a researcher to recover a matrix of proximate associations among genomic regions. With further analysis these associations can be used to produce a three-dimensional geometric map of the chromosomes as they are physically arranged in live nuclei. Such techniques describe the discrete spatial organization of chromosomes in live cells, and provide an accurate view of the functional interactions among chromosomal loci. One issue that plagued these functional studies was the presence of nonspecific interactions, associations present in the data that are attributable to nothing more than chromosomal proximity. In the disclosure, these nonspecific intrachromosomal interactions are captured by the methods presented herein so as to provide valuable information for assembly.

[00290] In some embodiments, the intrachromosomal interactions correlate with chromosomal connectivity. In some cases, the intrachromosomal data can aid genomic assembly. In some cases, the chromatin is reconstructed in vitro. This can be advantageous because chromatin – particularly histones, the major protein component of chromatin – is important for fixation under the most common “C” family of techniques for detecting chromatin conformation and structure through sequencing: 3C, 4C, 5C, and Hi-C. Chromatin is highly non-specific in terms of sequence and will generally assemble uniformly across the genome. In some cases, the genomes of species that do not use chromatin can be assembled on a reconstructed chromatin and thereby extend the horizon for the disclosure to all domains of life.

[00291] A chromatin conformation capture technique is summarized. In brief, cross-links are created between genome regions that are in close physical proximity. Crosslinking of proteins (such as histones) to the DNA molecule, e.g., genomic DNA, within chromatin can be accomplished according to a suitable method described in further detail elsewhere herein or otherwise known. In some cases, two or more nucleotide sequences can be cross-linked via proteins bound to one or more nucleotide sequences. One approach is to expose the chromatin to ultraviolet irradiation (Gilmour et al., Proc. Nat'l. Acad. Sci. USA 81:4275-4279, 1984). Crosslinking of polynucleotide segments may also be performed utilizing other approaches, such as chemical or physical (e.g., optical) crosslinking. Suitable chemical crosslinking agents include, but are not limited to, formaldehyde and psoralen (Solomon et al., Proc. Nat'l. Acad. Sci. USA 82:6470-6474, 1985; Solomon et al., Cell 53:937-947, 1988). For example, cross-linking can be

performed by adding 2% formaldehyde to a mixture comprising the DNA molecule and chromatin proteins. Other examples of agents that can be used to cross-link DNA include, but are not limited to, UV light, mitomycin C, nitrogen mustard, melphalan, 1,3-butadiene diepoxide, cis diamminedichloroplatinum(II), and cyclophosphamide. Suitably, the cross-linking agent will form cross-links that bridge relatively short distances—such as about 2 Å—thereby selecting intimate interactions that can be reversed.

[00292] In some embodiments, the DNA molecule may be immunoprecipitated prior to or after crosslinking. In some cases, the DNA molecule can be fragmented. Fragments may be contacted with a binding partner, such as an antibody that specifically recognizes and binds to acetylated histones, e.g., H3. Examples of such antibodies include, but are not limited to, Anti Acetylated Histone H3, available from Upstate Biotechnology, Lake Placid, N.Y. The polynucleotides from the immunoprecipitate can subsequently be collected from the immunoprecipitate. Prior to fragmenting the chromatin, the acetylated histones can be crosslinked to adjacent polynucleotide sequences. The mixture is then treated to fractionate polynucleotides in the mixture. Fractionation techniques herein comprise use of deoxyribonuclease (DNase) enzymes. DNases suitable for methods herein include, but are not limited to, DNase I, DNase II, and micrococcal nuclease. The resulting fragments can vary in size. The resulting fragments may also comprise a single-stranded overhang at the 5' or 3' end.

[00293] In some embodiments, fragments of about 145 bp to about 600 bp can be obtained. Alternatively, fragments of about 100 bp to about 2500 bp, about 100 bp to about 600 bp, or about 600 to about 2500 can be obtained. The sample can be prepared for sequencing of coupled sequence segments that are cross-linked. In some cases, a single, short stretch of polynucleotide can be created, for example, by ligating two sequence segments that were intramolecularly crosslinked. Sequence information may be obtained from the sample using any suitable sequencing technique described in further detail elsewhere herein or other suitable methods, such as a high-throughput sequencing method. For example, ligation products can be subjected to paired-end sequencing obtaining sequence information from each end of a fragment. Pairs of sequence segments can be represented in the obtained sequence information, associating haplotyping information over a linear distance separating the two sequence segments along the polynucleotide.

[00294] One feature of the data generated by Hi-C is that most reads pairs, when mapped back to the genome, are found to be in close linear proximity. That is, most read pairs are found to be close to one another in the genome. In the resulting data sets, the probability of intrachromosomal contacts is on average much higher than that of interchromosomal contacts, as expected if chromosomes occupy distinct territories. Moreover, although the probability of interaction decays rapidly with linear distance, even loci separated by > 200 Mb on the same chromosome are more likely to interact than loci on different chromosomes. In detecting long-range intra-chromosomal and especially inter-chromosomal contacts, this “background” of short and intermediate range intra-chromosomal contacts is background noise to be factored out using Hi-C analysis.

[00295] Notably, Hi-C experiments in eukaryotes have shown, in addition to species-specific and cell type-specific chromatin interactions, two canonical interaction patterns. One pattern, distance-dependent

decay (DDD), is a general trend of decay in interaction frequency as a function of genomic distance. The second pattern, cis-trans ratio (CTR), is a significantly higher interaction frequency between loci located on the same chromosome, even when separated by tens of megabases of sequence, versus loci on different chromosomes. These patterns may reflect general polymer dynamics, where proximal loci have a higher probability of randomly interacting, as well as specific nuclear organization features such as the formation of chromosome territories, the phenomenon of interphase chromosomes tending to occupy distinct volumes in the nucleus with little mixing. Although the exact details of these two patterns may vary between species, cell types and cellular conditions, they are ubiquitous and prominent. These patterns are so strong and consistent that they are used to assess experiment quality and are usually normalized out of the data in order to reveal detailed interactions. However, in the methods disclosed herein, genome assembly can take advantage of the three-dimensional structure of genomes. Features which make the canonical Hi-C interaction patterns a hindrance for the analysis of specific looping interactions, namely their ubiquity, strength, and consistency, can be used as powerful tool for estimating the genomic position of contigs.

[00296] In a particular implementation, examination of the physical distance between intra-chromosomal read pairs indicates several useful features of the data with respect to genome assembly. First, shorter range interactions are more common than longer-range interactions. That is, each read of a read-pair is more likely to be mated with a region close by in the actual genome than it is to be with a region that is far away. Second, there is a long tail of intermediate and long-range interactions. That is, read-pairs carry information about intra-chromosomal arrangement at kilobase (kB) or even megabase (Mb) distances. For example, read-pairs can provide sequence information over a span of greater than about 10 kB, about 50 kB, about 100 kB, about 200 kB, about 500 kB, about 1 Mb, about 2 Mb, about 5 Mb, about 10 Mb, or about 100 Mb. These features of the data simply indicate that regions of the genome that are nearby on the same chromosome are more likely to be in close physical proximity – an expected result because they are chemically linked to one another through the DNA backbone. It was speculated that genome-wide chromatin interaction data sets, such as those generated by Hi-C, would provide long-range information about the grouping and linear organization of sequences along entire chromosomes.

[00297] Although the experimental methods for Hi-C are straightforward and relatively low cost, current protocols for genome assembly and haplotyping require 3-5 million cells, a fairly large amount of material that may not be feasible to obtain, particularly from certain human patient samples. By contrast, the methods disclosed herein include methods that allow for accurate and predictive results for genotype assembly, haplotype phasing, and metagenomics with significantly less material from cells. For example, less than about 0.1 µg, about 0.2 µg, about 0.3 µg, about 0.4 µg, about 0.5 µg, about 0.6 µg, about 0.7 µg, about 0.8 µg, about 0.9 µg, about 1.0 µg, about 1.2 µg, about 1.4 µg, about 1.6 µg, about 1.8 µg, about 2.0 µg, about 2.5 µg, about 3.0 µg, about 3.5 µg, about 4.0 µg, about 4.5 µg, about 5.0 µg, about 6.0 µg, about 7.0 µg, about 8.0 µg, about 9.0 µg, about 10 µg, about 15 µg, about 20 µg, about 30 µg, about 40 µg, about 50 µg, about 60 µg, about 70 µg, about 80 µg, about 90 µg, about 100 µg, about 150 µg, about 200 µg, about 300 µg, about 400 µg, about 500 µg, about 600 µg, about 700 µg, about 800 µg, about 900 µg,

about 1000 µg, about 1200 µg, about 1400 µg, about 1600 µg, about 1800 µg, about 2000 µg, about 2200 µg, about 2400 µg, about 2600 µg, about 2800 µg, about 3000 µg, about 3200 µg, about 3400 µg, about 3600 µg, about 3800 µg, about 4000 µg, about 4200 µg, about 4400 µg, about 4600 µg, about 4800 µg, about 5000 µg, about 5200 µg, about 5400 µg, about 5600 µg, about 5800 µg, about 6000 µg, about 6200 µg, about 6400 µg, about 6600 µg, about 6800 µg, about 7000 µg, about 7200 µg, about 7400 µg, about 7600 µg, about 7800 µg, about 8000 µg, about 8200 µg, about 8400 µg, about 8600 µg, about 8800 µg, about 9000 µg, about 9200 µg, about 9400 µg, about 9600 µg, about 9800 µg, or about 10,000 µg of DNA can be used with the methods disclosed herein. In some examples, the DNA used in the methods disclosed herein can be extracted from less than about 3,000,000, about 2,500,000, about 2,000,000, about 1,500,000, about 1,000,000, about 500,000, about 100,000, about 50,000, about 10,000, about 5,000, about 1,000, about 500, or about 100 cells.

[00298] Universally, procedures for probing the physical layout of chromosomes, such as Hi-C based techniques, utilize chromatin that is formed within a cell/organism, such as chromatin isolated from cultured cells or primary tissue. The disclosure provides not only for the use of such techniques with chromatin isolated from a cell/organism but also with reconstituted chromatin. Reconstituted chromatin is differentiated from chromatin formed within a cell/organism over various features. First, for many samples, the collection of naked DNA samples can be achieved by using a variety of noninvasive to invasive methods, such as by collecting bodily fluids, swabbing buccal or rectal areas, taking epithelial samples, etc. Second, reconstituting chromatin substantially prevents the formation of inter-chromosomal and other long-range interactions that generate artifacts for genome assembly and haplotype phasing. In some cases, a sample may have less than about 20, 15, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0.5, 0.4, 0.3, 0.2, 0.1% or less inter-chromosomal or intermolecular crosslinking according to the methods and compositions of the disclosure. In some examples, the sample may have less than about 5% inter-chromosomal or intermolecular crosslinking. In some examples, the sample may have less than about 3% inter-chromosomal or intermolecular crosslinking. In further examples, may have less than about 1% inter-chromosomal or intermolecular crosslinking. Third, the frequency of sites that are capable of crosslinking and thus the frequency of intramolecular crosslinks within the polynucleotide can be adjusted. For example, the ratio of DNA to histones can be varied, such that the nucleosome density can be adjusted to a desired value. In some cases, the nucleosome density is reduced below the physiological level. Accordingly, the distribution of crosslinks can be altered to favor longer-range interactions. In some embodiments, sub-samples with varying cross-linking density may be prepared to cover both short- and long-range associations. For example, the crosslinking conditions can be adjusted such that at least about 1%, about 2%, about 3%, about 4%, about 5%, about 6%, about 7%, about 8%, about 9%, about 10%, about 11%, about 12%, about 13%, about 14%, about 15%, about 16%, about 17%, about 18%, about 19%, about 20%, about 25%, about 30%, about 40%, about 45%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, or about 100% of the crosslinks occur between DNA segments that are at least about 50 kb, about 60 kb, about 70 kb, about 80 kb, about 90 kb, about 100 kb, about 110 kb, about 120 kb, about 130 kb, about 140 kb, about 150 kb, about 160 kb, about 180 kb, about 200 kb, about

250 kb, about 300 kb, about 350 kb, about 400 kb, about 450 kb, or about 500 kb apart on the sample DNA molecule.

Contact Mapping and Topology

[00299] Read pairs generated by methods of the present disclosure can be used to analyze the three-dimensional structure of a genome and of chromosomes and nucleic acid molecules therein. As discussed herein, each read in a read pair can be mapped to different regions in the genome. It can be inferred that, for a given read pair, the two different regions in the genome that they map to would have been in spatial proximity to each other, in order to be able to be ligated together. By plotting read pairs from a sample according to the coordinates of both reads in the read pair, a contact map can be created for the sample.

[00300] Analysis of contacts throughout a sample can allow analysis of the structure of chromosomes and genomes. The organization of a genome into A and B compartments, active and inactive compartments, chromosomal compartments, euchromatin and heterochromatin, topologically-associating domains (TADs) including TAD subtypes, and other structures, can be analyzed, on scales as large as kilobase- or megabase-scale. Analysis of contact maps can also allow detection of genomic features such as structural variants such as rearrangements, translocations, copy number variations, inversions, deletions, and insertions.

[00301] Methods of the present disclosure can provide locations of protein binding, structural variation, or genome contact interactions at a resolution of less than or equal to about 1 bp, 2 bp, 3 bp, 4 bp, 5 bp, 6 bp, 7 bp, 8 bp, 9 bp, 10 bp, 20 bp, 30 bp, 40 bp, 50 bp, 60 bp, 70 bp, 80 bp, 90 bp, 100 bp, 200 bp, 300 bp, 400 bp, 500 bp, 600 bp, 700 bp, 800 bp, 900 bp, 1000 bp, 2000 bp, 3000 bp, 4000 bp, 5000 bp, 6000 bp, 7000 bp, 8000 bp, 9000 bp, 10 kb, 20 kb, 30 kb, 40 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb, or 100 kb. In some cases, protein binding sites, protein footprints, contact interactions, or other features can be mapped to within 1000 bp, within 900 bp, within 800 bp, within 700 bp, within 600 bp, within 500 bp, within 400 bp, within 300 bp, within 200 bp, within 190 bp, within 180 bp, within 170 bp, within 160 bp, within 150 bp, within 140 bp, within 130 bp, within 120 bp, within 110 bp, within 100 bp, within 90 bp, within 80 bp, within 70 bp, within 60 bp, within 50 bp, within 40 bp, within 30 bp, within 20 bp, within 10 bp, within 9 bp, within 8 bp, within 7 bp, within 6 bp, within 5 bp, within 4 bp, within 3 bp, within 2 bp, or within 1 bp. In an example, methods of the present disclosure can enable resolution of sites (e.g., protein binding sites such as CTCF sites) that are within 10,000 bp, 5,000 bp, 2,000 bp, or 1,000 bp of each other on a genome. In some cases, improved resolution or mapping can be achieved by the use of MNase or other endonucleases that degrade unprotected nucleic acids (e.g., nucleic acids not within the footprint of a binding protein), thereby resulting in proximity ligation events that occur at the edge of a protected region (e.g., a protein footprint).

Contig Mapping

[00302] In various embodiments, the disclosure provides a variety of methods that enable the mapping of the plurality of read pairs to the plurality of contigs. There are several publicly available computer programs for mapping reads to contig sequences. These read-mapping programs data also provide data describing how unique a particular read-mapping is within the genome. From the population of reads that

map uniquely, with high confidence within a contig, we can infer the distribution of distances between reads in each read pair. For read pairs whose reads map confidently to different contigs, this mapping data implies a connection between the two contigs in question. It also implies a distance between the two contigs that is proportional to the distribution of distances learned from the analysis described above. Thus, each read pair whose reads map to different contigs implies a connection between those two contigs in a correct assembly. The connections inferred from all such mapped read pairs can be summarized in an adjacency matrix wherein each contig is represented by both a row and column. Read pairs that connect contigs are marked as a non-zero value in the corresponding row and column denoting the contigs to which the reads in the read pair were mapped. Most of the read pairs will map within in a contig, and from which the distribution of distances between read pairs can be learned, and from which an adjacency matrix of contigs can be constructed using read pairs that map to different contigs.

[00303] In various embodiments, the disclosure provides methods comprising constructing an adjacency matrix of contigs using the read-mapping data from the read-pair data. In some embodiments, the adjacency matrix uses a weighting scheme for read pairs that incorporate the tendency for short-range interactions over long-range interactions. Read pairs spanning shorter distances are generally more common than read pairs that span longer distances. A function describing the probability of a particular distance can be fit using the read pair data that map to a single contig to learn this distribution. Therefore, one important feature of read pairs that map to different contigs is the position on the contig where they map. For read pairs that both map near one end of a contig, the inferred distance between these contigs can be short and therefore the distance between the joined reads small. Since shorter distances between read pairs are more common than longer distances, this configuration provides stronger evidence that these two contigs are adjacent than would reads mapping far from the edges of the contig. Therefore, the connections in the adjacency matrix are further weighted by the distance of the reads to the edge of the contigs. In further embodiments, the adjacency matrix can further be re-scaled to down-weight the high number of contacts on some contigs that represent promiscuous regions of the genome. These regions of the genome, identifiable by having a high proportion of reads mapping to them, are a priori more likely to contain spurious read mappings that might misinform assembly. In yet further embodiments, this scaling can be directed by searching for one or more conserved binding sites for one or more agents that regulate the scaffolding interactions of chromatin, such as transcriptional repressor CTCF, endocrine receptors, cohesins, or covalently modified histones.

[00304] In some embodiments, the disclosure provides for one or more methods disclosed herein that comprise a step of analyzing the adjacency matrix to determine a path through the contigs that represent their order and/or orientation to the genome. In other embodiments, the path through the contigs can be chosen so that each contig is visited exactly once. In further embodiments, the path through the contigs is chosen so that the path through the adjacency matrix maximizes the sum of edge-weights visited. In this way, the most probably contig connections are proposed for the correct assembly. In yet further embodiments, the path through the contigs can be chosen so that each contig is visited exactly once and that edge-weighting of adjacency matrix is maximized.

Haplotype Phasing

[00305] In diploid genomes, it is often important to know which allelic variants are linked on the same chromosome. This is known as the haplotype phasing. Short reads from high-throughput sequence data rarely allow one to directly observe which allelic variants are linked. Computational inference of haplotype phasing can be unreliable at long distances. The disclosure provides one or more methods that allow for determining which allelic variants are linked using allelic variants on read pairs. In some cases, phasing with methods of the present disclosure is conducted without imputation.

[00306] In various embodiments, the methods and compositions of the disclosure enable the haplotype phasing of diploid or polyploid genomes with regard to a plurality of allelic variants. The methods described herein can thus provide for the determination of linked allelic variants that are linked based on variant information from read pairs and/or assembled contigs using the same. Examples of allelic variants include, but are not limited to, those that are known from the 1000genomes, UK10K, HapMap and other projects for discovering genetic variation among humans. Disease association to a specific gene can be revealed more easily by having haplotype phasing data as demonstrated, for example, by the finding of unlinked, inactivating mutations in both copies of SH3TC2 leading to Charcot-Marie-Tooth neuropathy (Lupski JR, Reid JG, Gonzaga-Jauregui C, et al. N. Engl. J. Med. 362:1181–91, 2010) and unlinked, inactivating mutations in both copies of ABCG5 leading to hypercholesterolemia 9 (Rios J, Stein E, Shendure J, et al. Hum. Mol. Genet. 19:4313–18, 2010).

[00307] Humans are heterozygous at an average of 1 site in 1,000. In some cases, a single lane of data using high-throughput sequencing methods can generate at least about 150,000,000 read pairs. Read pairs can be about 100 base pairs long. From these parameters, one-tenth of all reads from a human sample is estimated to cover a heterozygous site. Thus, on average one-hundredth of all read pairs from a human sample is estimated to cover a pair of heterozygous sites. Accordingly, about 1,500,000 read pairs (one-hundredth of 150,000,000) provide phasing data using a single lane. With approximately 3 billion bases in the human genome, and one in one-thousand being heterozygous, there are approximately 3 million heterozygous sites in an average human genome. With about 1,500,000 read pairs that represent a pair of heterozygous sites, the average coverage of each heterozygous site to be phased using a single lane of a high-throughput sequence method is about (1X), using a typical high-throughput sequencing machine. A diploid human genome can therefore be reliably and completely phased with one lane of a high-throughput sequence data relating sequence variants from a sample that is prepared using the methods disclosed herein. In some examples, a lane of data can be a set of DNA sequence read data. In further examples, a lane of data can be a set of DNA sequence read data from a single run of a high-throughput sequencing instrument.

[00308] As the human genome consists of two homologous sets of chromosomes, understanding the true genetic makeup of an individual requires delineation of the maternal and paternal copies or haplotypes of the genetic material. Obtaining a haplotype in an individual is useful in several ways. First, haplotypes are useful clinically in predicting outcomes for donor-host matching in organ transplantation and are increasingly used as a means to detect disease associations. Second, in genes that show compound

heterozygosity, haplotypes provide information as to whether two deleterious variants are located on the same allele, greatly affecting the prediction of whether inheritance of these variants is harmful. Third, haplotypes from groups of individuals have provided information on population structure and the evolutionary history of the human race. Lastly, recently described widespread allelic imbalances in gene expression suggest that genetic or epigenetic differences between alleles may contribute to quantitative differences in expression. An understanding of haplotype structure will delineate the mechanisms of variants that contribute to allelic imbalances.

[00309] In certain embodiments, the methods disclosed herein comprise an in vitro technique to fix and capture associations among distant regions of a genome as needed for long-range linkage and phasing. In some cases, the method comprises constructing and sequencing an XLRP library to deliver very genomically distant read pairs. In some cases, the interactions primarily arise from the random associations within a single DNA fragment. In some examples, the genomic distance between segments can be inferred because segments that are near to each other in a DNA molecule interact more often and with higher probability, while interactions between distant portions of the molecule will be less frequent. Consequently, there is a systematic relationship between the number of pairs connecting two loci and their proximity on the input DNA. The disclosure can produce read pairs capable of spanning the largest DNA fragments in an extraction. The input DNA for this library had a maximum length of 150 kbp, which is the longest meaningful read pair observed from the sequencing data. This suggests that the present method can link still more genomically distant loci if provided larger input DNA fragments. By applying improved assembly software tools that are specifically adapted to handle the type of data produced by the present method, a complete genomic assembly may be possible.

[00310] Extremely high phasing accuracy can be achieved by the data produced using the methods and compositions of the disclosure. In comparison to previous methods, the methods described herein can phase a higher proportion of the variants. Phasing can be achieved while maintaining high levels of accuracy. The techniques herein can allow for phasing at an accuracy of greater than about 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, or 99.999%. The techniques herein can allow for accurate phasing with less than about 500x sequencing depth, 450x sequencing depth, 400x sequencing depth, 350x sequencing depth, 300x sequencing depth, 250x sequencing depth, 200x sequencing depth, 150x sequencing depth, 100x sequencing depth, or 50x sequencing depth. This phase information can be extended to longer ranges, for example, greater than about 200 kbp, about 300 kbp, about 400 kbp, about 500 kbp, about 600 kbp, about 700 kbp, about 800 kbp, about 900 kbp, about 1 Mbp, about 2 Mbp, about 3 Mbp, about 4 Mbp, about 5 Mbp, or about 10 Mbp. In some embodiments, more than 90% of the heterozygous SNPs for a human sample can be phased at an accuracy greater than 99% using less than about 250 million reads or read pairs, e.g., by using only 1 lane of Illumina HiSeq data. In other cases, more than about 40%, 50%, 60%, 70%, 80%, 90 %, 95%, or 99% of the heterozygous SNPs for a human sample can be phased at an accuracy greater than about 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, or 99.999% using less than about 250 million or about 500 million reads or read pairs, e.g., by using only 1 or 2 lanes of Illumina HiSeq data. For example, more than 95% or 99% of the

heterozygous SNPs for a human sample can be phase at an accuracy greater than about 95% or 99% using less about 250 million or about 500 million reads. In further cases, additional variants can be captured by increasing the read length to about 200 bp, 250 bp, 300 bp, 350 bp, 400 bp, 450 bp, 500 bp, 600 bp, 800 bp, 1000 bp, 1500 bp, 2 kbp, 3 kbp, 4 kbp, 5 kbp, 10 kbp, 20 kbp, 50 kbp, or 100 kbp.

[00311]In other embodiments of the disclosure, the data from an XLRP library can be used to confirm the phasing capabilities of the long-range read pairs. The accuracy of those results is on par with the best technologies previously available, but further extending to significantly longer distances. The current sample preparation protocol for a particular sequencing method recognizes variants located within a read-length, e.g., 150 bp, of a targeted site for phasing. In one example, from an XLRP library built for NA12878, a benchmark sample for assembly, 44% of the 1,703,909 heterozygous SNPs present were phased with an accuracy greater than 99%. In some cases, this proportion can be expanded to nearly all variable sites with the judicious choice of enzymes or with digestion conditions.

[00312]Haplotype phasing can include phasing the human leukocyte antigen (HLA) region (e.g., Class I HLA-A, B, and C; Class II HLA-DRB1/3/4/5, HLA-DQA1, HLA-DQB1, HLA-DPA1, and HLA-DPB1). The HLA region of the genome is densely polymorphic and can be difficult to sequence or phase with standard sequencing approaches. Techniques of the present disclosure can provide for improved sequencing and phasing accuracy of the HLA region of the genome. Using techniques of the present disclosure, the HLA region of the genome can be phased accurately as part of phasing larger regions (e.g., chromosome arms, chromosomes, whole genomes) or on its own (e.g., by targeted enrichment such as hybrid capture). In an example, the HLA region on its own was phased accurately at a sequencing depth of approximately 300x. These techniques can provide advantages over traditional approaches for HLA analysis, such as long-range PCR; for example, long-range PCR can involve complex protocols and many separate reactions. As discussed further herein, samples can be multiplexed for sequencing analysis, for example by including sample-identifying barcodes in bridge oligonucleotides or elsewhere, and demultiplexing the sequence information based on the barcodes. In an example, multiple samples are subjected to proximity ligation, barcoded with sample-identifying barcodes (e.g., in the bridge oligonucleotide), the HLA region is targeted (e.g., by hybrid capture), and multiplexed sequencing is conducted, allowing phasing of the HLA region for multiple samples. In some cases, phasing the HLA region is conducted without imputation.

[00313]Haplotype phasing can include phasing the killer cell immunoglobulin-like receptor (KIR) region. The KIR region of the genome is highly homologous and structurally dynamic due to transposon-mediated recombination, and can be difficult to sequence or phase with standard sequencing approaches. Techniques of the present disclosure can provide for improved sequencing and phasing accuracy of the KIR region of the genome. Using techniques of the present disclosure, the KIR region of the genome can be phased accurately as part of phasing larger regions (e.g., chromosome arms, chromosomes, whole genomes) or on its own (e.g., by targeted enrichment such as hybrid capture). These techniques can provide advantages over traditional approaches for HLA analysis, such as long-range PCR; for example, long-range PCR can involve complex protocols and many separate reactions. As discussed further herein,

samples can be multiplexed for sequencing analysis, for example by including sample-identifying barcodes in bridge oligonucleotides or elsewhere, and de-multiplexing the sequence information based on the barcodes. In an example, multiple samples are subjected to proximity ligation, barcoded with sample-identifying barcodes (e.g., in the bridge oligonucleotide), the KIR region is targeted (e.g., by hybrid capture), and multiplexed sequencing is conducted, allowing phasing of the KIR region for multiple samples. At least about 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, or more genes and/or pseudogenes can be phased. In some cases, phasing the KIR region is conducted without imputation.

Metagenomics Analysis

[00314] In some embodiments, the compositions and methods described herein allow for the investigation of meta-genomes, for example, those found in the human gut. Accordingly, the partial or whole genomic sequences of some or all organisms that inhabit a given ecological environment can be investigated.

Examples include random sequencing of all gut microbes, the microbes found on certain areas of skin, and the microbes that live in toxic waste sites. The composition of the microbe population in these environments can be determined using the compositions and methods described herein and as well as the aspects of interrelated biochemistries encoded by their respective genomes. The methods described herein can enable metagenomic studies from complex biological environments, for example, those that comprise more than 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1000, 5000, 10000 or more organisms and/or variants of organisms.

[00315] High degrees of accuracy required by cancer genome sequencing can be achieved using the methods and systems described herein. Inaccurate reference genomes can make base-calling challenges when sequencing cancer genomes. Heterogeneous samples and small starting materials, for example, a sample obtained by biopsy introduce additional challenges. Further, detection of large-scale structural variants and/or losses of heterozygosity is often crucial for cancer genome sequencing, as well as the ability to differentiate between somatic variants and errors in base-calling.

Improved Sequencing Accuracy

[00316] Systems and methods described herein may generate accurate long sequences from complex samples containing 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20 or more varying genomes. Mixed samples of normal, benign, and/or tumor origin may be analyzed, optionally without the need for a normal control. In some embodiments, starting samples as little as 100 ng or even as little as hundreds of genome equivalents are utilized to generate accurate long sequences. Systems and methods described herein may allow for detection of large scale structural variants and rearrangements. Phased variant calls may be obtained over long sequences spanning about 1 kbp, about 2 kbp, about 5 kbp, about 10 kbp, about 20 kbp, about 50 kbp, about 100 kbp, about 200 kbp, about 500 kbp, about 1 Mbp, about 2 Mbp, about 5 Mbp, about 10 Mbp, about 20 Mbp, about 50 Mbp, or about 100 Mbp or more nucleotides. For example, phase variant call may be obtained over long sequences spanning about 1 Mbp or about 2 Mbp.

[00317] Haplotypes determined using the methods and systems described herein may be assigned to computational resources, for example, computational resources over a network, such as a cloud system. Short variant calls can be corrected, if necessary, using relevant information that is stored in the

computational resources. Structural variants can be detected based on the combined information from short variant calls and the information stored in the computational resources. Problematic parts of the genome, such as segmental duplications, regions prone to structural variation, the highly variable and medically relevant MHC region, centromeric and telomeric regions, and other heterochromatic regions including, but not limited to, those with repeat regions, low sequence accuracy, high variant rates, ALU repeats, segmental duplications, or any other relevant problematic parts, can be reassembled for increased accuracy.

[00318] A sample type can be assigned to the sequence information either locally or in a networked computational resource, such as a cloud. In cases where the source of the information is known, for example, when the source of the information is from a cancer or normal tissue, the source can be assigned to the sample as part of a sample type. Other sample type examples generally include, but are not limited to, tissue type, sample collection method, presence of infection, type of infection, processing method, size of the sample, etc. In cases where a complete or partial comparison genome sequence is available, such as a normal genome in comparison to a cancer genome, the differences between the sample data and the comparison genome sequence can be determined and optionally output.

Clinical Applications

[00319] The methods of the present disclosure can be used in the analysis of genetic information of selective genomic regions of interest as well as genomic regions which may interact with the selective region of interest. Amplification methods as disclosed herein can be used in devices, kits, and methods for genetic analysis, such as, but not limited to, those found in U.S. Pat. Nos. 6,449,562, 6,287,766, 7,361,468, 7,414,117, 6,225,109, and 6,110,709. In some cases, amplification methods of the present disclosure can be used to amplify target nucleic acid for DNA hybridization studies to determine the presence or absence of polymorphisms. The polymorphisms, or alleles, can be associated with diseases or conditions such as genetic disease. In other cases, the polymorphisms can be associated with susceptibility to diseases or conditions, for example, polymorphisms associated with addiction, degenerative and age-related conditions, cancer, and the like. In other cases, the polymorphisms can be associated with beneficial traits such as increased coronary health, or resistance to diseases such as HIV or malaria, or resistance to degenerative diseases such as osteoporosis, Alzheimer's, or dementia.

[00320] The compositions and methods of the disclosure can be used for diagnostic, prognostic, therapeutic, patient stratification, drug development, treatment selection, and screening purposes. The present disclosure provides the advantage that many different target molecules can be analyzed at one time from a single biomolecular sample using the methods of the disclosure. This allows, for example, for several diagnostic tests to be performed on one sample.

[00321] The composition and methods of the disclosure can be used in genomics. The methods described herein can provide an answer rapidly which is very desirable for this application. The methods and composition described herein can be used in the process of finding biomarkers that may be used for diagnostics or prognostics and as indicators of health and disease. The methods and composition described herein can be used to screen for drugs, e.g., drug development, selection of treatment,

determination of treatment efficacy and/or identify targets for pharmaceutical development. The ability to test gene expression on screening assays involving drugs is very important because proteins are the final gene product in the body. In some embodiments, the methods and compositions described herein will measure both protein and gene expression simultaneously which will provide the most information regarding the particular screening being performed.

[00322] The composition and methods of the disclosure can be used in gene expression analysis. The methods described herein discriminate between nucleotide sequences. The difference between the target nucleotide sequences can be, for example, a single nucleic acid base difference, a nucleic acid deletion, a nucleic acid insertion, or rearrangement. Such sequence differences involving more than one base can also be detected. The process of the present disclosure is able to detect infectious diseases, genetic diseases, and cancer. It is also useful in environmental monitoring, forensics, and food science. Examples of genetic analyses that can be performed on nucleic acids include, e.g., SNP detection, STR detection, RNA expression analysis, promoter methylation, gene expression, virus detection, viral subtyping, and drug resistance.

[00323] The present methods can be applied to the analysis of biomolecular samples obtained or derived from a patient so as to determine whether a diseased cell type is present in the sample, the stage of the disease, the prognosis for the patient, the ability of the patient to respond to a particular treatment, or the best treatment for the patient. The present methods can also be applied to identify biomarkers for a particular disease.

[00324] In some embodiments, the methods described herein are used in the diagnosis of a condition. As used herein the term “diagnose” or “diagnosis” of a condition may include predicting or diagnosing the condition, determining predisposition to the condition, monitoring treatment of the condition, diagnosing a therapeutic response of the disease, or prognosis of the condition, condition progression, or response to particular treatment of the condition. For example, a blood sample can be assayed according to any of the methods described herein to determine the presence and/or quantity of markers of a disease or malignant cell type in the sample, thereby diagnosing or staging a disease or a cancer.

[00325] In some embodiments, the methods and composition described herein are used for the diagnosis and prognosis of a condition.

[00326] Numerous immunologic, proliferative, and malignant diseases and disorders are especially amenable to the methods described herein. Immunologic diseases and disorders include allergic diseases and disorders, disorders of immune function, and autoimmune diseases and conditions. Allergic diseases and disorders include, but are not limited to, allergic rhinitis, allergic conjunctivitis, allergic asthma, atopic eczema, atopic dermatitis, and food allergy. Immunodeficiencies include, but are not limited to, severe combined immunodeficiency (SCID), hypereosinophilic syndrome, chronic granulomatous disease, leukocyte adhesion deficiency I and II, hyper IgE syndrome, Chediak Higashi, neutrophilias, neutropenias, aplasias, Agammaglobulinemia, hyper-IgM syndromes, DiGeorge/Velocardial-facial syndromes and Interferon gamma-TH1 pathway defects. Autoimmune and immune dysregulation disorders include, but are not limited to, rheumatoid arthritis, diabetes, systemic lupus erythematosus,

Graves' disease, Graves ophthalmopathy, Crohn's disease, multiple sclerosis, psoriasis, systemic sclerosis, goiter and struma lymphomatosa (Hashimoto's thyroiditis, lymphadenoid goiter), alopecia areata, autoimmune myocarditis, lichen sclerosis, autoimmune uveitis, Addison's disease, atrophic gastritis, myasthenia gravis, idiopathic thrombocytopenic purpura, hemolytic anemia, primary biliary cirrhosis, Wegener's granulomatosis, polyarteritis nodosa, and inflammatory bowel disease, allograft rejection and tissue destructive from allergic reactions to infectious microorganisms or to environmental antigens.

[00327] Proliferative diseases and disorders that may be evaluated by the methods of the disclosure include, but are not limited to, hemangiomatosis in newborns; secondary progressive multiple sclerosis; chronic progressive myelodegenerative disease; neurofibromatosis; ganglioneuromatosis; keloid formation; Paget's Disease of the bone; fibrocystic disease (e.g., of the breast or uterus); sarcoidosis; Peronies and Duputren's fibrosis, cirrhosis, atherosclerosis, and vascular restenosis.

[00328] Malignant diseases and disorders that may be evaluated by the methods of the disclosure include both hematologic malignancies and solid tumors.

[00329] Hematologic malignancies are especially amenable to the methods of the disclosure when the sample is a blood sample, because such malignancies involve changes in blood-borne cells. Such malignancies include non-Hodgkin's lymphoma, Hodgkin's lymphoma, non-B cell lymphomas, and other lymphomas, acute or chronic leukemias, polycythemias, thrombocythemias, multiple myeloma, myelodysplastic disorders, myeloproliferative disorders, myelofibroses, atypical immune lymphoproliferations and plasma cell disorders.

[00330] Plasma cell disorders that may be evaluated by the methods of the disclosure include multiple myeloma, amyloidosis and Waldenstrom's macroglobulinemia.

[00331] Example of solid tumors include, but are not limited to, colon cancer, breast cancer, lung cancer, prostate cancer, brain tumors, central nervous system tumors, bladder tumors, melanomas, liver cancer, osteosarcoma and other bone cancers, testicular and ovarian carcinomas, head and neck tumors, and cervical neoplasms.

[00332] Genetic diseases can also be detected by the process of the present disclosure. This can be carried out by prenatal or post-natal screening for chromosomal and genetic aberrations or for genetic diseases. Examples of detectable genetic diseases include: 21 hydroxylase deficiency, cystic fibrosis, Fragile X Syndrome, Turner Syndrome, Duchenne Muscular Dystrophy, Down Syndrome or other trisomies, heart disease, single gene diseases, HLA typing, phenylketonuria, sickle cell anemia, Tay-Sachs Disease, thalassemia, Klinefelter Syndrome, Huntington Disease, autoimmune diseases, lipidosis, obesity defects, hemophilia, inborn errors of metabolism, and diabetes.

[00333] Methods of the present disclosure can be used to detect genetic or genomic features associated with genetic diseases including, but not limited to, gene fusions, structural variants, rearrangements, and changes in topology such as missing or altered TAD boundaries, changes in TAD subtype, changes in compartment, changes in chromatin type, and changes in modification status such as methylation status (e.g., CpG methylation, H3K4me3, H3K27me3, or other histone methylation).

[00334] The methods described herein can be used to diagnose pathogen infections, for example, infections by intracellular bacteria and viruses, by determining the presence and/or quantity of markers of bacterium or virus, respectively, in the sample.

[00335] A wide variety of infectious diseases can be detected by the process of the present disclosure. The infectious diseases can be caused by bacterial, viral, parasite, and fungal infectious agents. The resistance of various infectious agents to drugs can also be determined using the present disclosure.

[00336] Bacterial infectious agents which can be detected by the present disclosure include *Escherichia coli*, *Salmonella*, *Shigella*, *Klebsiella*, *Pseudomonas*, *Listeria monocytogenes*, *Mycobacterium tuberculosis*, *Mycobacterium aviumintracellulare*, *Yersinia*, *Francisella*, *Pasteurella*, *Brucella*, *Clostridia*, *Bordetella pertussis*, *Bacteroides*, *Staphylococcus aureus*, *Streptococcus pneumoniae*, *B-Hemolytic strep.*, *Corynebacteria*, *Legionella*, *Mycoplasma*, *Ureaplasma*, *Chlamydia*, *Neisseria gonorrhea*, *Neisseria meningitidis*, *Hemophilus influenza*, *Enterococcus faecalis*, *Proteus vulgaris*, *Proteus mirabilis*, *Helicobacter pylori*, *Treponema palladium*, *Borrelia burgdorferi*, *Borrelia recurrentis*, *Rickettsial* pathogens, *Nocardia*, and *Acitnomycetes*.

[00337] Fungal infectious agents which can be detected by the present disclosure include *Cryptococcus neoformans*, *Blastomyces dermatitidis*, *Histoplasma capsulatum*, *Coccidioides immitis*, *Paracoccidioides brasiliensis*, *Candida albicans*, *Aspergillus fumigatus*, *Phycomycetes (Rhizopus)*, *Sporothrix schenckii*, *Chromomycosis*, and *Maduromycosis*.

[00338] Viral infectious agents which can be detected by the present disclosure include human immunodeficiency virus, human T-cell lymphocytotropic virus, hepatitis viruses (e.g., Hepatitis B Virus and Hepatitis C Virus), Epstein-Barr virus, cytomegalovirus, human papillomaviruses, orthomyxo viruses, paramyxo viruses, adenoviruses, corona viruses, rhabdo viruses, polio viruses, toga viruses, bunya viruses, arena viruses, rubella viruses, and reo viruses.

[00339] Parasitic agents which can be detected by the present disclosure include *Plasmodium falciparum*, *Plasmodium malariae*, *Plasmodium vivax*, *Plasmodium ovale*, *Onchocerca volvulus*, *Leishmania*, *Trypanosoma* spp., *Schistosoma* spp., *Entamoeba histolytica*, *Cryptosporidium*, *Giardia* spp., *Trichomonas* spp., *Balantidium coli*, *Wuchereria bancrofti*, *Toxoplasma* spp., *Enterobius vermicularis*, *Ascaris lumbricoides*, *Trichuris trichiura*, *Dracunculus medinensis*, *Trematodes*, *Diphyllobothrium latum*, *Taenia* spp., *Pneumocystis carinii*, and *Necator americanus*.

[00340] The present disclosure is also useful for detection of drug resistance by infectious agents. For example, vancomycin-resistant *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus*, penicillin-resistant *Streptococcus pneumoniae*, multi-drug resistant *Mycobacterium tuberculosis*, and AZT-resistant human immunodeficiency virus can all be identified with the present disclosure.

[00341] Thus, the target molecules detected using the compositions and methods of the disclosure can be either patient markers (such as a cancer marker) or markers of infection with a foreign agent, such as bacterial or viral markers.

[00342] The compositions and methods of the disclosure can be used to identify and/or quantify a target molecule whose abundance is indicative of a biological state or disease condition, for example, blood markers that are upregulated or downregulated as a result of a disease state.

[00343] In some embodiments, the methods and compositions of the present disclosure can be used for cytokine expression. The low sensitivity of the methods described herein would be helpful for early detection of cytokines, e.g., as biomarkers of a condition, diagnosis, or prognosis of a disease such as cancer, and the identification of subclinical conditions.

[00344] Methods of the present disclosure can be used to detect genetic or genomic features associated with cancer including, but not limited to, gene fusions, structural variants, rearrangements, and changes in topology such as missing or altered TAD boundaries, changes in TAD subtype, changes in compartment, changes in chromatin type, and changes in modification status such as methylation status (e.g., CpG methylation, H3K4me3, H3K27me3, or other histone methylation).

Samples

[00345] The different samples from which the target polynucleotides are derived can comprise multiple samples from the same individual, samples from different individuals, or combinations thereof. In some embodiments, a sample comprises a plurality of polynucleotides from a single individual. In some embodiments, a sample comprises a plurality of polynucleotides from two or more individuals. An individual is any organism or portion thereof from which target polynucleotides can be derived, non-limiting examples of which include plants, animals, fungi, protists, monerans, viruses, mitochondria, and chloroplasts. Sample polynucleotides can be isolated from a subject, such as a cell sample, tissue sample, or organ sample derived therefrom, including, for example, cultured cell lines, biopsy, blood sample, or fluid sample containing a cell. The subject may be an animal including, but not limited to, an animal such as a cow, a pig, a mouse, a rat, a chicken, a cat, a dog, etc., and is usually a mammal, such as a human. Samples can also be artificially derived, such as by chemical synthesis. In some embodiments, the samples comprise DNA. In some embodiments, the samples comprise genomic DNA. In some embodiments, the samples comprise mitochondrial DNA, chloroplast DNA, plasmid DNA, bacterial artificial chromosomes, yeast artificial chromosomes, oligonucleotide tags, or combinations thereof. In some embodiments, the samples comprise DNA generated by primer extension reactions using any suitable combination of primers and a DNA polymerase including, but not limited to, polymerase chain reaction (PCR), reverse transcription, and combinations thereof. Where the template for the primer extension reaction is RNA, the product of reverse transcription is referred to as complementary DNA (cDNA). Primers useful in primer extension reactions can comprise sequences specific to one or more targets, random sequences, partially random sequences, and combinations thereof. Reaction conditions suitable for primer extension reactions are known. In general, sample polynucleotides comprise any polynucleotide present in a sample, which may or may not include target polynucleotides.

[00346] In some embodiments, nucleic acid template molecules (e.g., DNA or RNA) are isolated from a biological sample containing a variety of other components, such as proteins, lipids, and non-template nucleic acids. Nucleic acid template molecules can be obtained from any cellular material, obtained from

an animal, plant, bacterium, fungus, or any other cellular organism. Biological samples for use in the present disclosure include viral particles or preparations. Nucleic acid template molecules can be obtained directly from an organism or from a biological sample obtained from an organism, e.g., from blood, urine, cerebrospinal fluid, seminal fluid, saliva, sputum, stool, and tissue. Any tissue or body fluid specimen may be used as a source for nucleic acid for use in the disclosure. Nucleic acid template molecules can also be isolated from cultured cells, such as a primary cell culture or a cell line. The cells or tissues from which template nucleic acids are obtained can be infected with a virus or other intracellular pathogen. A sample can also be total RNA extracted from a biological specimen, a cDNA library, viral, or genomic DNA. A sample may also be isolated DNA from a non-cellular origin, e.g., amplified/isolated DNA from the freezer.

[00347] Methods for the extraction and purification of nucleic acids are known. For example, nucleic acids can be purified by organic extraction with phenol, phenol/chloroform/isoamyl alcohol, or similar formulations, including TRIzol and TriReagent. Other non-limiting examples of extraction techniques include: (1) organic extraction followed by ethanol precipitation, e.g., using a phenol/chloroform organic reagent (Ausubel et al., 1993), with or without the use of an automated nucleic acid extractor, e.g., the Model 341 DNA Extractor available from Applied Biosystems (Foster City, Calif.); (2) stationary phase adsorption methods (U.S. Pat. No. 5,234,809; Walsh et al., 1991); and (3) salt-induced nucleic acid precipitation methods (Miller et al., (1988), such precipitation methods being typically referred to as “salting-out” methods. Another example of nucleic acid isolation and/or purification includes the use of magnetic particles to which nucleic acids can specifically or non-specifically bind, followed by isolation of the beads using a magnet, and washing and eluting the nucleic acids from the beads (see, e.g., U.S. Pat. No. 5,705,628). In some embodiments, the above isolation methods may be preceded by an enzyme digestion step to help eliminate unwanted protein from the sample, e.g., digestion with proteinase K, or other like proteases (see, e.g., U.S. Pat. No. 7,001,724). If desired, RNase inhibitors may be added to the lysis buffer. For certain cell or sample types, it may be desirable to add a protein denaturation/digestion step to the protocol. Purification methods may be directed to isolate DNA, RNA, or both. When both DNA and RNA are isolated together during or subsequent to an extraction procedure, further steps may be employed to purify one or both separately from the other. Sub-fractions of extracted nucleic acids can also be generated, for example, purification by size, sequence, or other physical or chemical characteristic. In addition to an initial nucleic isolation step, purification of nucleic acids can be performed after any step in the methods of the disclosure, such as to remove excess or unwanted reagents, reactants, or products.

[00348] Nucleic acid template molecules can be obtained as described in U.S. Patent Application Publication Number US2002/0190663 A1, published Oct. 9, 2003. Generally, nucleic acid can be extracted from a biological sample by a variety of techniques such as those described by Maniatis, et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor, N.Y., pp. 280-281 (1982). In some cases, the nucleic acids can be first extracted from the biological samples and then cross-linked in vitro. In some cases, native association proteins (e.g., histones) can be further removed from the nucleic acids.

[00349] In other embodiments, the disclosure can be easily applied to any high molecular weight double stranded DNA including, for example, DNA isolated from tissues, cell culture, bodily fluids, animal tissue, plant, bacteria, fungi, viruses, etc.

[00350] In some embodiments, each of the plurality of independent samples can independently comprise at least about 1 ng, 2 ng, 5 ng, 10 ng, 20 ng, 30 ng, 40 ng, 50 ng, 75 ng, 100 ng, 150 ng, 200 ng, 250 ng, 300 ng, 400 ng, 500 ng, 1 µg, 1.5 µg, 2 µg, 5 µg, 10 µg, 20 µg, 50 µg, 100 µg, 200 µg, 500 µg, or 1000 µg, or more of nucleic acid material. In some embodiments, each of the plurality of independent samples can independently comprise less than about 1 ng, 2 ng, 5 ng, 10 ng, 20 ng, 30 ng, 40 ng, 50 ng, 75 ng, 100 ng, 150 ng, 200 ng, 250 ng, 300 ng, 400 ng, 500 ng, 1 µg, 1.5 µg, 2 µg, 5 µg, 10 µg, 20 µg, 50 µg, 100 µg, 200 µg, 500 µg, or 1000 µg, or more of nucleic acid.

[00351] In some embodiments, end repair is performed to generate blunt end 5' phosphorylated nucleic acid ends using commercial kits, such as those available from Epicentre Biotechnologies (Madison, WI).

Adaptors

[00352] An adaptor oligonucleotide includes any oligonucleotide having a sequence, at least a portion of which is known, that can be joined to a target polynucleotide. Adaptor oligonucleotides can comprise DNA, RNA, nucleotide analogues, non-canonical nucleotides, labeled nucleotides, modified nucleotides, or combinations thereof. Adaptor oligonucleotides can be single-stranded, double-stranded, or partial duplex. In general, a partial-duplex adaptor comprises one or more single-stranded regions and one or more double-stranded regions. Double-stranded adaptors can comprise two separate oligonucleotides hybridized to one another (also referred to as an "oligonucleotide duplex"), and hybridization may leave one or more blunt ends, one or more 3' overhangs, one or more 5' overhangs, one or more bulges resulting from mismatched and/or unpaired nucleotides, or any combination of these. In some embodiments, a single-stranded adaptor comprises two or more sequences that are able to hybridize with one another. When two such hybridizable sequences are contained in a single-stranded adaptor, hybridization yields a hairpin structure (hairpin adaptor). When two hybridized regions of an adaptor are separated from one another by a non-hybridized region, a "bubble" structure results. Adaptors comprising a bubble structure can consist of a single adaptor oligonucleotide comprising internal hybridizations, or may comprise two or more adaptor oligonucleotides hybridized to one another. Internal sequence hybridization, such as between two hybridizable sequences in an adaptor, can produce a double-stranded structure in a single-stranded adaptor oligonucleotide. Adaptors of different kinds can be used in combination, such as a hairpin adaptor and a double-stranded adaptor, or adaptors of different sequences. Hybridizable sequences in a hairpin adaptor may or may not include one or both ends of the oligonucleotide. When neither of the ends are included in the hybridizable sequences, both ends are "free" or "overhanging." When only one end is hybridizable to another sequence in the adaptor, the other end forms an overhang, such as a 3' overhang or a 5' overhang. When both the 5'-terminal nucleotide and the 3'-terminal nucleotide are included in the hybridizable sequences, such that the 5'-terminal nucleotide and the 3'-terminal nucleotide are complementary and hybridize with one another, the end is referred to as "blunt." Different adaptors can be joined to target polynucleotides in sequential reactions or

simultaneously. For example, the first and second adaptors can be added to the same reaction. Adaptors can be manipulated prior to combining with target polynucleotides. For example, terminal phosphates can be added or removed.

[00353] Adaptors can contain one or more of a variety of sequence elements including, but not limited to, one or more amplification primer annealing sequences or complements thereof, one or more sequencing primer annealing sequences or complements thereof, one or more barcode sequences, one or more common sequences shared among multiple different adaptors or subsets of different adaptors, one or more restriction enzyme recognition sites, one or more overhangs complementary to one or more target polynucleotide overhangs, one or more probe binding sites (e.g., for attachment to a sequencing platform, such as a flow cell for massive parallel sequencing, such as developed by Illumina, Inc.), one or more random or near-random sequences (e.g., one or more nucleotides selected at random from a set of two or more different nucleotides at one or more positions, with each of the different nucleotides selected at one or more positions represented in a pool of adaptors comprising the random sequence), and combinations thereof. Two or more sequence elements can be non-adjacent to one another (e.g., separated by one or more nucleotides), adjacent to one another, partially overlapping, or completely overlapping. For example, an amplification primer annealing sequence can also serve as a sequencing primer annealing sequence. Sequence elements can be located at or near the 3' end, at or near the 5' end, or in the interior of the adaptor oligonucleotide. When an adaptor oligonucleotide is capable of forming secondary structure, such as a hairpin, sequence elements can be located partially or completely outside the secondary structure, partially or completely inside the secondary structure, or in between sequences participating in the secondary structure. For example, when an adaptor oligonucleotide comprises a hairpin structure, sequence elements can be located partially or completely inside or outside the hybridizable sequences (the "stem"), including in the sequence between the hybridizable sequences (the "loop"). In some embodiments, the first adaptor oligonucleotides in a plurality of first adaptor oligonucleotides having different barcode sequences comprise a sequence element common among all first adaptor oligonucleotides in the plurality. In some embodiments, all second adaptor oligonucleotides comprise a sequence element common among all second adaptor oligonucleotides that is different from the common sequence element shared by the first adaptor oligonucleotides. A difference in sequence elements can be any such that at least a portion of different adaptors do not completely align, for example, due to changes in sequence length, deletion, or insertion of one or more nucleotides, or a change in the nucleotide composition at one or more nucleotide positions (such as a base change or base modification). In some embodiments, an adaptor oligonucleotide comprises a 5' overhang, a 3' overhang, or both that is complementary to one or more target polynucleotides. Complementary overhangs can be one or more nucleotides in length including, but not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more nucleotides in length. For example, the complementary overhangs can be about 1, 2, 3, 4, 5 or 6 nucleotides in length. Complementary overhangs may comprise a fixed sequence. Complementary overhangs may comprise a random sequence of one or more nucleotides, such that one or more nucleotides are selected at random from a set of two or more different nucleotides at one or more

positions, with each of the different nucleotides selected at one or more positions represented in a pool of adaptors with complementary overhangs comprising the random sequence. In some embodiments, an adaptor overhang consists of an adenine or a thymine.

[00354] Adaptor oligonucleotides can have any suitable length, at least sufficient to accommodate the one or more sequence elements of which they are comprised. In some embodiments, adaptors are about, less than about, or more than about, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 200, or more nucleotides in length. In some examples, the adaptors can be about 10 to about 50 nucleotides in length. In further examples, the adaptors can be about 20 to about 40 nucleotides in length.

[00355] As used herein, the term “barcode” refers to a known nucleic acid sequence that allows some feature of a polynucleotide with which the barcode is associated to be identified. In some embodiments, the feature of the polynucleotide to be identified is the sample from which the polynucleotide is derived. In some embodiments, barcodes can be at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more nucleotides in length. For example, barcodes can be at least 10, 11, 12, 13, 14, or 15 nucleotides in length. In some embodiments, barcodes can be shorter than 10, 9, 8, 7, 6, 5, or 4 nucleotides in length. For example, barcodes can be shorter than 10 nucleotides in length. In some embodiments, barcodes associated with some polynucleotides are of different length than barcodes associated with other polynucleotides. In general, barcodes are of sufficient length and comprise sequences that are sufficiently different to allow the identification of samples based on barcodes with which they are associated. In some embodiments, a barcode, and the sample source with which it is associated, can be identified accurately after the mutation, insertion, or deletion of one or more nucleotides in the barcode sequence, such as the mutation, insertion, or deletion of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides. In some examples, 1, 2 or 3 nucleotides can be mutated, inserted and/or deleted. In some embodiments, each barcode in a plurality of barcodes differ from every other barcode in the plurality at least two nucleotide positions, such as at least 2, 3, 4, 5, 6, 7, 8, 9, 10, or more positions. In some examples, each barcode can differ from every other barcode by in at least 2, 3, 4 or 5 positions. In some embodiments, both a first site and a second site comprise at least one of a plurality of barcode sequences. In some embodiments, barcodes for second sites are selected independently from barcodes for first adaptor oligonucleotides. In some embodiments, first sites and second sites having barcodes are paired, such that sequences of the pair comprise the same or different one or more barcodes. In some embodiments, the methods of the disclosure further comprise identifying the sample from which a target polynucleotide is derived based on a barcode sequence to which the target polynucleotide is joined. In general, a barcode may comprise a nucleic acid sequence that when joined to a target polynucleotide serves as an identifier of the sample from which the target polynucleotide was derived.

[00356] Adaptor oligonucleotides may be coupled, linked, or tethered to an immunoglobulin or an immunoglobulin binding protein or fragment thereof. For example, after in situ genomic digestion of a crosslinked sample with a DNase, such as MNase, one or more antibodies may be added to the sample to bind the digested chromatin, such as at methylated sites or transcription factor binding sites. Next, a biotinylated adaptor oligonucleotide coupled, linked, or tethered to an immunoglobulin binding protein or

fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L, may be added to the sample to target the adaptors to one or more specific sites in the chromatin. The sample may then be treated with a ligase to effect proximity ligation. Moreover, streptavidin may be used to isolate DNA that has been ligated to the adaptors. Crosslinks may then be reversed before amplifying the sample using PCR and sequencing. Alternatively, adaptor linked oligonucleotides may comprise modified nucleotides capable of linking to a purification reagent using click chemistry.

Bridge Oligonucleotides

[00357] Methods provided herein can comprise attaching a first segment and a second segment of a plurality of segments at a junction. In some cases, attaching can comprise filling in sticky ends using biotin tagged nucleotides and ligating the blunt ends. In certain cases, attaching can comprise contacting at least the first segment and the second segment to a bridge oligonucleotide. The ends are polished and polyadenylated before ligating a bridge oligonucleotide to each of the first segment and the second segment. The first segment and the second segment are then ligated to create a junction comprising a bridge oligonucleotide. In various cases, attaching can comprise contacting at least the first segment and the second segment to a barcode.

[00358] In some embodiments, bridge oligonucleotides as provided herein can be from at least about 5 nucleotides in length to about 50 nucleotides in length. In certain embodiments, the bridge oligonucleotides can be from about 15 nucleotides in length to about 18 nucleotides in length. In various embodiments, the bridge oligonucleotides can be at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, or more nucleotides in length. In an example, the bridge oligonucleotides are at least 10 nucleotides in length. In another example, the bridge oligonucleotides are 12 nucleotides in length or about 12 nucleotides in length. In some cases, bridge oligonucleotides of at least 10 bp can increase stability and reduce adverse proximity ligation events, such as short inserts, interchromosomal ligations, non-specific ligations, and bridge self-ligations.

[00359] In some embodiments, the bridge oligonucleotides may comprise a barcode. In certain embodiments, the bridge oligonucleotides can comprise multiple barcodes (e.g., two or more barcodes). In various embodiments, the bridge oligonucleotides can comprise multiple bridge oligonucleotides coupled or connected together. In some embodiments, the bridge oligonucleotides may be coupled or linked to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L. In some cases, coupled bridge oligonucleotides may be delivered to a location in the sample nucleic acid where an antibody is bound.

[00360] A splitting and pooling approach can be employed to produce bridge oligonucleotides with unique barcodes. A population of samples can be split into multiple groups, bridge oligonucleotides can be attached to the samples such that the bridge oligonucleotide barcodes are different between groups but the same within a group, the groups of samples can be pooled together again, and this process can be repeated multiple times. For example, a population of polynucleotides can be split into Group A and Group B. First

bridge oligonucleotides can be attached to the polynucleotides in Group A and second bridge oligonucleotides can be attached to the polynucleotides in Group B. Accordingly, the bridge oligonucleotide barcodes are the same within Group A, but the bridge oligonucleotides are different between Group A and Group B. Iterating this process can ultimately result in each sample in the population having a unique series of bridge oligonucleotide barcodes, allowing single-sample (e.g., single cell, single nucleus, single chromosome) analysis. In one illustrative example, a sample of crosslinked digested nuclei attached to a solid support of beads is split across 8 tubes, each containing 1 of 8 unique members of a first adaptor group (first iteration) comprising double-stranded DNA (dsDNA) adaptors to be ligated. Each of the 8 adaptors can have the same 5' overhang sequence for ligation to the nucleic acid ends of the cross-linked chromatin aggregates in the nuclei, but otherwise has a unique dsDNA sequence. After the first adaptor group is ligated, the nuclei can be pooled back together and washed to remove the ligation reaction components. The scheme of distributing, ligating, and pooling can be repeated 2 additional times (2 iterations). Following ligation of members from each adaptor group, a cross-linked chromatin aggregate can be attached to multiple barcodes in series. In some cases, the sequential ligation of a plurality of members of a plurality of adaptor groups (iterations) results in barcode combinations. The number of barcode combinations available depends on the number of groups per iteration and the total number of barcode oligonucleotides used. For example, 3 iterations comprising 8 members each can have 83 possible combinations. In some cases, barcode combinations are unique. In some cases, barcode combinations are redundant. The total number of barcode combinations can be adjusted by increasing or decreasing the number of groups receiving unique barcodes and/or increasing or decreasing the number of iterations. When more than one adaptor group is used, a distributing, attaching, and pooling scheme can be used for iterative adaptor attachment. In some cases, the scheme of distributing, attaching, and pooling can be repeated at least 3, 4, 5, 6, 7, 8, 9, or 10 additional times. In some cases, the members of the last adaptor group include a sequence for subsequent enrichment of adaptor-attached DNA, for example, during sequencing library preparation through PCR amplification.

[00361] Iterating this process (of splitting and pooling) can ultimately result in each sample in the population having a unique series of bridge oligonucleotide barcodes, allowing single-sample (e.g., single cell, single nucleus, and single chromosome) analysis. In an exemplary workflow using a splitting and pooling approach, the nucleic acid is digested in situ and then end polished and polyadenylated. Single cells are dispensed, and a barcode is ligated to the ends present in each cell (e.g., barcode bc1). Cells are pooled and then single cells are isolated, and a second barcode is ligated to the ends present in each cell (e.g., barcode bc2). Cells are pooled again and separated into single cells before ligating a bridge adaptor (e.g., Bio-Bridge), which can be ligated to another DNA segment forming a junction between two segments having a unique combination of barcodes and adaptors identifying the cell from which the junction was derived (e.g., barcodes bc1 and bc2). The bridge adaptor can comprise one or more affinity reagents, such as biotin, for subsequent pull-down or other purification.

[00362] In another illustrative example, a sample of crosslinked digested nuclei attached to a solid support of beads can be split across eight tubes, each containing one of eight unique members of a first adaptor

group (first iteration) comprising double-stranded DNA (dsDNA) adaptors to be ligated. Each of the eight adaptors can have the same 5' overhang sequence for ligation to the nucleic acid ends of the cross-linked chromatin aggregates in the nuclei, but otherwise have a unique dsDNA sequence. After the first adaptor group is ligated, the nuclei can be pooled back together and washed to remove the ligation reaction components. The scheme of distributing, ligating, and pooling can be repeated two additional times (two iterations). Following ligation of members from each adaptor group, a cross-linked chromatin aggregate can be attached to multiple barcodes in series.

[00363] In some cases, the sequential ligation of a plurality of members of a plurality of adaptor groups (iterations) can result in barcode combinations. The number of barcode combinations available can depend on the number of groups per iteration and the total number of barcode oligonucleotides used. For example, three iterations comprising eight members each can have 83 possible combinations. In some cases, barcode combinations are unique. In certain cases, barcode combinations are redundant. The total number of barcode combinations can be adjusted by increasing or decreasing the number of groups receiving unique barcodes and/or increasing or decreasing the number of iterations. When more than one adaptor group is used, a distributing, attaching, and pooling scheme can be used for iterative adaptor attachment. In various cases, the scheme of distributing, attaching, and pooling can be repeated at least 3, 4, 5, 6, 7, 8, 9, 10, or more additional times. In some cases, the members of the last adaptor group may include a sequence for subsequent enrichment of adaptor-attached DNA, for example, during sequencing library preparation through PCR amplification.

[00364] In some cases, a three oligo design may be used, allowing for a split-pool strategy whereby two 96-well plates combined with eight different biotinylated oligos may be used, allowing for distinct barcoding of 73,728 different molecules. In certain cases, the first two sets of eight oligos are not biotinylated and the third set of eight oligos is biotinylated. In various cases, each barcoded oligonucleotide is directional allowing only one oligo to be added in each round. The bridge oligonucleotide can have a sequence that allows it to match up with a corresponding end.

[00365] In certain cases, the barcodes and adaptors may have a shorter sequence to reduce the amount of sequence space taken by the fully ligated bridges. In various cases, the bridge may take up 30 bp of sequence space. In some cases, the bridge may take up 54 bp of sequence space but offer additional positions for unique molecular identifiers (UMIs). In certain cases, UMIs may enable single-cell identification with 73,728 different combinations. In various cases, the first two oligo sets are unmodified and the third oligo set is biotinylated.

[00366] Barcode sequences in bridge adapters can be used to allow multiplexed sequencing of samples. For example, proximity ligation can be conducted on several different samples, with each sample using bridge oligonucleotides with different barcode sequences. The samples can then be pooled for multiplexed sequencing analysis, and sequence information can be de-multiplexed back to the individual samples based on the barcode sequences.

Phased Read-Sets for Genome Assembly and Haplotype Phasing

[00367] Provided herein are methods for generating read sets, including phased read-sets, for applications including genome assembly and haplotype phasing, using long-read or short-read sequencing technologies. Some such methods are provided in greater detail at WO2017/147279, which is incorporated by reference herein in its entirety. In such methods, nucleic acid molecules can be bound (e.g., in a chromatin structure), cleaved to expose internal ends, re-attached at junctions to other exposed ends, freed from binding, and sequenced. This technique can produce nucleic acid molecules comprising multiple sequence segments. The multiple sequence segments within a nucleic acid molecule can have phase information preserved while being rearranged relative to their natural or starting position and orientation. Sequence segments on either side of a junction can be confidently considered to come from the same phase of a sample nucleic acid molecule.

[00368] Nucleic acid molecules, including high molecular weight DNA, can be bound or immobilized on at least one nucleic acid binding moiety. For example, DNA assembled into *in vitro* chromatin aggregates and fixed with formaldehyde treatment are consistent with methods herein. Nucleic acid binding or immobilizing approaches include, but are not limited to, *in vitro* or reconstituted chromatin assembly, native chromatin, DNA-binding protein aggregates, nanoparticles, DNA-binding beads, or beads coated using a DNA-binding substance, polymers, synthetic DNA-binding molecules or other solid or substantially solid affinity molecules. In some cases, the beads are solid phase reversible immobilization (SPRI) beads (e.g., beads with negatively charged carboxyl groups such as Beckman-Coulter Agencourt AMPure XP beads).

[00369] Nucleic acids bound to a nucleic acid binding moiety such as those described herein can be held such that a nucleic acid molecule having a first segment and a second segment separated on the nucleic acid molecule by a distance greater than a read distance on a sequencing device (10 kb, 50 kb, 100 kb or greater, for example) are bound together independent of their common phosphodiester bonds. Upon cleavage of such a bound nucleic acid molecule, exposed ends of the first segment and the second segment may ligate to one another. In some cases, the nucleic acid molecules are bound at a concentration such that there is little or no overlap between bound nucleic acid molecules on a solid surface, such that exposed internal ends of cleaved molecules are likely to re-ligate or become reattached only to exposed ends from other segments that were in phase on a common nucleic acid source prior to cleavage. Consequently, a DNA molecule can be cleaved and cleaved exposed internal ends can be re-ligated, for example at random, without loss of phase information.

[00370] A bound nucleic acid molecule can be cleaved to expose internal ends through one of any number of enzymatic and non-enzymatic approaches. For example, a nucleic acid molecule can be digested using a restriction enzyme, such as a restriction endonuclease that leaves a single stranded overhang. MboI digest, for example, is suitable for this purpose, although other restriction endonucleases are contemplated. Lists of restriction endonucleases are available, for example, in most molecular biology product catalogues. Other non-limiting techniques for nucleic acid cleavage include using a transposase, tagmentation enzyme complex, topoisomerase, nonspecific endonuclease, DNA repair enzyme, RNA-

guided nuclease, fragmentase, or alternate enzyme. Transposase, for example, can be used in combination with unlinked left and right borders to create a sequence-independent break in a nucleic acid that is marked by attachment of transposase-delivered oligonucleotide sequence. Physical means can also be used to generate cleavage, including mechanical means (e.g., sonication, shear), thermal means (e.g., temperature change), or electromagnetic means (e.g., irradiation, such as UV irradiation).

[00371] Immobilization of nucleic acids at this stage can keep the cleaved nucleic acid molecule fragments in close physical proximity, such that phase information for the initial molecule is preserved. For example, resulting chromatin aggregates form one nucleic acid binding moiety. A benefit of the fixation, e.g. to chromatin aggregates, is that separate regions of a common nucleic acid molecule can be held together independent of their phosphodiester backbone, such that their phase information is not lost upon cleavage of the phosphodiester backbone. This benefit is also conveyed through alternate scaffolds to which a nucleic acid molecule is attached prior to cleavage.

[00372] Optionally, single stranded “sticky” end overhangs are modified to prevent reannealing and re-ligation. For example, sticky ends are partially filled-in, such as by adding one nucleotide and a polymerase. In this way, the entire single-stranded end cannot be filled in, but the end is modified to prevent re-ligation with a formerly complementary end. In the example of MboI digestion, which leaves a 5′ GATC 5-prime overhang, only the Guanosine nucleotide triphosphate is added. This results in only a “G” fill-in of the first complementary base (“C”) and result in a 5′ GAT overhang. This step renders the free sticky ends incompatible for re-ligation to one another, but preserves sticky ends for downstream applications. Alternately, blunt ends are generated through completely filling in the overhangs, restriction digest with blunt-end generating enzymes, treatment with a single-strand DNA exonuclease, or nonspecific cleavage. In some cases, a transposase is used to attach adapter ends having blunt or sticky ends to the exposed internal ends of the DNA molecule.

[00373] Optionally, a “punctuation oligonucleotide” is introduced. This punctuation oligonucleotide marks cleavage/re-ligation sites. Some punctuation oligonucleotides have single-stranded overhangs on both ends that are compatible with the partially filled-in overhangs generated on the exposed nucleic acid sample internal ends. An example of a punctuation oligonucleotide is shown below. In some cases, the double-stranded oligonucleotide having single-stranded overhangs is modified, such as by 5′ phosphate removal at its 5′ ends, so that it cannot form concatemers during ligation. Alternately, blunt punctuation oligonucleotides are used, or cleavage sites are not marked using a distinct punctuation oligonucleotide. In some systems, such as when a transposase is used, punctuation is accomplished through addition of transpososome border sequences, followed by ligation of border sequences to one another or to a punctuation oligo. An exemplary punctuation oligo is presented below. However, alternate punctuation oligos are consistent with the disclosure herein, varying in sequence, length, overhang presence or sequence, or modification such as 5′ de-phosphorylation.

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5' ATCACGCGC 3'
3' TCGCGCTA 5'

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In some cases, the double-stranded region of the punctuation oligonucleotide will vary. A relevant feature of the punctuation oligonucleotide is the sequence of its overhang, allowing ligation to the nucleic acid sample but optionally modified precluding auto-ligation or concatemer formation. It is often preferred that the punctuation oligonucleotide comprise sequence that does not occur or is less likely to occur in a target nucleic acid molecule, such that it is easily identified in a downstream sequence reaction. Punctuation oligos are optionally barcoded, for example with a known barcode sequence or with a randomly generated unique identifier sequence. Unique identifier sequences can be designed to make it highly unlikely for multiple junctions in a nucleic acid molecule or in a sample to be barcoded with the same unique identifier.

[00374] Cleaved ends can be attached to one another directly or through an oligo (e.g., a punctuation oligo), for example using a ligase or similar enzyme. Ligation can proceed such that the free single-stranded ends of an immobilized high-molecular weight nucleic acid molecule are ligated directly or to the punctuation oligonucleotide. Because the punctuation oligonucleotide, if utilized, can have two ligatable ends, this ligation can effectively chain regions of the high molecular weight nucleic acid molecule together. Alternative approaches resulting in affixing a punctuating sequence or molecule between two exposed ends can also be employed, as can approaches for directly connecting two exposed ends without punctuation.

[00375] Nucleic acids can then be liberated from the nucleic acid binding moiety. In the case of *in vitro* chromatin aggregates, this can be accomplished by reversing the cross-links, or digesting the protein components, or both reversing the crosslinking and digesting protein components. A suitable approach is treatment of complexes with proteinase K, though many alternatives are also contemplated. For other binding techniques, suitable methods can be employed, such as the severing of linker molecules or the degradation of a substrate.

[00376] Nucleic acid molecules resulting from such techniques can have a variety of relevant features. Sequence segments within a nucleic acid molecule can be rearranged relative to their natural or starting positions and orientations, but with phase information preserved. Consequently, sequence segments on either side of a junction can be confidently assigned to a common phase of a common sample molecule. Thus, segments far removed from one another on a molecule can be, by such techniques, brought together or in proximity such that portions or the entirety of each segment is sequenced in a single run of a single molecule sequencing device, allowing definitive phase assignment. Alternately, in some cases originally adjacent segments can become separated from one in the resultant nucleic acid. In some cases, the nucleic acid molecules can be re-ligated such that at least about 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, 99.999%, or 100% of re-ligations are between segments that were in phase on a common nucleic acid source prior to cleavage.

[00377] Another relevant feature of the resultant molecules is that, in some cases, most or all the original molecular sequence is preserved, though perhaps rearranged, in the final punctuated or rearranged molecule. For example, in some cases no more than 1%, 2%, 3%, 4%, 5%, 10%, 15%, or 20% of the original molecule is lost in producing the resultant molecule or molecules. Consequently, in addition to

being useful as a phase determinant, the resultant molecule retains a substantial proportion of the original molecule sequence, such that the resultant molecule is optionally used to concurrently generate sequence information such as contig information useful in de novo sequencing or as independent verification of previously generated contig information.

[00378] Another feature of libraries of some resultant molecules is that cleavage junctions are not common to multiple members of a population of resultant molecules. That is, that different copies of the same starting nucleic acid molecule can end up with different patterns of junction and rearrangement. Random cleavage junctions can be generated with a non-specific cleavage molecule, or through variation in restriction endonuclease selection or digestion parameters.

[00379] A consequence of having molecule-specific cleavage sites is that in some cases punctuation oligonucleotides are optionally excluded from the process that results in the 'punctuation molecule' re-shuffling and re-ligation to no ill effect. By aligning segments of three or more reshuffled molecules, one observes that cleavage sites are readily identified by their absence in the majority of other members of a library. That is, when three or more reshuffled molecules are locally aligned, a segment can be found to be common to all of the molecules, but the edges of the segment can vary among the molecules. By noting where segment local sequence similarity ends, one can map cleavage junctions in an 'unpunctuated' rearranged nucleic acid molecule.

[00380] The resulting nucleic acid molecules can be sequenced, for example on a long-read sequencer. The resulting sequence reads contain segments that alternate between nucleic acid sequence from the original input molecule and, if they are used, sequences of the punctuation oligo. These reads can be processed by a computer to split sequence data from each read using the punctuation oligonucleotide sequence, or are otherwise processed to identify junctions. The sequence segments within each read can be segments from a single input high molecular weight DNA molecule. The original nucleic acid molecule can comprise a genome sequence or fraction thereof, such as a chromosome. The sets of segment reads can be discontinuous in the original nucleic acid molecule but reveal long-range, haplotype-phased data. These data can be used for de novo genome assembly and phasing heterozygous positions in the input genome. Sequence between junctions indicates contiguous nucleic acid sequence in the source nucleic acid sample, while sequence across a junction is indicative of a nucleic acid segment that is in phase in the nucleic acid sample but that may be far removed in the arranged scaffold from the adjacent segment.

[00381] Junctions can be identified by a variety of approaches. If punctuation oligos are used, junctions can be identified at reads containing the punctuation oligo sequence. Alternately, junctions can be identified by comparison to a second sequence source (and, preferably, a third sequence source) for a nucleic acid molecule, such as a previously generated contig sequence dataset or a second, independently generated DNA chain molecule having independently derived junctions. As the sequence is aligned, for example, the quality or confidence of alignment to a particular location can indicate where one segment ends and another begins. If restriction enzymes are used to generate cleavages, sequences containing the restriction enzyme recognition site can be evaluated for potentially containing a junction. Note that not

every restriction enzyme recognition site may contain a junction, as some restriction enzyme recognition sites may not have been physically accessible by the enzyme while the nucleic acid was bound to the support, for example. Statistical information can also be employed in identifying junctions; for example, the length segments between junctions may be predicted to be of a certain average value or to follow a certain distribution.

[00382] A benefit of the manipulations herein is that they can preserve molecular phase information while bringing nonadjacent regions of the molecule in proximity such that they are included in a single nucleic acid molecule at a distance suitable for sequencing in a single read, such as a long read. Thus, regions that are separated in the starting sample by greater than the distance of a single long read operation (for example 10 kb, 15 kb, 20 kb, 30 kb, 50 kb, 100 kb or greater) are brought into local proximity such that they are within the distance covered by a single read of a long-range sequencing reaction. Thus, regions that are separated by more than the range of the sequencing technology for a single read in the original sample are read in a single reaction in the phase-preserved, rearranged molecule.

[00383] Resultant rearranged molecules can be sequenced and their sequence information mapped to independently or concurrently generated sequence reads or contig information, or to a known reference genome sequence (for example, the known sequence of the human genome). Segments adjacent on the resultant rearranged molecule reads are presumed to be in phase. Accordingly, when these segments are mapped to disparate contigs or long range sequence reads, the reads are assigned to a common phase of a common molecule in the sequence assembly.

[00384] Alternately, if multiple independently generated resultant rearranged molecules are sequenced concurrently, phased sample data is optionally generated from these molecules alone, such that segment sequences separated by junctions are inferred to be in phase, while sequences not separated by junctions are inferred to represent stretches of nucleic acids contiguous in the sample itself and useful for, for example, de novo sequence determination as well as being useful for phase determination. However, additionally or as an alternative, multiple independently generated resultant rearranged molecules sequenced concurrently can still be compared to independently generated scaffold or contig information

[00385] Methods and compositions presented herein can preserve long-range phase information, particularly for molecule segments separated by greater than the length of a read in a sequencing technology (10 kb, 20 kb, 50 kb, 100 kb, 500 kb or greater, for example), while providing such nonadjacent segments in a rearranged or often ‘punctuated’ molecule where the segments are adjacent or close enough to be covered by a single read.

[00386] In some instances, resultant rearranged molecules are combined with native molecules for sequencing. The native molecules can be recognized and utilized informatically by the lack of punctuation sequences, if employed. Native molecules are sequenced using short or long read technology, and their assembly is guided by the phase information and segment sequence information generated through sequencing of the rearranged molecule or library.

Punctuation Oligonucleotides

[00387] In some cases, punctuation oligonucleotides can be utilized in connecting exposed cleaved ends. A punctuation oligonucleotide includes any oligonucleotide that can be joined to a target polynucleotide, so as to bridge two cleaved internal ends of a sample molecule undergoing phase-preserving rearrangement. Punctuation oligonucleotides can comprise DNA, RNA, nucleotide analogues, non-canonical nucleotides, labeled nucleotides, modified nucleotides, or combinations thereof. In many examples, double-stranded punctuation oligonucleotides comprise two separate oligonucleotides hybridized to one another (also referred to as an “oligonucleotide duplex”), and hybridization may leave one or more blunt ends, one or more 3' overhangs, one or more 5' overhangs, one or more bulges resulting from mismatched and/or unpaired nucleotides, or any combination of these. In some instances, different punctuation oligonucleotides are joined to target polynucleotides in sequential reactions or simultaneously. For example, the first and second punctuation oligonucleotides can be added to the same reaction. Alternately, punctuation oligo populations are uniform in some cases.

[00388] Punctuation oligonucleotides can be manipulated prior to combining with target polynucleotides. For example, terminal phosphates can be removed. Such a modification precludes location of punctuation oligos to one another rather than to cleaved internal ends of a sample molecule.

[00389] Punctuation oligonucleotides contain one or more of a variety of sequence elements, including but not limited to, one or more amplification primer annealing sequences or complements thereof, one or more sequencing primer annealing sequences or complements thereof, one or more barcode sequences, one or more common sequences shared among multiple different punctuation oligonucleotides or subsets of different punctuation oligonucleotides, one or more restriction enzyme recognition sites, one or more overhangs complementary to one or more target polynucleotide overhangs, one or more probe binding sites, one or more random or near-random sequences, and combinations thereof. In some examples, two or more sequence elements are non-adjacent to one another (e.g. separated by one or more nucleotides), adjacent to one another, partially overlapping, or completely overlapping. For example, an amplification primer annealing sequence also serves as a sequencing primer annealing sequence. In certain instances, sequence elements are located at or near the 3' end, at or near the 5' end, or in the interior of the punctuation oligonucleotide.

[00390] In alternate embodiments, the punctuation oligo comprises a minimal complement of bases to maintain integrity of the double-stranded molecule, so as to minimize the amount of sequence information it occupies in a sequencing reaction, or the punctuation oligo comprises an optimal number of bases for ligation, or the punctuation oligo length is arbitrarily determined.

[00391] In some embodiments, a punctuation oligonucleotide comprises a 5' overhang, a 3' overhang, or both that is complementary to one or more target polynucleotides. In certain instances, complementary overhangs are one or more nucleotides in length, including but not limited to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more nucleotides in length. For example, the complementary overhang is about 1, 2, 3, 4, 5 or 6 nucleotides in length. In some embodiments, a punctuation oligonucleotide overhang is

complementary to a target polynucleotide overhang produced by restriction endonuclease digestion or other DNA cleavage method.

[00392] Punctuation oligonucleotides can have any suitable length, at least sufficient to accommodate the one or more sequence elements of which they are comprised. In some embodiments, punctuation oligonucleotides are about, less than about, or more than about 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 200, or more nucleotides in length. In some examples, the punctuation oligonucleotide is 5 to 15 nucleotides in length. In further examples, the punctuation oligonucleotide is about 20 to about 40 nucleotides in length.

[00393] Preferably, punctuation oligonucleotides are modified, for example by 5' phosphate excision (via calf alkaline phosphatase treatment, or de novo by synthesis in the absence of such moieties), so that they do not ligate with one another to form multimers. 3' OH (hydroxyl) moieties are able to ligate to 5' phosphates on the cleaved nucleic acids, thereby supporting ligation to a first or a second nucleic acid segment.

Adapter Oligonucleotides

[00394] An adapter includes any oligonucleotide having a sequence that can be joined to a target polynucleotide. In various examples, adapter oligonucleotides comprise DNA, RNA, nucleotide analogues, non-canonical nucleotides, labeled nucleotides, modified nucleotides, or combinations thereof. In some instances, adapter oligonucleotides are single-stranded, double-stranded, or partial duplex. In general, a partial-duplex adapter oligonucleotide comprises one or more single-stranded regions and one or more double-stranded regions. Double-stranded adapter oligonucleotides can comprise two separate oligonucleotides hybridized to one another (also referred to as an "oligonucleotide duplex"), and hybridization may leave one or more blunt ends, one or more 3' overhangs, one or more 5' overhangs, one or more bulges resulting from mismatched and/or unpaired nucleotides, or any combination of these. In some embodiments, a single-stranded adapter oligonucleotide comprises two or more sequences that can hybridize with one another. When two such hybridizable sequences are contained in a single-stranded adapter, hybridization yields a hairpin structure (hairpin adapter). When two hybridized regions of an adapter oligonucleotides are separated from one another by a non-hybridized region, a "bubble" structure results. Adapter oligonucleotides comprising a bubble structure consist of a single adapter oligonucleotide comprising internal hybridizations, or comprise two or more adapter oligonucleotides hybridized to one another. Internal sequence hybridization, such as between two hybridizable sequences in adapter oligonucleotides, produce, in some instances, a double-stranded structure in a single-stranded adapter oligonucleotide. In some examples, adapter oligonucleotides of different kinds are used in combination, such as a hairpin adapter and a double-stranded adapter, or adapters of different sequences. In certain cases, hybridizable sequences in a hairpin adapter include one or both ends of the oligonucleotide. When neither of the ends are included in the hybridizable sequences, both ends are "free" or "overhanging." When only one end is hybridizable to another sequence in the adapter, the other end forms an overhang, such as a 3' overhang or a 5' overhang. When both the 5'-terminal nucleotide and the 3'-terminal nucleotide are included in the hybridizable sequences, such that the 5'-terminal nucleotide and the 3'-

terminal nucleotide are complementary and hybridize with one another, the end is referred to as “blunt.” In some cases, different adapter oligonucleotides are joined to target polynucleotides in sequential reactions or simultaneously. For example, the first and second adapter oligonucleotides is added to the same reaction. In some examples, adapter oligonucleotides are manipulated prior to combining with target polynucleotides. For example, terminal phosphates can be added or removed.

[00395] Adapter oligonucleotides contain one or more of a variety of sequence elements, including but not limited to, one or more amplification primer annealing sequences or complements thereof, one or more sequencing primer annealing sequences or complements thereof, one or more barcode sequences, one or more common sequences shared among multiple different adapters or subsets of different adapters, one or more restriction enzyme recognition sites, one or more overhangs complementary to one or more target polynucleotide overhangs, one or more probe binding sites (e.g. for attachment to a sequencing platform, such as a flow cell for massive parallel sequencing, such as developed by Illumina, Inc.), one or more random or near-random sequences (e.g. one or more nucleotides selected at random from a set of two or more different nucleotides at one or more positions, with each of the different nucleotides selected at one or more positions represented in a pool of adapters comprising the random sequence), and combinations thereof. In many examples, two or more sequence elements can be non-adjacent to one another (e.g. separated by one or more nucleotides), adjacent to one another, partially overlapping, or completely overlapping. For example, an amplification primer annealing sequence also serves as a sequencing primer annealing sequence. Sequence elements are located at or near the 3' end, at or near the 5' end, or in the interior of the adapter oligonucleotide. When an adapter oligonucleotide can form secondary structure, such as a hairpin, sequence elements can be located partially or completely outside the secondary structure, partially or completely inside the secondary structure, or in between sequences participating in the secondary structure. For example, when an adapter oligonucleotide comprises a hairpin structure, sequence elements can be located partially or completely inside or outside the hybridizable sequences (the “stem”), including in the sequence between the hybridizable sequences (the “loop”). In some embodiments, the first adapter oligonucleotides in a plurality of first adapter oligonucleotides having different barcode sequences comprise a sequence element common among all first adapter oligonucleotides in the plurality. In some embodiments, all second adapter oligonucleotides comprise a sequence element common to all second adapter oligonucleotides that is different from the common sequence element shared by the first adapter oligonucleotides. A difference in sequence elements can be any such that at least a portion of different adapters do not completely align, for example, due to changes in sequence length, deletion, or insertion of one or more nucleotides, or a change in the nucleotide composition at one or more nucleotide positions (such as a base change or base modification). In some embodiments, an adapter oligonucleotide comprises a 5' overhang, a 3' overhang, or both that is complementary to one or more target polynucleotides. Complementary overhangs can be one or more nucleotides in length, including but not limited to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more nucleotides in length. For example, the complementary overhang can be about 1, 2, 3, 4, 5 or 6 nucleotides in length. Complementary overhangs may comprise a fixed sequence. Complementary

overhangs may additionally or alternatively comprise a random sequence of one or more nucleotides, such that one or more nucleotides are selected at random from a set of two or more different nucleotides at one or more positions, with each of the different nucleotides selected at one or more positions represented in a pool of adapter oligonucleotides with complementary overhangs comprising the random sequence. In some embodiments, an adapter oligonucleotides overhang is complementary to a target polynucleotide overhang produced by restriction endonuclease digestion. In some embodiments, an adapter oligonucleotide overhang consists of an adenine or a thymine.

[00396] Adapter oligonucleotides can have any suitable length, at least sufficient to accommodate the one or more sequence elements of which they are comprised. In some embodiments, adapter oligonucleotides are about, less than about, or more than about 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, 200, or more nucleotides in length. In some examples, the adapter oligonucleotides are 5 to 15 nucleotides in length. In further examples, the adapter oligonucleotides are about 20 to about 40 nucleotides in length.

[00397] Preferably, adapter oligonucleotides are modified, for example by 5' phosphate excision (via calf alkaline phosphatase treatment, or de novo by synthesis in the absence of such moieties), so that they do not ligate with one another to form multimers. 3' OH (hydroxyl) moieties are able to ligate to 5' phosphates on the cleaved nucleic acids, thereby supporting ligation to a first or a second nucleic acid segment.

Determining Phase Information of a Nucleic Acid Sample

[00398] To determine phase information of a nucleic acid sample, a nucleic acid is first acquired, for example by extraction methods discussed herein. In many cases, the nucleic acid is then attached to a solid surface so as to preserve phase information subsequent to cleavage of the nucleic acid molecule. Preferably, the nucleic acid molecule is assembled in vitro with nucleic acid-binding proteins to generate reconstituted chromatin, though other suitable solid surfaces include nucleic acid-binding protein aggregates, nanoparticles, nucleic acid-binding beads, or beads coated using a nucleic acid-binding substance, polymers, synthetic nucleic acid-binding molecules, or other solid or substantially solid affinity molecules. A nucleic acid sample can also be obtained already attached to a solid surface, such as in the case of native chromatin. Native chromatin can be obtained having already been fixed, such as in the form of a formalin-fixed paraffin-embedded (FFPE) or similarly preserved sample.

[00399] Following attachment to a nucleic acid binding moiety, the bound nucleic acid molecule can be cleaved. Cleavage is performed with any suitable nucleic acid cleavage entity, including any number of enzymatic and non-enzymatic approaches. Preferably, DNA cleavage is performed with a restriction endonuclease, fragmentase, or transposase. Alternatively or additionally, nucleic acid cleavage is achieved with other restriction enzymes, topoisomerase, non-specific endonuclease, nucleic acid repair enzyme, RNA-guided nuclease, or alternate enzyme. Physical means can also be used to generate cleavage, including mechanical means (e.g., sonication, shear), thermal means (e.g., temperature change), or electromagnetic means (e.g., irradiation, such as UV irradiation). Nucleic acid cleavage produces free nucleic acid ends, either having 'sticky' overhangs or blunt ends, depending on the cleavage method used.

When sticky overhang ends are generated, the sticky ends are optionally partially filled in to prevent re-ligation. Alternatively, the overhangs are completely filled in to produce blunt ends.

[00400] In many cases, overhang ends are partially or completely filled in with dNTPs, which are optionally labeled. In such cases, dNTPs can be biotinylated, sulphated, attached to a fluorophore, dephosphorylated, or any other number of nucleotide modifications. Nucleotide modifications can also include epigenetic modifications, such as methylation (e.g., 5-mC, 5-hmC, 5-fC, 5-caC, 4-mC, 6-mA, 8-oxoG, 8-oxoA). Labels or modifications can be selected from those detectable during sequencing, such as epigenetic modifications detectable by nanopore sequencing; in this way, the locations of ligation junctions can be detected during sequencing. These labels or modifications can also be targeted for binding or enrichment; for example, antibodies targeting methyl-cytosine can be used to capture, target, bind, or label blunt ends filled in with methyl-cytosine. Non-natural nucleotides, non-canonical or modified nucleotides, and nucleic acid analogs can also be used to label the locations of blunt-end fill-in. Non-canonical or modified nucleotides can include pseudouridine (Ψ), dihydrouridine (D), inosine (I), 7-methylguanosine (m7G), xanthine, hypoxanthine, purine, 2,6-diaminopurine, and 6,8-diaminopurine. Nucleic acid analogs can include peptide nucleic acid (PNA), Morpholino and locked nucleic acid (LNA), glycol nucleic acid (GNA), and threose nucleic acid (TNA). In some cases, overhangs are filled in with un-labeled dNTPs, such as dNTPs without biotin. In some cases, such as cleavage with a transposon, blunt ends are generated that do not require filling in. These free blunt ends are generated when the transposase inserts two unlinked punctuation oligonucleotides. The punctuation oligonucleotides, however, are synthesized to have sticky or blunt ends as desired. Proteins associated with sample nucleic acids, such as histones, can also be modified. For example, histones can be acetylated (e.g., at lysine residues) and/or methylated (e.g., at lysine and arginine residues).

[00401] Next, while the cleaved nucleic acid molecule is still bound to the solid surface, the free nucleic acid ends are linked together, resulting in a proximity-linked nucleic acid molecule. Linking occurs, in some cases, through ligation, either between free ends, or with a separate entity, such as an oligonucleotide. In some cases, the oligonucleotide is a punctuation oligonucleotide. In such cases, the punctuation molecule ends are compatible with the free ends of the cleaved nucleic acid molecule. In many cases, the punctuation molecule is dephosphorylated to prevent concatemerization of the oligonucleotides. In most cases, the punctuation molecule is ligated on each end to a free nucleic acid end of the cleaved nucleic acid molecule. In many cases, this ligation step results in rearrangements of the cleaved nucleic acid molecule such that two free ends that were not originally adjacent to one another in the starting nucleic acid molecule are now proximity-linked in a paired end.

[00402] Following linking of the free ends of the cleaved nucleic acid molecule, the rearranged nucleic acid sample is released from the nucleic acid binding moiety using any number of standard enzymatic and non-enzymatic approaches. For example, in the case of in vitro reconstituted chromatin, the rearranged nucleic acid molecule is released by denaturing or degradation of the nucleic acid-binding proteins. In other examples, cross-linking is reversed. In yet other examples, affinity interactions are reversed or blocked. The released nucleic acid molecule is rearranged compared to the input nucleic acid molecule. In

cases where punctuation molecules are used, the resulting rearranged molecule is referred to as a punctuated molecule due to the punctuation oligonucleotides that are interspersed throughout the rearranged nucleic acid molecule. In these cases, the nucleic acid segments flanking the punctuations make up a paired end.

[00403] During the cleavage and linking steps of the methods disclosed herein, phase information is maintained since the nucleic acid molecule is bound to a solid surface throughout these processes. This can enable the analysis of phase information without relying on information from other markers, such as single nucleotide polymorphisms (SNPs). Using the methods and compositions disclosed herein, in some cases, two nucleic acid segments within the nucleic acid molecule are rearranged such that they are closer in proximity than they were on the original nucleic acid molecule. In many examples, the original separation distance of the two nucleic acid segments in the starting nucleic acid sample is greater than the average read length of standard sequencing technologies. For example, the starting separation distance between the two nucleic acid segments within the input nucleic acid sample is about 10 kb, 12.5 kb, 15 kb, 17.5 kb, 20 kb, 25 kb, 30 kb, 35 kb, 40 kb, 45 kb, 50 kb, 60 kb, 70 kb, 80 kb, 90 kb, 100 kb, 125 kb, 150 kb, 200 kb, 300 kb, 400 kb, 500 kb, 600 kb, 700 kb, 800 kb, 900 kb, 1 Mb, or greater. In preferred examples, the separation distance between the two rearranged DNA segments is less than the average read length of standard sequencing technologies. For example, the distance separating the two rearranged DNA segments within the rearranged DNA molecule is less than about 50 kb, 40 kb, 30 kb, 25 kb, 20 kb, 17 kb, 15 kb, 14 kb, 13 kb, 12 kb, 11 kb, 10 kb, 9 kb, 8 kb, 7 kb, 6 kb, 5 kb, or less. In preferred cases, the separation distance is less than that of the average read length of a long-read sequencing machine. In these cases, when the rearranged DNA sample is released from the nucleic acid binding moiety and sequenced, phase information is determined and sequence information is generated sufficient to generate a de novo sequence scaffold.

Barcoding a Rearranged Nucleic Acid Molecule

[00404] In some examples, the released rearranged nucleic acid molecule described herein is further processed prior to sequencing. For example, the nucleic acid segments comprised within the rearranged nucleic acid molecule can be barcoded. Barcoding can allow for easier grouping of sequence reads. For example, barcodes can be used to identify sequences originating from the same rearranged nucleic acid molecule. Barcodes can also be used to uniquely identify individual junctions. For example, each junction can be marked with a unique (e.g., randomly generated) barcode which can uniquely identify the junction. Multiple barcodes can be used together, such as a first barcode to identify sequences originating from the same rearranged nucleic acid molecule and a second barcode that uniquely identifies individual junctions.

[00405] Barcoding can be achieved through a number of techniques. In some cases, barcodes can be included as a sequence within a punctuation oligo. In other cases, the released rearranged nucleic acid molecule can be contacted to oligonucleotides comprising at least two segments: one segment contains a barcode and a second segment contains a sequence complementary to a punctuation sequence. After annealing to the punctuation sequences, the barcoded oligonucleotides are extended with polymerase to yield barcoded molecules from the same punctuated nucleic acid molecule. Since the punctuated nucleic

acid molecule is a rearranged version of the input nucleic acid molecule, in which phase information is preserved, the generated barcoded molecules are also from the same input nucleic acid molecule. These barcoded molecules comprise a barcode sequence, the punctuation complementary sequence, and genomic sequence.

[00406] For rearranged nucleic acid molecules with or without punctuation, molecules can be barcoded by other means. For example, rearranged nucleic acid molecules can be contacted with barcoded oligonucleotides which can be extended to incorporate sequence from the rearranged nucleic acid molecule. Barcodes can hybridize to punctuation sequences, to restriction enzyme recognition sites, to sites of interest (e.g., genomic regions of interest), or to random sites (e.g., through a random n-mer sequence on the barcode oligonucleotide). Rearranged nucleic acid molecules can be contacted to the barcodes using appropriate concentrations and/or separations (e.g., spatial or temporal separation) from other rearranged nucleic acid molecules in the sample such that multiple rearranged nucleic acid molecules are not given the same barcode sequence. For example, a solution comprising rearranged nucleic acid molecules can be diluted to such a concentration that only one rearranged nucleic acid molecule will be contacted to a barcode or group of barcodes with a given barcode sequence. Barcodes can be contacted to rearranged nucleic acid molecules in free solution, in fluidic partitions (e.g., droplets or wells), or on an array (e.g., at particular array spots).

[00407] Barcoded nucleic acid molecules (e.g., extension products) can be sequenced, for example, on a short-read sequencing machine and phase information is determined by grouping sequence reads having the same barcode into a common phase. Alternatively, prior to sequencing, the barcoded products can be linked together, for example through bulk ligation, to generate long molecules which are sequenced, for example, using long-read sequencing technology. In these cases, the embedded read pairs are identifiable via the amplification adapters and punctuation sequences. Further phase information is obtained from the barcode sequence of the read pair.

Determining Phase Information with Paired Ends

[00408] Further provided herein are methods and compositions for determining phase information from paired ends. Paired ends can be generated by any of the methods disclosed or those further illustrated in the provided Examples. For example, in the case of a nucleic acid molecule bound to a solid surface which was subsequently cleaved, following re-ligation of free ends, re-ligated nucleic acid segments are released from the solid-phase attached nucleic acid molecule, for example, by restriction digestion. This release results in a plurality of paired ends. In some cases, the paired ends are ligated to amplification adapters, amplified, and sequenced with short reach technology. In these cases, paired ends from multiple different nucleic acid binding moiety-bound nucleic acid molecules are within the sequenced sample. However, it is confidently concluded that for either side of a paired end junction, the junction adjacent sequence is derived from a common phase of a common molecule. In cases where paired ends are linked with a punctuation oligonucleotide, the paired end junction in the sequencing read is identified by the punctuation oligonucleotide sequence. In other cases, the pair ends were linked by modified nucleotides, which can be identified based on the sequence of the modified nucleotides used.

[00409] Alternatively, following release of paired ends, the free paired ends can be ligated to amplification adapters and amplified. In these cases, the plurality of paired ends is then bulk ligated together to generate long molecules which are read using long-read sequencing technology. In other examples, released paired ends are bulk ligated to each other without the intervening amplification step. In either case, the embedded read pairs are identifiable via the native DNA sequence adjacent to the linking sequence, such as a punctuation sequence or modified nucleotides. The concatenated paired ends are read on a long-sequence device, and sequence information for multiple junctions is obtained. Since the paired ends derived from multiple different nucleic acid binding moiety-bound DNA molecules, sequences spanning two individual paired ends, such as those flanking amplification adapter sequences, are found to map to multiple different DNA molecules. However, it is confidently concluded that for either side of a paired end junction, the junction-adjacent sequence is derived from a common phase of a common molecule. For example, in the case of paired ends derived from a punctuated molecule, sequences flanking the punctuation sequence are confidently assigned to a common DNA molecule. In preferred cases, because the individual paired ends are concatenated using the methods and compositions disclosed herein, one can sequence multiple paired ends in a single read.

[00410] Upon sequencing the punctuated nucleic acid using a long-read sequencing device, one observes stretches of sequence that correspond to uncleaved segments, for which local order and orientation, as well as phase information is derived. One also observes regions of long sequence reads that span punctuation oligo sequence. These sequence segments on either side of a punctuation oligo are known to be in phase with one another (and in phase with other segments on the punctuated molecule), but are unlikely to be in the correct order and orientation. A benefit of the rearrangement process is that segments far apart from one another on the sample molecule are brought into proximity such that they are spanned in a single read. Another benefit is that the sequence information of the original sample molecule is largely preserved, such that de novo contig information is concurrently generated.

Nucleic Acids

[00411] In eukaryotes, genomic DNA is packed into chromatin to consist as chromosomes within the nucleus. The basic structural unit of chromatin is the nucleosome, which consists of 146 base pairs (bp) of DNA wrapped around a histone octamer. The histone octamer consists of two copies each of the core histone H2A-H2B dimers and H3-H4 dimers. Nucleosomes are regularly spaced along the DNA in what is commonly referred to as “beads on a string.”

[00412] The assembly of core histones and DNA into nucleosomes is mediated by chaperone proteins and associated assembly factors. Nearly all of these factors are core histone-binding proteins. Some of the histone chaperones, such as nucleosome assembly protein-1 (NAP-1), exhibit a preference for binding to histones H3 and H4. It has also been observed that newly synthesized histones are acetylated and then subsequently deacetylated after assembly into chromatin. The factors that mediate histone acetylation or deacetylation therefore play an important role in the chromatin assembly process.

[00413] In general, two in vitro methods have been developed for reconstituting or assembling chromatin. One method is ATP-independent, while the second is ATP-dependent. The ATP-independent method for

reconstituting chromatin involves the DNA and core histones plus either a protein like NAP-1 or salt to act as a histone chaperone. This method results in a random arrangement of histones on the DNA that does not accurately mimic the native core nucleosome particle in the cell. These particles are often referred to as mononucleosomes because they are not regularly ordered, extended nucleosome arrays and the DNA sequence used is usually not longer than 250 bp (Kundu, T. K. et al., Mol. Cell 6: 551-561, 2000). To generate an extended array of ordered nucleosomes on a greater length of DNA sequence, the chromatin can be assembled through an ATP-dependent process.

[00414] The ATP-dependent assembly of periodic nucleosome arrays, which are similar to those seen in native chromatin, requires the DNA sequence, core histone particles, a chaperone protein and ATP-utilizing chromatin assembly factors. ACF (ATP-utilizing chromatin assembly and remodeling factor) or RSF (remodeling and spacing factor) are two widely researched assembly factors that are used to generate extended ordered arrays of nucleosomes into chromatin in vitro (Fyodorov, D.V., and Kadonaga, J.T. Method Enzymol. 371: 499-515, 2003; Kundu, T. K. et al. Mol. Cell 6: 551-561, 2000).

[00415] In particular embodiments, the methods of the disclosure can be easily applied to any type of fragmented double stranded DNA including, but not limited to, for example, free DNA isolated from plasma, serum, and/or urine; apoptotic DNA from cells and/or tissues; and/or DNA fragmented enzymatically in vitro (for example, by DNase I).

[00416] Nucleic acid obtained from biological samples can be fragmented to produce suitable fragments for analysis. Template nucleic acids may be fragmented to desired length, using a variety of enzymatic methods. DNA may be randomly sheared brief exposure to a DNase. RNA may be fragmented by brief exposure to an RNase, heat plus magnesium, or by shearing. The RNA may be converted to cDNA. If fragmentation is employed, the RNA may be converted to cDNA before or after fragmentation. Nucleic acid molecules may be single-stranded, double-stranded, or double-stranded with single-stranded regions (for example, stem- and loop-structures).

[00417] In some embodiments, cross-linked DNA molecules may be subjected to a size selection step. Size selection of the nucleic acids may be performed to cross-linked DNA molecules below or above a certain size. Size selection may further be affected by the frequency of cross-links and/or by the fragmentation method. In some embodiments, a composition may be prepared comprising cross-linking a DNA molecule in the range of about 145 bp to about 600 bp, about 100 bp to about 2500 bp, about 600 to about 2500 bp, about 350 bp to about 1000 bp, or any range bounded by any of these values (e.g., about 100 bp to about 2500 bp).

[00418] In some embodiments, sample polynucleotides are fragmented into a population of fragmented DNA molecules of one or more specific size range(s). In some embodiments, fragments can be generated from at least about 1, about 2, about 5, about 10, about 20, about 50, about 100, about 200, about 500, about 1000, about 2000, about 5000, about 10,000, about 20,000, about 50,000, about 100,000, about 200,000, about 500,000, about 1,000,000, about 2,000,000, about 5,000,000, about 10,000,000, or more genome-equivalents of starting DNA. Fragmentation may be accomplished by DNase treatment. In some embodiments, the fragments have an average length from about 10 to about 10,000, about 20,000, about

30,000, about 40,000, about 50,000, about 60,000, about 70,000, about 80,000, about 90,000, about 100,000, about 150,000, about 200,000, about 300,000, about 400,000, about 500,000, about 600,000, about 700,000, about 800,000, about 900,000, about 1,000,000, about 2,000,000, about 5,000,000, about 10,000,000, or more nucleotides. In some embodiments, the fragments have an average length from about 145 bp to about 600 bp, about 100 bp to about 2500 bp, about 600 to about 2500 bp, about 350 bp to about 1000 bp, or any range bounded by any of these values (e.g., about 100 bp to about 2500 bp). In some embodiments, the fragments have an average length less than about 2500 bp, less than about 1200 bp, less than about 1000 bp, less than about 800 bp, less than about 600 bp, less than about 350 bp, or less than about 200 bp. In other embodiments, the fragments have an average length more than about 100 bp, more than about 350 bp, more than about 600 bp, more than about 800 bp, more than about 1000 bp, more than about 1200 bp, or more than about 2000 bp. Non-limiting examples of DNases include DNase I, DNase II, micrococcal nuclease, variants thereof, and combinations thereof. For example, digestion with DNase I can induce random double-stranded breaks in DNA in the absence of Mg^{++} and in the presence of Mn^{++} . Fragmentation can produce fragments having 5' overhangs, 3' overhangs, blunt ends, or a combination thereof. In some embodiments, the method includes the step of size selecting the fragments via standard methods such as column purification or isolation from an agarose gel.

Targeted Nuclease Enzymes

[00419] Fragmented DNA as provided herein may be created or generated by digestion, such as by in situ digestion with any number of nucleases (e.g., restriction endonucleases) or DNases (e.g., MNase). In some cases, enzymes may be used in combination to achieve the desired digestion or fragmentation. In various cases, nucleases (or domains or fragments thereof) may be targeted to certain genomic sites using one or more antibodies. For example, the crosslinked sample may be contacted to an antibody that binds to certain regions of the DNA, such as a histone binding site, a transcription factor binding site, or a methylated DNA site. A nuclease linked or fused to an immunoglobulin binding protein or fragment thereof, such as a Protein A, a Protein G, a Protein A/G, or a Protein L, can then be added to the sample and the nuclease may digest the DNA only in the region where the antibody bound. This may be done in combination, for example, where a first antibody is bound to the DNA sample, then the nuclease is targeted to the first antibody, then a second antibody is bound to the DNA sample and the nuclease is targeted to the second antibody, and so on to achieve the desired digestion pattern.

Ligation

[00420] In some embodiments, the 5' and/or 3' end nucleotide sequences of fragmented DNA are not modified prior to ligation. For example, cleavage by an enzyme that leaves a predictable blunt end can be followed by ligation of blunt-ended DNA fragments to nucleic acids, such as adaptors, oligonucleotides, or polynucleotides, comprising a blunt end. In some embodiments, the fragmented DNA molecules are blunt-end polished (or "end repaired") to produce DNA fragments having blunt ends, prior to being joined to adaptors. The blunt-end polishing step may be accomplished by incubation with a suitable enzyme, such as a DNA polymerase that has both 3' to 5' exonuclease activity and 5' to 3' polymerase activity, for example, T4 polymerase. In some embodiments, end repair can be followed by an addition of 1, 2, 3, 4, 5,

6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more nucleotides, such as one or more adenine, one or more thymine, one or more guanine, or one or more cytosine, to produce an overhang. For example, the end pair can be followed by an addition of 1, 2, 3, 4, 5, or 6 nucleotides. DNA fragments having an overhang can be joined to one or more nucleic acids, such as oligonucleotides, adaptor oligonucleotides, or polynucleotides, having a complementary overhang, such as in a ligation reaction. For example, a single adenine can be added to the 3' ends of end repaired DNA fragments using a template independent polymerase, followed by ligation to one or more adaptors each having a thymine at a 3' end. In some embodiments, nucleic acids, such as oligonucleotides or polynucleotides can be joined to blunt end double-stranded DNA molecules which have been modified by extension of the 3' end with one or more nucleotides followed by 5' phosphorylation. In some cases, extension of the 3' end may be performed with a polymerase such as, Klenow polymerase or any of the suitable polymerases provided herein, or by use of a terminal deoxynucleotide transferase, in the presence of one or more dNTPs in a suitable buffer that can contain magnesium. In some embodiments, target polynucleotides having blunt ends are joined to one or more adaptors comprising a blunt end. Phosphorylation of 5' ends of DNA fragment molecules may be performed, for example, with T4 polynucleotide kinase in a suitable buffer containing ATP and magnesium. The fragmented DNA molecules may optionally be treated to dephosphorylate 5' ends or 3' ends, for example, by using enzymes such as phosphatases.

[00421] The terms “connecting,” “joining,” and “ligation” as used herein, with respect to two polynucleotides, such as an adaptor oligonucleotide and a target polynucleotide, refers to the covalent attachment of two separate DNA segments to produce a single larger polynucleotide with a contiguous backbone. Methods for joining two DNA segments include, without limitation, enzymatic and non-enzymatic (e.g., chemical) methods. Examples of ligation reactions that are non-enzymatic include the non-enzymatic ligation techniques described in U.S. Pat. Nos. 5,780,613 and 5,476,930, which are herein incorporated by reference. In some embodiments, an adaptor oligonucleotide is joined to a target polynucleotide by a ligase, for example, a DNA ligase or RNA ligase. Multiple ligases, each having characterized reaction conditions include, without limitation, NAD⁺-dependent ligases including tRNA ligase, Taq DNA ligase, *Thermus filiformis* DNA ligase, *Escherichia coli* DNA ligase, Tth DNA ligase, *Thermus scotoductus* DNA ligase (I and II), thermostable ligase, Ampligase thermostable DNA ligase, VanC-type ligase, 9° N DNA Ligase, Tsp DNA ligase, and novel ligases discovered by bioprospecting; ATP-dependent ligases including T4 RNA ligase, T4 DNA ligase, T3 DNA ligase, T7 DNA ligase, Pfu DNA ligase, DNA ligase I, DNA ligase III, DNA ligase IV, and novel ligases discovered by bioprospecting; and wild-type, mutant isoforms, and genetically engineered variants thereof.

[00422] Ligation can be between DNA segments having hybridizable sequences, such as complementary overhangs. Ligation can also be between two blunt ends. Generally, a 5' phosphate is utilized in a ligation reaction. The 5' phosphate can be provided by the target polynucleotide, the adaptor oligonucleotide, or both. 5' phosphates can be added to or removed from DNA segments to be joined, as needed. Methods for the addition or removal of 5' phosphates include, without limitation, enzymatic and chemical processes. Enzymes useful in the addition and/or removal of 5' phosphates include kinases, phosphatases, and

polymerases. In some embodiments, both of the two ends joined in a ligation reaction (e.g., an adaptor end and a target polynucleotide end) provide a 5' phosphate, such that two covalent linkages are made in joining the two ends. In some embodiments, only one of the two ends joined in a ligation reaction (e.g., only one of an adaptor end and a target polynucleotide end) provides a 5' phosphate, such that only one covalent linkage is made in joining the two ends.

[00423] In some embodiments, only one strand at one or both ends of a target polynucleotide is joined to an adaptor oligonucleotide. In some embodiments, both strands at one or both ends of a target polynucleotide are joined to an adaptor oligonucleotide. In some embodiments, 3' phosphates are removed prior to ligation. In some embodiments, an adaptor oligonucleotide is added to both ends of a target polynucleotide, wherein one or both strands at each end are joined to one or more adaptor oligonucleotides. When both strands at both ends are joined to an adaptor oligonucleotide, joining can be followed by a cleavage reaction that leaves a 5' overhang that can serve as a template for the extension of the corresponding 3' end, which 3' end may or may not include one or more nucleotides derived from the adaptor oligonucleotide. In some embodiments, a target polynucleotide is joined to a first adaptor oligonucleotide on one end and a second adaptor oligonucleotide on the other end. In some embodiments, two ends of a target polynucleotide are joined to the opposite ends of a single adaptor oligonucleotide. In some embodiments, the target polynucleotide and the adaptor oligonucleotide to which it is joined comprise blunt ends. In some embodiments, separate ligation reactions can be carried out for each sample, using a different first adaptor oligonucleotide comprising at least one barcode sequence for each sample, such that no barcode sequence is joined to the target polynucleotides of more than one sample. A DNA segment or a target polynucleotide that has an adaptor oligonucleotide joined to it is considered "tagged" by the joined adaptor.

[00424] In some cases, the ligation reaction can be performed at a DNA segment or target polynucleotide concentration of about 0.1 ng/μL, about 0.2 ng/μL, about 0.3 ng/μL, about 0.4 ng/μL, about 0.5 ng/μL, about 0.6 ng/μL, about 0.7 ng/μL, about 0.8 ng/μL, about 0.9 ng/μL, about 1.0 ng/μL, about 1.2 ng/μL, about 1.4 ng/μL, about 1.6 ng/μL, about 1.8 ng/μL, about 2.0 ng/μL, about 2.5 ng/μL, about 3.0 ng/μL, about 3.5 ng/μL, about 4.0 ng/μL, about 4.5 ng/μL, about 5.0 ng/μL, about 6.0 ng/μL, about 7.0 ng/μL, about 8.0 ng/μL, about 9.0 ng/μL, about 10 ng/μL, about 15 ng/μL, about 20 ng/μL, about 30 ng/μL, about 40 ng/μL, about 50 ng/μL, about 60 ng/μL, about 70 ng/μL, about 80 ng/μL, about 90 ng/μL, about 100 ng/μL, about 150 ng/μL, about 200 ng/μL, about 300 ng/μL, about 400 ng/μL, about 500 ng/μL, about 600 ng/μL, about 800 ng/μL, or about 1000 ng/μL. For example, the ligation can be performed at a DNA segment or target polynucleotide concentration of about 100 ng/μL, about 150 ng/μL, about 200 ng/μL, about 300 ng/μL, about 400 ng/μL, or about 500 ng/μL.

[00425] In some cases, the ligation reaction can be performed at a DNA segment or target polynucleotide concentration of about 0.1 to 1000 ng/μL, about 1 to 1000 ng/μL, about 1 to 800 ng/μL, about 10 to 800 ng/μL, about 10 to 600 ng/μL, about 100 to 600 ng/μL, or about 100 to 500 ng/μL.

[00426] In some cases, the ligation reaction can be performed for more than about 5 minutes, about 10 minutes, about 20 minutes, about 30 minutes, about 40 minutes, about 50 minutes, about 60 minutes,

about 90 minutes, about 2 hours, about 3 hours, about 4 hours, about 5 hours, about 6 hours, about 8 hours, about 10 hours, about 12 hours, about 18 hours, about 24 hours, about 36 hours, about 48 hours, or about 96 hours. In other cases, the ligation reaction can be performed for less than about 5 minutes, about 10 minutes, about 20 minutes, about 30 minutes, about 40 minutes, about 50 minutes, about 60 minutes, about 90 minutes, about 2 hours, about 3 hours, about 4 hours, about 5 hours, about 6 hours, about 8 hours, about 10 hours, about 12 hours, about 18 hours, about 24 hours, about 36 hours, about 48 hours, or about 96 hours. For example, the ligation reaction can be performed for about 30 minutes to about 90 minutes. In some embodiments, joining of an adaptor to a target polynucleotide produces a joined product polynucleotide having a 3' overhang comprising a nucleotide sequence derived from the adaptor.

[00427] In some embodiments, after joining at least one adaptor oligonucleotide to a target polynucleotide, the 3' end of one or more target polynucleotides is extended using the one or more joined adaptor oligonucleotides as template. For example, an adaptor comprising two hybridized oligonucleotides that is joined to only the 5' end of a target polynucleotide allows for the extension of the unjoined 3' end of the target using the joined strand of the adaptor as template, concurrently with or following displacement of the unjoined strand. Both strands of an adaptor comprising two hybridized oligonucleotides may be joined to a target polynucleotide such that the joined product has a 5' overhang, and the complementary 3' end can be extended using the 5' overhang as template. As a further example, a hairpin adaptor oligonucleotide can be joined to the 5' end of a target polynucleotide. In some embodiments, the 3' end of the target polynucleotide that is extended comprises one or more nucleotides from an adaptor oligonucleotide. For target polynucleotides to which adaptors are joined on both ends, extension can be carried out for both 3' ends of a double-stranded target polynucleotide having 5' overhangs. This 3' end extension, or "fill-in" reaction, generates a complementary sequence, or "complement," to the adaptor oligonucleotide template that is hybridized to the template, thus filling in the 5' overhang to produce a double-stranded sequence region. Where both ends of a double-stranded target polynucleotide have 5' overhangs that are filled in by extension of the complementary strands' 3' ends, the product is completely double-stranded. Extension can be carried out by any suitable polymerase, such as a DNA polymerase, many of which are commercially available. DNA polymerases can comprise DNA-dependent DNA polymerase activity, RNA-dependent DNA polymerase activity, or DNA-dependent and RNA-dependent DNA polymerase activity. DNA polymerases can be thermostable or non-thermostable. Examples of DNA polymerases include, but are not limited to, Taq polymerase, Tth polymerase, Tli polymerase, Pfu polymerase, PfuTubo polymerase, Pyrobest polymerase, Pwo polymerase, KOD polymerase, Bst polymerase, Sac polymerase, Sso polymerase, Poc polymerase, Pab polymerase, Mth polymerase, Pho polymerase, ES4 polymerase, VENT polymerase, DEEPVENT polymerase, EX-Taq polymerase, LA-Taq polymerase, Expand polymerases, Platinum Taq polymerases, Hi-Fi polymerase, Tbr polymerase, Tfi polymerase, Tru polymerase, Tac polymerase, Tne polymerase, Tma polymerase, Tih polymerase, Tfi polymerase, Klenow fragment, and variants, modified products and derivatives thereof 3' end extension can be performed before or after pooling of target polynucleotides from independent samples.

Target Enrichment

[00428] In certain embodiments, the disclosure provides methods for the enrichment of a target nucleic acids and analysis of the target nucleic acids. In some cases, the methods for enrichment is in a solution-based format. In some cases, the target nucleic acid can be labeled with a labeling agent. In other cases, the target nucleic acid can be crosslinked to one or more association molecules that are labeled with a labeling agent. Examples of labeling agents include, but are not limited to, biotin, polyhistidine tags, and chemical tags (e.g., alkyne and azide derivatives used in Click Chemistry methods). Further, the labeled target nucleic acid can be captured and thereby enriched by using a capturing agent. The capturing agent can be streptavidin and/or avidin, an antibody, a chemical moiety (e.g., alkyne, azide), and any biological, chemical, physical, or enzymatic agents used for affinity purification.

[00429] In some cases, immobilized or non-immobilized nucleic acid probes can be used to capture the target nucleic acids. For example, the target nucleic acids can be enriched from a sample by hybridization to the probes on a solid support or in solution. In some examples, the sample can be a genomic sample. In some examples, the probes can be an amplicon. The amplicon can comprise a predetermined sequence. Further, the hybridized target nucleic acids can be washed and/or eluted off of the probes. The target nucleic acid can be a DNA, RNA, cDNA, or mRNA molecule.

[00430] In some cases, the enrichment method can comprise contacting the sample comprising the target nucleic acid to the probes and binding the target nucleic acid to a solid support. In some cases, the sample can be fragmented using enzymatic methods to yield the target nucleic acids. In some cases, the probes can be specifically hybridized to the target nucleic acids. In some cases, the target nucleic acids can have an average size of about 145 bp to about 600 bp, about 100 bp to about 2500 bp, about 600 to about 2500 bp, or about 350 bp to about 1000 bp. The target nucleic acids can be further separated from the unbound nucleic acids in the sample. The solid support can be washed and/or eluted to provide the enriched target nucleic acids. In some examples, the enrichment steps can be repeated for about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 times. For example, the enrichment steps can be repeated for about 1, 2, or 3 times.

[00431] In some cases, the enrichment method can comprise providing probe derived amplicons wherein said probes for amplification are attached to a solid support. The solid support can comprise support-immobilized nucleic acid probes to capture specific target nucleic acid from a sample. The probe derived amplicons can hybridize to the target nucleic acids. Following hybridization to the probe amplicons, the target nucleic acids in the sample can be enriched by capturing (e.g., via capturing agents as biotin, antibodies, etc.) and washing and/or eluting the hybridized target nucleic acids from the captured probes. The target nucleic acid sequence(s) may be further amplified using, for example, PCR methods to produce an amplified pool of enriched PCR products.

[00432] In some cases, the solid support can be a microarray, a slide, a chip, a microwell, a column, a tube, a particle, or a bead. In some examples, the solid support can be coated with streptavidin and/or avidin. In other examples, the solid support can be coated with an antibody. Further, the solid support can comprise a glass, metal, ceramic or polymeric material. In some embodiments, the solid support can be a

nucleic acid microarray (e.g., a DNA microarray). In other embodiments, the solid support can be a paramagnetic bead.

[00433] In particular embodiments, the disclosure provides methods for amplifying the enriched DNA. In some cases, the enriched DNA is a read-pair. The read-pair can be obtained by the methods of the present disclosure.

[00434] In some embodiments, the one or more amplification and/or replication steps are used for the preparation of a library to be sequenced. Any suitable amplification method may be used. Examples of amplification techniques that can be used include, but are not limited to, quantitative PCR, quantitative fluorescent PCR (QF-PCR), multiplex fluorescent PCR (MF-PCR), real time PCR (RTPCR), single cell PCR, restriction fragment length polymorphism PCR (PCR-RFLP), PCK-RFLPIRT-PCR-IRFLP, hot start PCR, nested PCR, in situ polonony PCR, in situ rolling circle amplification (RCA), bridge PCR, ligation mediated PCR, Qb replicase amplification, inverse PCR, picotiter PCR and emulsion PCR. Other suitable amplification methods include the ligase chain reaction (LCR), transcription amplification, self-sustained sequence replication, selective amplification of target polynucleotide sequences, consensus sequence primed polymerase chain reaction (CP-PCR), arbitrarily primed polymerase chain reaction (AP-PCR), degenerate oligonucleotide-primed PCR (DOP-PCR) and nucleic acid-based sequence amplification (NABSA). Other amplification methods that can be used herein include those described in U.S. Patent Nos. 5,242,794; 5,494,810; 4,988,617; and 6,582,938.

[00435] In particular embodiments, PCR is used to amplify DNA molecules after they are dispensed into individual partitions. In some cases, one or more specific priming sequences within amplification adaptors are utilized for PCR amplification. The amplification adaptors may be ligated to fragmented DNA molecules before or after dispensing into individual partitions. Polynucleotides comprising amplification adaptors with suitable priming sequences on both ends can be PCR amplified exponentially. Polynucleotides with only one suitable priming sequence due to, for example, imperfect ligation efficiency of amplification adaptors comprising priming sequences, may only undergo linear amplification. Further, polynucleotides can be eliminated from amplification, for example, PCR amplification, all together, if no adaptors comprising suitable priming sequences are ligated. In some embodiments, the number of PCR cycles vary between 10-30, but can be as low as 9, 8, 7, 6, 5, 4, 3, 2 or less or as high as 40, 45, 50, 55, 60 or more. As a result, exponentially amplifiable fragments carrying amplification adaptors with a suitable priming sequence can be present in much higher (1000 fold or more) concentration compared to linearly amplifiable or un-amplifiable fragments, after a PCR amplification. Benefits of PCR, as compared to whole genome amplification techniques (such as amplification with randomized primers or Multiple Displacement Amplification using phi29 polymerase) include, but are not limited to, a more uniform relative sequence coverage - as each fragment can be copied at most once per cycle and as the amplification is controlled by thermocycling program, a substantially lower rate of forming chimeric molecules than, for example, MDA (Lasken et al., 2007, BMC Biotechnology) - as chimeric molecules pose significant challenges for accurate sequence assembly by presenting nonbiological sequences in the assembly graph, which may result in higher rate of

misassemblies or highly ambiguous and fragmented assembly, reduced sequence specific biases that may result from binding of randomized primers commonly used in MDA versus using specific priming sites with a specific sequence, a higher reproducibility in the amount of final amplified DNA product, which can be controlled by selection of the number of PCR cycles, and a higher fidelity in replication with the polymerases that are commonly used in PCR as compared to common whole genome amplification techniques.

[00436] In some embodiments, the fill-in reaction is followed by or performed as part of amplification of one or more target polynucleotides using a first primer and a second primer, wherein the first primer comprises a sequence that is hybridizable to at least a portion of the complement of one or more of the first adaptor oligonucleotides, and further wherein the second primer comprises a sequence that is hybridizable to at least a portion of the complement of one or more of the second adaptor oligonucleotides. Each of the first and second primers may be of any suitable length, such as about, less than about, or more than about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 100, or more nucleotides, any portion or all of which may be complementary to the corresponding target sequence (e.g., about, less than about, or more than about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, or more nucleotides). For example, about 10 to 50 nucleotides can be complementary to the corresponding target sequence.

[00437] “Amplification” refers to any process by which the copy number of a target sequence is increased. In some cases, a replication reaction may produce only a single complementary copy/replica of a polynucleotide. Methods for primer-directed amplification of target polynucleotides include, without limitation, methods based on the polymerase chain reaction (PCR). Conditions favorable to the amplification of target sequences by PCR can be optimized at a variety of steps in the process, and depend on characteristics of elements in the reaction, such as target type, target concentration, sequence length to be amplified, sequence of the target and/or one or more primers, primer length, primer concentration, polymerase used, reaction volume, ratio of one or more elements to one or more other elements, and others, some or all of which can be altered. In general, PCR involves the steps of denaturation of the target to be amplified (if double stranded), hybridization of one or more primers to the target, and extension of the primers by a DNA polymerase, with the steps repeated (or “cycled”) in order to amplify the target sequence. Steps in this process can be optimized for various outcomes, such as to enhance yield, decrease the formation of spurious products, and/or increase or decrease specificity of primer annealing. Methods of optimization include, without limitation, adjustments to the type or number of elements in the amplification reaction and/or to the conditions of a given step in the process, such as temperature at a particular step, duration of a particular step, and/or number of cycles.

[00438] In some embodiments, an amplification reaction can comprise at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more cycles. In some examples, an amplification reaction can comprise at least about 20, 25, 30, 35 or 40 cycles. In some embodiments, an amplification reaction comprises no more than about 5, 10, 15, 20, 25, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more cycles. Cycles can contain any number of steps, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more steps. Steps can comprise any temperature or gradient of temperatures, suitable for achieving the purpose of the given step

including, but not limited to, 3' end extension (e.g., adaptor fill-in), primer annealing, primer extension, and strand denaturation. Steps can be of any duration including, but not limited to, about, less than about, or more than about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 70, 80, 90, 100, 120, 180, 240, 300, 360, 420, 480, 540, 600, 1200, 1800, or more seconds, including indefinitely until manually interrupted. Cycles of any number comprising different steps can be combined in any order. In some embodiments, different cycles comprising different steps are combined such that the total number of cycles in the combination is about, less than about, or more than about 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200 or more cycles. In some embodiments, amplification is performed following the fill-in reaction.

[00439] In some embodiments, the amplification reaction can be carried out on at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 800, 1000 ng of the target DNA molecule. In other embodiments, the amplification reaction can be carried out on less than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 25, 30, 40, 50, 100, 200, 300, 400, 500, 600, 800, 1000 ng of the target DNA molecule.

[00440] Amplification can be performed before or after pooling of target polynucleotides from independent samples.

[00441] Methods of the disclosure involve determining an amount of amplifiable nucleic acid present in a sample. Any known method may be used to quantify amplifiable nucleic acid, and an exemplary method is the polymerase chain reaction (PCR), specifically quantitative polymerase chain reaction (qPCR).

qPCR is a technique based on the polymerase chain reaction, and is used to amplify and simultaneously quantify a targeted nucleic acid molecule. qPCR allows for both detection and quantification (as absolute number of copies or relative amount when normalized to DNA input or additional normalizing genes) of a specific sequence in a DNA sample. The procedure follows the general principle of polymerase chain reaction, with the additional feature that the amplified DNA is quantified as it accumulates in the reaction in real time after each amplification cycle. QPCR is described, for example, in Kurnit et al. (U.S. patent number 6,033,854), Wang et al. (U.S. patent number 5,567,583 and 5,348,853), Ma et al. (The Journal of American Science, 2(3), 2006), Heid et al. (Genome Research 986-994, 1996), Sambrook and Russell (Quantitative PCR, Cold Spring Harbor Protocols, 2006), and Higuchi (U.S. patent numbers 6,171,785 and 5,994,056). The contents of these are incorporated by reference herein in their entirety.

[00442] Other methods of quantification include use of fluorescent dyes that intercalate with double-stranded DNA, and modified DNA oligonucleotide probes that fluoresce when hybridized with a complementary DNA. These methods can be broadly used but are also specifically adapted to real-time PCR as described in further detail as an example. In the first method, a DNA-binding dye binds to all double-stranded (ds)DNA in PCR, resulting in fluorescence of the dye. An increase in DNA product during PCR therefore leads to an increase in fluorescence intensity and is measured at each cycle, thus allowing DNA concentrations to be quantified. The reaction is prepared similarly to a standard PCR reaction, with the addition of fluorescent (ds)DNA dye. The reaction is run in a thermocycler, and after each cycle, the levels of fluorescence are measured with a detector; the dye only fluoresces when bound to the (ds)DNA (i.e., the PCR product). With reference to a standard dilution, the (ds)DNA concentration in

the PCR can be determined. Like other real-time PCR methods, the values obtained do not have absolute units associated with it. A comparison of a measured DNA/RNA sample to a standard dilution gives a fraction or ratio of the sample relative to the standard, allowing relative comparisons between different tissues or experimental conditions. To ensure accuracy in the quantification and/or expression of a target gene can be normalized with respect to a stably expressed gene. Copy numbers of unknown genes can similarly be normalized relative to genes of known copy number.

[00443] The second method uses a sequence-specific RNA or DNA-based probe to quantify only the DNA containing a probe sequence; therefore, use of the reporter probe significantly increases specificity, and allows quantification even in the presence of some non-specific DNA amplification. This allows for multiplexing, i.e., assaying for several genes in the same reaction by using specific probes with differently colored labels, provided that all genes are amplified with similar efficiency.

[00444] This method is commonly carried out with a DNA-based probe with a fluorescent reporter (e.g., 6-carboxyfluorescein) at one end and a quencher (e.g., 6-carboxy-tetramethylrhodamine) of fluorescence at the opposite end of the probe. The close proximity of the reporter to the quencher prevents detection of its fluorescence. Breakdown of the probe by the 5' to 3' exonuclease activity of a polymerase (e.g., Taq polymerase) breaks the reporter-quencher proximity and thus allows unquenched emission of fluorescence, which can be detected. An increase in the product targeted by the reporter probe at each PCR cycle results in a proportional increase in fluorescence due to breakdown of the probe and release of the reporter. The reaction is prepared similarly to a standard PCR reaction, and the reporter probe is added. As the reaction commences, during the annealing stage of the PCR both probe and primers anneal to the DNA target. Polymerization of a new DNA strand is initiated from the primers, and once the polymerase reaches the probe, its 5'-3'-exonuclease degrades the probe, physically separating the fluorescent reporter from the quencher, resulting in an increase in fluorescence. Fluorescence is detected and measured in a real-time PCR thermocycler, and geometric increase of fluorescence corresponding to exponential increase of the product is used to determine the threshold cycle in each reaction.

[00445] Relative concentrations of DNA present during the exponential phase of the reaction are determined by plotting fluorescence against cycle number on a logarithmic scale (so an exponentially increasing quantity will give a straight line). A threshold for detection of fluorescence above background is determined. The cycle at which the fluorescence from a sample crosses the threshold is called the cycle threshold, Ct. Since the quantity of DNA doubles every cycle during the exponential phase, relative amounts of DNA can be calculated, e.g., a sample with a Ct of 3 cycles earlier than another has $2^3 = 8$ times more template. Amounts of nucleic acid (e.g., RNA or DNA) are then determined by comparing the results to a standard curve produced by a real-time PCR of serial dilutions (e.g., undiluted, 1:4, 1:16, 1:64) of a known amount of nucleic acid.

[00446] In certain embodiments, the qPCR reaction involves a dual fluorophore approach that takes advantage of fluorescence resonance energy transfer (FRET), e.g., LIGHTCYCLER hybridization probes, where two oligonucleotide probes anneal to the amplicon (see, e.g., U.S. patent number 6,174,670). The oligonucleotides are designed to hybridize in a head-to-tail orientation with the fluorophores separated at a

distance that is compatible with efficient energy transfer. Other examples of labeled oligonucleotides that are structured to emit a signal when bound to a nucleic acid or incorporated into an extension product include: SCORPIONS probes (e.g., Whitcombe et al., Nature Biotechnology 17:804-807, 1999, and U.S. patent number 6,326,145), Sunrise (or AMPLIFLOUR) primers (e.g., Nazarenko et al., Nuc. Acids Res. 25:2516-2521, 1997, and U.S. patent number 6,117,635), and LUX primers and MOLECULAR BEACONS probes (e.g., Tyagi et al., Nature Biotechnology 14:303-308, 1996 and U.S. patent number 5,989,823).

[00447] In other embodiments, a qPCR reaction uses fluorescent Taqman methodology and an instrument capable of measuring fluorescence in real time (e.g., ABI Prism 7700 Sequence Detector). The Taqman reaction uses a hybridization probe labeled with two different fluorescent dyes. One dye is a reporter dye (6-carboxyfluorescein), the other is a quenching dye (6-carboxy-tetramethylrhodamine). When the probe is intact, fluorescent energy transfer occurs and the reporter dye fluorescent emission is absorbed by the quenching dye. During the extension phase of the PCR cycle, the fluorescent hybridization probe is cleaved by the 5'-3' nucleolytic activity of the DNA polymerase. On cleavage of the probe, the reporter dye emission is no longer transferred efficiently to the quenching dye, resulting in an increase of the reporter dye fluorescent emission spectra. Any nucleic acid quantification method, including real-time methods or single-point detection methods may be used to quantify the amount of nucleic acid in the sample. The detection can be performed by several different methodologies (e.g., staining, hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of ³²P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment), as well as any other suitable detection method for nucleic acid quantification. The quantification may or may not include an amplification step.

[00448] In some embodiments, the disclosure provides labels for identifying or quantifying the proximity-linked DNA segments. In some cases, the proximity-linked DNA segments can be labeled in order to assist in downstream applications, such as array hybridization. For example, the proximity-linked DNA segments can be labeled using random priming or nick translation.

[00449] A wide variety of labels (e.g., reporters) may be used to label the nucleotide sequences described herein including, but not limited to, during the amplification step. Suitable labels include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as ligands, cofactors, inhibitors, magnetic particles, and the like. Examples of such labels are included in U.S. Pat. No. 3,817,837; U.S. Pat. No. 3,850,752; U.S. Pat. No. 3,939,350; U.S. Pat. No. 3,996,345; U.S. Pat. No. 4,277,437; U.S. Pat. No. 4,275,149 and U.S. Pat. No. 4,366,241, which are incorporated by reference in its entirety.

[00450] Additional labels include, but are not limited to, β -galactosidase, invertase, green fluorescent protein, luciferase, chloramphenicol, acetyltransferase, β -glucuronidase, exo-glucanase and glucoamylase. Fluorescent labels may also be used, as well as fluorescent reagents specifically synthesized with particular chemical properties. A wide variety of ways to measure fluorescence are available. For example, some fluorescent labels exhibit a change in excitation or emission spectra, some exhibit resonance energy transfer where one fluorescent reporter loses fluorescence, while a second gains in

fluorescence, some exhibit a loss (quenching) or appearance of fluorescence, while some report rotational movements.

[00451] Further, in order to obtain sufficient material for labeling, multiple amplifications may be pooled, instead of increasing the number of amplification cycles per reaction. Alternatively, labeled nucleotides can be incorporated into the last cycles of the amplification reaction, e.g., 30 cycles of PCR (no label) +10 cycles of PCR (plus label).

[00452] In particular embodiments, the disclosure provides probes that can attach to the proximity-linked DNA segments. As used herein, the term “probe” refers to a molecule (e.g., an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification), that is capable of hybridizing to another molecule of interest (e.g., another oligonucleotide). When probes are oligonucleotides, they may be single-stranded or double-stranded. Probes are useful in the detection, identification, and isolation of particular targets (e.g., gene sequences). In some cases, the probes may be associated with a label so that is detectable in any detection system including, but not limited to, enzyme (e.g., ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems

[00453] With respect to arrays and microarrays, the term “probe” is used to refer to any hybridizable material that is affixed to the array for the purpose of detecting a nucleotide sequence that has hybridized to said probe. In some cases, the probes can be about 10 bp to 500 bp, about 10 bp to 250 bp, about 20 bp to 250 bp, about 20 bp to 200 bp, about 25 bp to 200 bp, about 25 bp to 100 bp, about 30 bp to 100 bp, or about 30 bp to 80 bp. In some cases, the probes can be greater than about 10 bp, about 20 bp, about 30 bp, about 40 bp, about 50 bp, about 60 bp, about 70 bp, about 80 bp, about 90 bp, about 100 bp, about 150 bp, about 200 bp, about 250 bp, about 300 bp, about 400 bp, or about 500 bp in length. For example, the probes can be about 20 to about 50 bp in length. Examples and rationale for probe design can be found in WO95/11995, EP 717,113 and WO97/29212

[00454] The probes, array of probes or set of probes can be immobilized on a support. Supports (e.g., solid supports) can be made of a variety of materials—such as glass, silica, plastic, nylon, or nitrocellulose. Supports can be rigid and have a planar surface. Supports can have from about 1 to 10,000,000 resolved loci. For example, a support can have about 10 to 10,000,000, about 10 to 5,000,000, about 100 to 5,000,000, about 100 to 4,000,000, about 1000 to 4,000,000, about 1000 to 3,000,000, about 10,000 to 3,000,000, about 10,000 to 2,000,000, about 100,000 to 2,000,000, or about 100,000 to 1,000,000 resolved loci. The density of resolved loci can be at least about 10, about 100, about 1000, about 10,000, about 100,000 or about 1,000,000 resolved loci within a square centimeter. In some cases, each resolved locus can be occupied by >95% of a single type of oligonucleotide. In other cases, each resolved locus can be occupied by pooled mixtures of probes or a set of probes. In further cases, some resolved loci are occupied by pooled mixtures of probes or a set of probes, and other resolved loci are occupied by >95% of a single type of oligonucleotide.

[00455] In some cases, the number of probes for a given nucleotide sequence on the array can be in large excess to the DNA sample to be hybridized to such array. For example, the array can have about 10, about

100, about 1000, about 10,000, about 100,000, about 1,000,000, about 10,000,000, or about 100,000,000 times the number of probes relative to the amount of DNA in the input sample.

[00456] In some cases, an array can have about 10, about 100, about 1000, about 10,000, about 100,000, about 1,000,000, about 10,000,000, about 100,000,000, or about 1,000,000,000 probes.

[00457] Arrays of probes or sets of probes may be synthesized in a step-by-step manner on a support or can be attached in presynthesized form. One method of synthesis is VLSIPS™ (as described in U.S. Pat. No. 5,143,854 and EP 476,014), which entails the use of light to direct the synthesis of oligonucleotide probes in high-density, miniaturized arrays. Algorithms for design of masks to reduce the number of synthesis cycles are described in U.S. Pat. No. 5,571,639 and U.S. Pat. No. 5,593,839. Arrays can also be synthesized in a combinatorial fashion by delivering monomers to cells of a support by mechanically constrained flowpaths, as described in EP 624,059. Arrays can also be synthesized by spotting reagents on to a support using an ink jet printer (see, for example, EP 728,520).

[00458] In some embodiments, the present disclosure provides methods for hybridizing the proximity-linked DNA segments onto an array. A “substrate” or an “array” is an intentionally created collection of nucleic acids which can be prepared either synthetically or biosynthetically and screened for biological activity in a variety of different formats (e.g., libraries of soluble molecules; and libraries of oligonucleotides tethered to resin beads, silica chips, or other solid supports). Additionally, the term “array” includes those libraries of nucleic acids which can be prepared by spotting nucleic acids of essentially any length (e.g., from 1 to about 1000 nucleotide monomers in length) onto a substrate.

[00459] Array technology and the various associated techniques and applications are described generally in numerous textbooks and documents. For example, these include Lemieux et al., 1998, *Molecular Breeding* 4, 277-289; Schena and Davis, *Parallel Analysis with Biological Chips*. in *PCR Methods Manual* (eds. M. Innis, D. Gelfand, J. Sninsky); Schena and Davis, 1999, *Genes, Genomes and Chips*. In *DNA Microarrays: A Practical Approach* (ed. M. Schena), Oxford University Press, Oxford, UK, 1999); *The Chipping Forecast* (Nature Genetics special issue; January 1999 Supplement); Mark Schena (Ed.), *Microarray Biochip Technology*, (Eaton Publishing Company); Cortes, 2000, *The Scientist* 14[17]:25; Gwynn and Page, *Microarray analysis: the next revolution in molecular biology*, *Science*, 1999 Aug. 6; and Eakins and Chu, 1999, *Trends in Biotechnology*, 17, 217-218.

[00460] In general, any library may be arranged in an orderly manner into an array, by spatially separating the members of the library. Examples of suitable libraries for arraying include nucleic acid libraries (including DNA, cDNA, oligonucleotide, etc. libraries), peptide, polypeptide, and protein libraries, as well as libraries comprising any molecules, such as ligand libraries, among others.

[00461] The library can be fixed or immobilized onto a solid phase (e.g., a solid substrate), to limit diffusion and admixing of the members. In some cases, libraries of DNA binding ligands may be prepared. In particular, the libraries may be immobilized to a substantially planar solid phase, including membranes and non-porous substrates such as plastic and glass. Furthermore, the library can be arranged in such a way that indexing (i.e., reference or access to a particular member) is facilitated. In some examples, the members of the library can be applied as spots in a grid formation. Common assay systems

may be adapted for this purpose. For example, an array may be immobilized on the surface of a microplate, either with multiple members in a well, or with a single member in each well. Furthermore, the solid substrate may be a membrane, such as a nitrocellulose or nylon membrane (for example, membranes used in blotting experiments). Alternative substrates include glass, or silica-based substrates. Thus, the library can be immobilized by any suitable method, for example, by charge interactions, or by chemical coupling to the walls or bottom of the wells, or the surface of the membrane. Other means of arranging and fixing may be used, for example, pipetting, drop-touch, piezoelectric means, ink-jet and bubblejet technology, electrostatic application, etc. In the case of silicon-based chips, photolithography may be utilized to arrange and fix the libraries on the chip.

[00462] The library may be arranged by being “spotted” onto the solid substrate; this may be done by hand or by making use of robotics to deposit the members. In general, arrays may be described as macroarrays or microarrays, the difference being the size of the spots. Macroarrays can contain spot sizes of about 300 microns or larger and may be easily imaged by existing gel and blot scanners. The spot sizes in microarrays can be less than 200 microns in diameter and these arrays usually contain thousands of spots. Thus, microarrays may require specialized robotics and imaging equipment, which may need to be custom made. Instrumentation is described generally in a review by Cortese, 2000, *The Scientist* 14[11]:26.

[00463] Techniques for producing immobilized libraries of DNA molecules have been described. Generally, most such methods describe how to synthesize single-stranded nucleic acid molecule libraries, using, for example, masking techniques to build up various permutations of sequences at the various discrete positions on the solid substrate. U.S. Pat. No. 5,837,832 describes an improved method for producing DNA arrays immobilized to silicon substrates based on very large-scale integration technology. In particular, U.S. Pat. No. 5,837,832 describes a strategy called “tiling” to synthesize specific sets of probes at spatially-defined locations on a substrate which may be used to produce the immobilized DNA libraries of the present disclosure. U.S. Pat. No. 5,837,832 also provides references for earlier techniques that may also be used. In other cases, arrays may also be built using photo deposition chemistry.

[00464] Arrays of peptides (or peptidomimetics) may also be synthesized on a surface in a manner that places each distinct library member (e.g., unique peptide sequence) at a discrete, predefined location in the array. The identity of each library member is determined by its spatial location in the array. The locations in the array where binding interactions between a predetermined molecule (e.g., a target or probe) and reactive library members occur is determined, thereby identifying the sequences of the reactive library members on the basis of spatial location. These methods are described in U.S. Pat. No. 5,143,854; WO90/15070 and WO92/10092; Fodor et al. (1991) *Science*, 251: 767; Dower and Fodor (1991) *Ann. Rep. Med. Chem.*, 26: 271

[00465] To aid detection, labels can be used (as discussed above)—such as any readily detectable reporter, for example, a fluorescent, bioluminescent, phosphorescent, radioactive, etc. reporter. Such reporters, their detection, coupling to targets/probes, etc. are discussed elsewhere in this document. Labelling of probes and targets is also disclosed in Shalon et al., 1996, *Genome Res* 6(7):639-45.

[00466] Examples of some commercially available microarray formats are set out in Marshall and Hodgson, 1998, Nature Biotechnology, 16(1), 27-31.

[00467] In order to generate data from array-based assays a signal can be detected to signify the presence of or absence of hybridization between a probe and a nucleotide sequence. Further, direct and indirect labeling techniques can also be utilized. For example, direct labeling incorporates fluorescent dyes directly into the nucleotide sequences that hybridize to the array associated probes (e.g., dyes are incorporated into nucleotide sequence by enzymatic synthesis in the presence of labeled nucleotides or PCR primers). Direct labeling schemes can yield strong hybridization signals, for example, by using families of fluorescent dyes with similar chemical structures and characteristics, and can be simple to implement. In cases comprising direct labeling of nucleic acids, cyanine or alexa analogs can be utilized in multiple-fluor comparative array analyses. In other embodiments, indirect labeling schemes can be utilized to incorporate epitopes into the nucleic acids either prior to or after hybridization to the microarray probes. One or more staining procedures and reagents can be used to label the hybridized complex (e.g., a fluorescent molecule that binds to the epitopes, thereby providing a fluorescent signal by virtue of the conjugation of dye molecule to the epitope of the hybridized species).

Sequencing

[00468] In various embodiments, suitable sequencing methods described herein or otherwise known will be used to obtain sequence information from nucleic acid molecules within a sample. Sequencing can be accomplished through classic Sanger sequencing methods. Sequence can also be accomplished using high-throughput systems some of which allow detection of a sequenced nucleotide immediately after or upon its incorporation into a growing strand, i.e., detection of sequence in real time or substantially real time. In some cases, high-throughput sequencing generates at least 1,000, at least 5,000, at least 10,000, at least 20,000, at least 30,000, at least 40,000, at least 50,000, at least 100,000 or at least 500,000 sequence reads per hour; where the sequencing reads can be at least about 50, about 60, about 70, about 80, about 90, about 100, about 120, about 150, about 180, about 210, about 240, about 270, about 300, about 350, about 400, about 450, about 500, about 600, about 700, about 800, about 900, or about 1000 bases per read.

[00469] Sequencing can be whole-genome, with or without enrichment of particular regions of interest. Sequencing can be targeted to particular regions of the genome. Regions of the genome that can be enriched for or targeted include but are not limited to single genes (or regions thereof), gene panels, gene fusions, human leukocyte antigen (HLA) loci (e.g., Class I HLA-A, B, and C; Class II HLA-DRB1/3/4/5, HLA-DQA1, HLA-DQB1, HLA-DPA1, and HLA-DPB1), exonic regions, exome, and other loci. Genomic regions can be relevant to immune response, immune repertoire, immune cell diversity, transcription (e.g., exome), cancers (e.g., BRCA1, BRCA2, panels of genes or regions thereof such as hotspot regions, somatic variants, SNVs, amplifications, fusions, tumor mutational burden (TMB), microsatellite instability (MSI)), cardiac diseases, inherited diseases, and other diseases or conditions. A variety of methods can be used to enrich for or target regions of interest, including but not limited to

sequence capture. In some cases, Capture Hi-C (CHi-C) or CHi-C-like protocols are employed, employing a sequence capture step (e.g., by target enrichment array) before or after library preparation.

[00470] In some embodiments, high-throughput sequencing involves the use of technology available by Illumina's Genome Analyzer IIX, MiSeq personal sequencer, or HiSeq systems, such as those using HiSeq 2500, HiSeq 1500, HiSeq 2000, or HiSeq 1000 machines. These machines use reversible terminator-based sequencing by synthesis chemistry. These machines can do 200 billion DNA reads or more in eight days. Smaller systems may be utilized for runs within 3, 2, 1 days or less time.

[00471] In some embodiments, high-throughput sequencing involves the use of technology available by ABI Solid System. This genetic analysis platform that enables massively parallel sequencing of clonally-amplified DNA fragments linked to beads. The sequencing methodology is based on sequential ligation with dye-labeled oligonucleotides.

[00472] The next generation sequencing can comprise ion semiconductor sequencing (e.g., using technology from Life Technologies (Ion Torrent)). Ion semiconductor sequencing can take advantage of the fact that when a nucleotide is incorporated into a strand of DNA, an ion can be released. To perform ion semiconductor sequencing, a high-density array of micromachined wells can be formed. Each well can hold a single DNA template. Beneath the well can be an ion sensitive layer, and beneath the ion sensitive layer can be an ion sensor. When a nucleotide is added to a DNA, H⁺ can be released, which can be measured as a change in pH. The H⁺ ion can be converted to voltage and recorded by the semiconductor sensor. An array chip can be sequentially flooded with one nucleotide after another. No scanning, light, or cameras can be required. In some cases, an IONPROTON™ Sequencer is used to sequence nucleic acid. In some cases, an IONPGM™ Sequencer is used. The Ion Torrent Personal Genome Machine (PGM). The PGM can do 10 million reads in two hours.

[00473] In some embodiments, high-throughput sequencing involves the use of technology available by Helicos BioSciences Corporation (Cambridge, Massachusetts) such as the Single Molecule Sequencing by Synthesis (SMSS) method. SMSS is unique because it allows for sequencing the entire human genome in up to 24 hours. Finally, SMSS is described in part in US Publication Application Nos. 20060024711; 20060024678; 20060012793; 20060012784; and 20050100932.

[00474] In some embodiments, high-throughput sequencing involves the use of technology available by 454 Lifesciences, Inc. (Branford, Connecticut) such as the PicoTiterPlate device which includes a fiber optic plate that transmits chemiluminescent signal generated by the sequencing reaction to be recorded by a CCD camera in the instrument. This use of fiber optics allows for the detection of a minimum of 20 million base pairs in 4.5 hours.

[00475] Methods for using bead amplification followed by fiber optics detection are described in Marguiles, M., et al. "Genome sequencing in microfabricated high-density picolitre reactors," Nature, doi:10.1038/nature03959; and well as in US Publication Application Nos. 20020012930; 20030068629; 20030100102; 20030148344; 20040248161; 20050079510, 20050124022; and 20060078909.

[00476] In some embodiments, high-throughput sequencing is performed using Clonal Single Molecule Array (Solexa, Inc.) or sequencing-by-synthesis (SBS) utilizing reversible terminator chemistry. These

technologies are described in part in US Patent Nos. 6,969,488; 6,897,023; 6,833,246; 6,787,308; and US Publication Application Nos. 20040106110; 20030064398; 20030022207; and Constans, A., *The Scientist* 2003, 17(13):36.

[00477] The next generation sequencing technique can comprise real-time (SMRT™) technology by Pacific Biosciences. In SMRT, each of four DNA bases can be attached to one of four different fluorescent dyes. These dyes can be phospho linked. A single DNA polymerase can be immobilized with a single molecule of template single stranded DNA at the bottom of a zero-mode waveguide (ZMW). A ZMW can be a confinement structure which enables observation of incorporation of a single nucleotide by DNA polymerase against the background of fluorescent nucleotides that can rapidly diffuse in and out of the ZMW (in microseconds). It can take several milliseconds to incorporate a nucleotide into a growing strand. During this time, the fluorescent label can be excited and produce a fluorescent signal, and the fluorescent tag can be cleaved off. The ZMW can be illuminated from below. Attenuated light from an excitation beam can penetrate the lower 20-30 nm of each ZMW. A microscope with a detection limit of 20 zepto liters (20×10^{-21} liters) can be created. The tiny detection volume can provide 1000-fold improvement in the reduction of background noise. Detection of the corresponding fluorescence of the dye can indicate which base was incorporated. The process can be repeated.

[00478] In some cases, the next generation sequencing is nanopore sequencing (see, e.g., Soni GV and Meller A. (2007) *Clin Chem* 53: 1996-2001). A nanopore can be a small hole, of the order of about one nanometer in diameter. Immersion of a nanopore in a conducting fluid and application of a potential across it can result in a slight electrical current due to conduction of ions through the nanopore. The amount of current which flows can be sensitive to the size of the nanopore. As a DNA molecule passes through a nanopore, each nucleotide on the DNA molecule can obstruct the nanopore to a different degree. Thus, the change in the current passing through the nanopore as the DNA molecule passes through the nanopore can represent a reading of the DNA sequence. The nanopore sequencing technology can be from Oxford Nanopore Technologies, e.g., a GridION system. A single nanopore can be inserted in a polymer membrane across the top of a microwell. Each microwell can have an electrode for individual sensing. The microwells can be fabricated into an array chip, with 100,000 or more microwells (e.g., more than 200,000, 300,000, 400,000, 500,000, 600,000, 700,000, 800,000, 900,000, or 1,000,000) per chip. An instrument (or node) can be used to analyze the chip. Data can be analyzed in real-time. One or more instruments can be operated at a time. The nanopore can be a protein nanopore, e.g., the protein alpha-hemolysin, a heptameric protein pore. The nanopore can be a solid-state nanopore made, e.g., a nanometer sized hole formed in a synthetic membrane (e.g., SiNx, or SiO₂). The nanopore can be a hybrid pore (e.g., an integration of a protein pore into a solid-state membrane). The nanopore can be a nanopore with an integrated sensor (e.g., tunneling electrode detectors, capacitive detectors, or graphene based nano-gap or edge state detectors (see e.g., Garaj et al. (2010) *Nature* vol. 67, doi: 10.1038/nature09379)). A nanopore can be functionalized for analyzing a specific type of molecule (e.g., DNA, RNA, or protein). Nanopore sequencing can comprise “strand sequencing” in which intact DNA polymers can be passed through a protein nanopore with sequencing in real time as the DNA translocates the pore. An enzyme can separate

strands of a double stranded DNA and feed a strand through a nanopore. The DNA can have a hairpin at one end, and the system can read both strands. In some cases, nanopore sequencing is “exonuclease sequencing” in which individual nucleotides can be cleaved from a DNA strand by a processive exonuclease, and the nucleotides can be passed through a protein nanopore. The nucleotides can transiently bind to a molecule in the pore (e.g., cyclodextran). A characteristic disruption in current can be used to identify bases.

[00479] Nanopore sequencing technology from GENIA can be used. An engineered protein pore can be embedded in a lipid bilayer membrane. “Active Control” technology can be used to enable efficient nanopore-membrane assembly and control of DNA movement through the channel. In some cases, the nanopore sequencing technology is from NABsys. Genomic DNA can be fragmented into strands of average length of about 100 kb. The 100 kb fragments can be made single stranded and subsequently hybridized with a 6-mer probe. The genomic fragments with probes can be driven through a nanopore, which can create a current-versus- time tracing. The current tracing can provide the positions of the probes on each genomic fragment. The genomic fragments can be lined up to create a probe map for the genome. The process can be done in parallel for a library of probes. A genome-length probe map for each probe can be generated. Errors can be fixed with a process termed “moving window Sequencing By Hybridization (mwSBH).” In some cases, the nanopore sequencing technology is from IBM/Roche. An electron beam can be used to make a nanopore sized opening in a microchip. An electrical field can be used to pull or thread DNA through the nanopore. A DNA transistor device in the nanopore can comprise alternating nanometer sized layers of metal and dielectric. Discrete charges in the DNA backbone can get trapped by electrical fields inside the DNA nanopore. Turning off and on gate voltages can allow the DNA sequence to be read.

[00480] The next generation sequencing can comprise DNA nanoball sequencing (as performed, e.g., by Complete Genomics; see e.g., Drmanac et al. (2010) Science 327: 78-81). DNA can be isolated, fragmented, and size selected. For example, DNA can be fragmented (e.g., by sonication) to a mean length of about 500 bp. Adaptors (Adl) can be attached to the ends of the fragments. The adaptors can be used to hybridize to anchors for sequencing reactions. DNA with adaptors bound to each end can be PCR amplified. The adaptor sequences can be modified so that complementary single strand ends bind to each other forming circular DNA. The DNA can be methylated to protect it from cleavage by a type IIS restriction enzyme used in a subsequent step. An adaptor (e.g., the right adaptor) can have a restriction recognition site, and the restriction recognition site can remain non-methylated. The non-methylated restriction recognition site in the adaptor can be recognized by a restriction enzyme (e.g., Acul), and the DNA can be cleaved by Acul 13 bp to the right of the right adaptor to form linear double stranded DNA. A second round of right and left adaptors (Ad2) can be ligated onto either end of the linear DNA, and all DNA with both adaptors bound can be PCR amplified (e.g., by PCR). Ad2 sequences can be modified to allow them to bind each other and form circular DNA. The DNA can be methylated, but a restriction enzyme recognition site can remain non-methylated on the left Adl adaptor. A restriction enzyme (e.g., Acul) can be applied, and the DNA can be cleaved 13 bp to the left of the Adl to form a linear DNA

fragment. A third round of right and left adaptor (Ad3) can be ligated to the right and left flank of the linear DNA, and the resulting fragment can be PCR amplified. The adaptors can be modified so that they can bind to each other and form circular DNA. A type III restriction enzyme (e.g., EcoP15) can be added; EcoP15 can cleave the DNA 26 bp to the left of Ad3 and 26 bp to the right of Ad2. This cleavage can remove a large segment of DNA and linearize the DNA once again. A fourth round of right and left adaptors (Ad4) can be ligated to the DNA, the DNA can be amplified (e.g., by PCR), and modified so that they bind each other and form the completed circular DNA template.

[00481] Rolling circle replication (e.g., using Phi 29 DNA polymerase) can be used to amplify small fragments of DNA. The four adaptor sequences can contain palindromic sequences that can hybridize, and a single strand can fold onto itself to form a DNA nanoball (DNB™) which can be approximately 200-300 nanometers in diameter on average. A DNA nanoball can be attached (e.g., by adsorption) to a microarray (sequencing flowcell). The flow cell can be a silicon wafer coated with silicon dioxide, titanium and hexamethyldisilazane (HMDS) and a photoresist material. Sequencing can be performed by unchained sequencing by ligating fluorescent probes to the DNA. The color of the fluorescence of an interrogated position can be visualized by a high-resolution camera. The identity of nucleotide sequences between adaptor sequences can be determined.

[00482] In some embodiments, high-throughput sequencing can take place using AnyDot.chips (Genovox, Germany). In particular, the AnyDot.chips allow for 10x – 50x enhancement of nucleotide fluorescence signal detection. AnyDot.chips and methods for using them are described in part in International Publication Application Nos. WO 02088382, WO 03020968, WO 03031947, WO 2005044836, PCT/EP 05/05657, PCT/EP 05/05655; and German Patent Application Nos. DE 101 49 786, DE 102 14 395, DE 103 56 837, DE 10 2004 009 704, DE 10 2004 025 696, DE 10 2004 025 746, DE 10 2004 025 694, DE 10 2004 025 695, DE 10 2004 025 744, DE 10 2004 025 745, and DE 10 2005 012 301.

[00483] Other high-throughput sequencing systems include those disclosed in Venter, J., et al. Science 16 February 2001; Adams, M. et al. Science 24 March 2000; and M. J. Levene, et al. Science 299:682-686, January 2003; as well as US Publication Application No. 20030044781 and 2006/0078937. Overall such systems involve sequencing a target nucleic acid molecule having a plurality of bases by the temporal addition of bases via a polymerization reaction that is measured on a molecule of nucleic acid, i.e., the activity of a nucleic acid polymerizing enzyme on the template nucleic acid molecule to be sequenced is followed in real time. Sequence can then be deduced by identifying which base is being incorporated into the growing complementary strand of the target nucleic acid by the catalytic activity of the nucleic acid polymerizing enzyme at each step in the sequence of base additions. A polymerase on the target nucleic acid molecule complex is provided in a position suitable to move along the target nucleic acid molecule and extend the oligonucleotide primer at an active site. A plurality of labeled types of nucleotide analogs are provided proximate to the active site, with each distinguishable type of nucleotide analog being complementary to a different nucleotide in the target nucleic acid sequence. The growing nucleic acid strand is extended by using the polymerase to add a nucleotide analog to the nucleic acid strand at the

active site, where the nucleotide analog being added is complementary to the nucleotide of the target nucleic acid at the active site. The nucleotide analog added to the oligonucleotide primer as a result of the polymerizing step is identified. The steps of providing labeled nucleotide analogs, polymerizing the growing nucleic acid strand, and identifying the added nucleotide analog are repeated so that the nucleic acid strand is further extended, and the sequence of the target nucleic acid is determined.

Kits

[00484] In particular embodiments, the present disclosure further provides kits comprising one or more components of the disclosure. The kits can be used for any suitable application, including, without limitation, those described above. The kits can comprise, for example, a plurality of association molecules, a fixative agent, a nuclease, a ligase, and/or a combination thereof. In some cases, the association molecules can be proteins including, for example, histones. In some cases, the fixative agent can be formaldehyde or any other DNA crosslinking agent, including DSG, EGS, or DSS.

[00485] In some cases, the kit can further comprise a plurality of beads. The beads can be paramagnetic and/or are coated with a capturing agent. For example, the beads can be coated with streptavidin and/or an antibody.

[00486] In some cases, the kit can comprise adaptor oligonucleotides and/or sequencing primers. Further, the kit can comprise a device capable of amplifying the read-pairs using the adaptor oligonucleotides and/or sequencing primers.

[00487] In some cases, the kit can also comprise other reagents including, but not limited to, lysis buffers, ligation reagents (e.g., dNTPs, polymerase, polynucleotide kinase, and/or ligase buffer, etc.), and PCR reagents (e.g., dNTPs, polymerase, and/or PCR buffer, etc.).

[00488] The kit can also include instructions for using the components of the kit and/or for generating the read-pairs.

Computers and Systems

[00489] The computer system 500 illustrated in FIG. 1 may be understood as a logical apparatus that can read instructions from media 511 and/or a network port 505, which can optionally be connected to server 509 having fixed media 512. The system, such as shown in FIG. 1 can include a CPU 501, disk drives 503, optional input devices such as keyboard 515 and/or mouse 516 and optional monitor 507. Data communication can be achieved through the indicated communication medium to a server at a local or a remote location. The communication medium can include any means of transmitting and/or receiving data. For example, the communication medium can be a network connection, a wireless connection, or an internet connection. Such a connection can provide for communication over the World Wide Web. It is envisioned that data relating to the present disclosure can be transmitted over such networks or connections for reception and/or review by a party 522 as illustrated in FIG. 1.

[00490] FIG. 2 is a block diagram illustrating a first example architecture of a computer system 100 that can be used in connection with example embodiments of the present disclosure. As depicted in FIG. 2, the example computer system can include a processor 102 for processing instructions. Non-limiting examples of processors include: Intel Xeon™ processor, AMD Opteron™ processor, Samsung 32-bit RISC ARM

1176JZ(F)-S v1.0™ processor, ARM Cortex-A8 Samsung S5PC100™ processor, ARM Cortex-A8 Apple A4™ processor, Marvell PXA 930™ processor, or a functionally-equivalent processor. Multiple threads of execution can be used for parallel processing. In some embodiments, multiple processors or processors with multiple cores can also be used, whether in a single computer system, in a cluster, or distributed across systems over a network comprising a plurality of computers, cell phones, and/or personal data assistant devices.

[00491] As illustrated in **FIG. 2**, a high-speed cache **104** can be connected to, or incorporated in, the processor **102** to provide a high-speed memory for instructions or data that have been recently, or are frequently, used by processor **102**. The processor **102** is connected to a north bridge **106** by a processor bus **108**. The north bridge **106** is connected to random access memory (RAM) **110** by a memory bus **112** and manages access to the RAM **110** by the processor **102**. The north bridge **106** is also connected to a south bridge **114** by a chipset bus **116**. The south bridge **114** is, in turn, connected to a peripheral bus **118**. The peripheral bus can be, for example, PCI, PCI-X, PCI Express, or other peripheral bus. The north bridge and south bridge are often referred to as a processor chipset and manage data transfer between the processor, RAM, and peripheral components on the peripheral bus **118**. In some alternative architectures, the functionality of the north bridge can be incorporated into the processor instead of using a separate north bridge chip.

[00492] In some embodiments, system **100** can include an accelerator card **122** attached to the peripheral bus **118**. The accelerator can include field programmable gate arrays (FPGAs) or other hardware for accelerating certain processing. For example, an accelerator can be used for adaptive data restructuring or to evaluate algebraic expressions used in extended set processing.

[00493] Software and data are stored in external storage **124** and can be loaded into RAM **110** and/or cache **104** for use by the processor. The system **100** includes an operating system for managing system resources; non-limiting examples of operating systems include: Linux, Windows™, MacOS™, BlackBerry OS™, iOS™, and other functionally-equivalent operating systems, as well as application software running on top of the operating system for managing data storage and optimization in accordance with example embodiments of the present disclosure.

[00494] In this example, system **100** also includes network interface cards (NICs) **120** and **121** connected to the peripheral bus for providing network interfaces to external storage, such as Network Attached Storage (NAS) and other computer systems that can be used for distributed parallel processing.

[00495] **FIG. 3** is a diagram showing a network **200** with a plurality of computer systems **202a**, and **202b**, a plurality of cell phones and personal data assistants **202c**, and Network Attached Storage (NAS) **204a**, and **204b**. In example embodiments, systems **202a**, **202b**, and **202c** can manage data storage and optimize data access for data stored in Network Attached Storage (NAS) **204a** and **204b**. A mathematical model can be used for the data and be evaluated using distributed parallel processing across computer systems **202a**, and **202b**, and cell phone and personal data assistant systems **202c**. Computer systems **202a**, and **202b**, and cell phone and personal data assistant systems **202c** can also provide parallel processing for adaptive data restructuring of the data stored in Network Attached Storage (NAS) **204a** and **204b**. **FIG. 3**

illustrates an example only, and a wide variety of other computer architectures and systems can be used in conjunction with the various embodiments of the present disclosure. For example, a blade server can be used to provide parallel processing. Processor blades can be connected through a back plane to provide parallel processing. Storage can also be connected to the back plane or as Network Attached Storage (NAS) through a separate network interface.

[00496] In some example embodiments, processors can maintain separate memory spaces and transmit data through network interfaces, back plane, or other connectors for parallel processing by other processors. In other embodiments, some or all of the processors can use a shared virtual address memory space.

[00497] FIG. 4 is a block diagram of a multiprocessor computer system 300 using a shared virtual address memory space in accordance with an example embodiment. The system includes a plurality of processors 302a-f that can access a shared memory subsystem 304. The system incorporates a plurality of programmable hardware memory algorithm processors (MAPs) 306a-f in the memory subsystem 304. Each MAP 306a-f can comprise a memory 308a-f and one or more field programmable gate arrays (FPGAs) 310a-f. The MAP provides a configurable functional unit and particular algorithms, or portions of algorithms, can be provided to the FPGAs 310a-f for processing in close coordination with a respective processor. For example, the MAPs can be used to evaluate algebraic expressions regarding the data model and to perform adaptive data restructuring in example embodiments. In this example, each MAP is globally accessible by all of the processors for these purposes. In one configuration, each MAP can use Direct Memory Access (DMA) to access an associated memory 308a-f, allowing it to execute tasks independently of, and asynchronously from, the respective microprocessor 302a-f. In this configuration, a MAP can feed results directly to another MAP for pipelining and parallel execution of algorithms.

[00498] The above computer architectures and systems are examples only, and a wide variety of other computer, cell phone, and personal data assistant architectures and systems can be used in connection with example embodiments, including systems using any combination of general processors, co-processors, FPGAs and other programmable logic devices, system on chips (SOCs), application specific integrated circuits (ASICs), and other processing and logic elements. In some embodiments, all or part of the computer system can be implemented in software or hardware. Any variety of data storage media can be used in connection with example embodiments, including random access memory, hard drives, flash memory, tape drives, disk arrays, Network Attached Storage (NAS) and other local or distributed data storage devices and systems.

[00499] In example embodiments, the computer system can be implemented using software modules executing on any of the above or other computer architectures and systems. In other embodiments, the functions of the system can be implemented partially or completely in firmware, programmable logic devices such as field programmable gate arrays (FPGAs), system on chips (SOCs), application specific integrated circuits (ASICs), or other processing and logic elements. For example, the Set Processor and Optimizer can be implemented with hardware acceleration through the use of a hardware accelerator card, such as accelerator card 122 illustrated in FIG. 2.

Definitions

[00500] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. Although any methods and reagents similar or equivalent to those described herein can be used in the practice of the disclosed methods and compositions, the exemplary methods and materials are now described.

[00501] As used herein and in the appended claims, the singular forms “a,” “and,” and “the” include plural referents unless the context clearly dictates otherwise. Thus, for example, reference to “contig” includes a plurality of such contigs and reference to “probing the physical layout of chromosomes” includes reference to one or more methods for probing the physical layout of chromosomes and equivalents thereof known to those skilled in the art, and so forth.

[00502] Also, the use of “and” means “and/or” unless stated otherwise. Similarly, “comprise,” “comprises,” “comprising,” “include,” “includes,” and “including” are interchangeable and not intended to be limiting.

[00503] It is to be further understood that where descriptions of various embodiments use the term “comprising,” those skilled in the art would understand that in some specific instances, an embodiment can be alternatively described using language “consisting essentially of” or “consisting of.”

[00504] The term “sequencing read” as used herein, refers to a fragment of DNA in which the sequence has been determined.

[00505] The term “contigs” as used herein, refers to contiguous regions of DNA sequence. “Contigs” can be determined by any number methods known in the art, such as, by comparing sequencing reads for overlapping sequences, and/or by comparing sequencing reads against a database of known sequences in order to identify which sequencing reads have a high probability of being contiguous.

[00506] The term “subject” as used herein can refer to any eukaryotic or prokaryotic organism.

[00507] The term “read pair” or “read-pair” as used herein can refer to two or more elements that are linked to provide sequence information. In some cases, the number of read-pairs can refer to the number of mappable read-pairs. In other cases, the number of read-pairs can refer to the total number of generated read-pairs.

[00508] The term “stabilized” as used herein can describe a sample that has been preserved or otherwise protected from degradation. In some cases, a stabilized sample is crosslinked or treated with a fixative or crosslinking agent. In some cases, a stabilized sample is treated with formaldehyde, formalin, paraformaldehyde, glutaraldehyde, osmium tetroxide, or the like.

[00509] The term “about” as used herein can describe a number, unless otherwise specified, as a range of values including that number plus or minus 10% of that number.

[00510] As used herein, “exposed internal ends of a nucleic acid” can refer to exposed ends generated through generation of cleavage sites introduced into stabilized or non-stabilized nucleic acids, such as those introduced so as to access the end-adjacent nucleic acid sequence information to facilitate phase or local three-dimensional structural information.

[00511] As used herein, the term “about” a number refers to a range spanning +/- 10% of that number, while “about” a range refers to 10% lower than a stated range limit spanning to 10% greater than a stated range limit.

[00512] As used herein, a sequence segment on a linker or otherwise is partition designating, or cell designating when identification of its sequence facilitates assigning adjacent nucleic acid sequence to a particular first partition or cell of origin to the exclusion of a second partition or cell of origin. A distinguishing sequence is in some cases unique to a partition or cell, such that it distinguishes from all other cells, and when this is technically feasible, unique tags facilitate downstream analysis. However, unique sequence is not in all cases required. In some cases, redundant barcoding is resolved computationally downstream, such that a tag that is not unique is nonetheless sufficient to distinguish nucleic acids of a first partition or cell from a second partition or cell.

[00513] As used herein, a cluster is a region of a nucleic acid reference to which a plurality of distinct end adjacent sequences or sequence tags map. In some cases, the proximity of one region to a second region is assessed at least in part by counting the number of cluster constituents of a first cluster that co-occur in paired end reads with cluster constituents of a second cluster.

EXAMPLES

[00514] The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion. The present examples, along with the methods described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses which are encompassed within the spirit of the invention as defined by the scope of the claims will occur to those skilled in the art.

Example 1: Proximity Ligation Method with Circularization

[00515] A nucleic acid sample was fragmented using a Tn5 transposase. Nucleic acids were bound to capture beads and a ligase was used to join adjacent tagged fragments creating a proximity-linked nucleic acid product that has the two fragments optionally joined by a bridge oligonucleotide adaptor. Ends of the proximity-linked nucleic acid products were removed and crosslinks were reversed prior to nucleic acid isolation. The isolated proximity-linked nucleic acid products were circularized and the sample nucleic acids were amplified using PCR. PCR products were purified and subjected to size selection prior to sequencing (FIG. 6 and FIG. 7). The method resulted in improved long range information compared to methods using recombinase (FIG. 10).

Example 2: Analysis of Long Non-Coding RNA Binding Sites

[00516] A biological sample is crosslinked and chromatin is prepared and treated with RNase H to deplete the sample of ribosomal RNA. The chromatin is fragmented using Tn5 transposase which also adds a adenylated/biotinylated oligonucleotide to the cleaved ends. RNA bound to the chromatin is ligated to the adenylated adaptor using T4 RNA ligase and the sample is treated with proteinase K and crosslinks are reversed. The second strand of ligated RNA is extended with reverse transcriptase, a second strand is

produced and DNA is purified. A streptavidin tagged endonuclease is bound to the fragments which digests DNA near the biotin tagged oligonucleotide. A sequencing library is prepared and DNA having the biotin tag is purified using beads resulting in a library with the cDNA, the adaptor, and the bound DNA. This method is illustrated in FIG. 5.

Example 3: Methods of Sample Preparation

[00517] The standard sample preparation was modified to include treatment of nuclei with 0.3% SDS at 62 °C. Samples treated with SDS had improved coverage uniformity and similar library statistics for % valid reads, % cis > 1 kb, % cis > 10 kb, % cis > 1 Mb, and complexity at 400 Mb (FIG. 9A and FIG. 9B).

[00518] Titration of exonuclease treatment was done to find a concentration optimal for removing ends while maintaining genomic fragment length. It was found that treatment of chromatin protected the fragment from complete chew back and made the reaction more robust. With T5 exonuclease treatment of chromatin, recovery was about 80% compared to treatment of naked DNA where recovery was 0% (FIG. 13). T5 exonuclease treatment using between 1 U and 100 U on crosslinked chromatin removed ends while leaving nucleosome protected fragment (FIG. 14).

Example 4: Proximity Ligation Method with Circularization – Biotin-Free Isolation

[00519] A nucleic acid sample was fragmented using a Tn5 transposase. Nucleic acids were bound to capture beads and a ligase was used to join adjacent tagged fragments creating a proximity-linked nucleic acid product without biotin that has the two fragments optionally joined by a bridge oligonucleotide adaptor. Ends of the proximity-linked nucleic acid products were removed and crosslinks were reversed prior to nucleic acid isolation. The isolated proximity-linked nucleic acid products were circularized. Circularized nucleic acids were found to contain proximity-linked nucleic acids versus unlinked nucleic acids because of the efficiency of circularization favors the length of the proximity-linked nucleic acids. The unlinked nucleic acids were not able to circularize as efficiently. The sample nucleic acids were amplified using PCR. PCR products were purified and subjected to size selection prior to sequencing. The method resulted in equal or better performance in HLA typing compared with the method including biotinylated proximity-linked nucleic acids and streptavidin purification of proximity-linked nucleic acids or use of the OmniC protocol. Specifically, the method without use of biotin-streptavidin purification resulted in equal or better final library concentration, total read pairs obtained, fewer inter-chromosomal junctions, equal or better size fragments obtained, and equal or better library complexity compared with a comparable method using biotin-streptavidin or the OmniC method (Table 1). Use of this method also saved time and reagent cost compared with previous methods.

Table 1: HLA Panel Performance – Pre-capture QC							
	Lib prep input	Final lib ng/ul	Total Read Pair	Inter-chrom.	<1 kb	>1 kb	Complexity @ 400M
C1-TLv1	200 ng	21.6	1,721,786	40%	17%	42%	219,675,958
NoC1-TLv2	200 ng	18.9	867,337	19%	34%	47%	224,365,562
noC1-TLv2	500 ng	43.4	1,456,461	19%	40%	40%	264,129,021
noC1-TLv2	1000 ng	80.8	1,219,547	18%	45%	37%	250,274,481
OmniC	1000 ng	56.3	1,890,882	25%	19%	57%	325,186,278
*C1-TLv1 lib PCR 14 cycles, other samples 12 cycles							

[00520] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments described herein may be employed. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

WHAT IS CLAIMED IS:

1. A method of nucleic acid processing, comprising:
 - (a) obtaining a stabilized sample comprising a nucleic acid molecule complexed to at least one nucleic acid binding protein;
 - (b) cleaving the nucleic acid molecule into a plurality of segments comprising at least a first segment and a second segment, wherein the cleaving is effected by a transposase; and
 - (c) ligating the first segment to the second segment, thereby creating a proximity-linked nucleic acid comprising a first sequence from the first segment and a second sequence from the second segment.
2. The method of claim 1, wherein the transposase is a Tn5 transposase.
3. The method of claim 1, further comprising circularizing the proximity-linked nucleic acid by ligating a 5' end of the proximity-linked nucleic acid to a 3' end of the proximity-linked nucleic acid, thereby creating a circularized proximity-linked nucleic acid.
4. The method of claim 1, further comprising sequencing at least a portion of the proximity-linked nucleic acid.
5. The method of claim 4, wherein the sequencing comprises sequencing at least a portion of the first sequence and at least a portion of the second sequence.
6. The method of claim 5, further comprising mapping at least a portion of the first sequence and at least a portion of the second sequence to a genome.
7. The method of claim 4, further comprising conducting three-dimensional genomic analysis using information from the sequencing.
8. The method of claim 1, wherein the stabilized sample is a crosslinked sample.
9. The method of claim 1, wherein obtaining the stabilized sample comprises obtaining a sample and stabilizing the sample.
10. The method of claim 1, wherein obtaining the stabilized sample comprises obtaining a sample that was previously stabilized.
11. The method of claim 1, wherein the nucleic acid binding protein comprises chromatin or a constituent thereof.
12. The method of claim 1, wherein a linker sequence is ligated between the first segment and the second segment.
13. The method of claim 12, wherein the linker sequence comprises a barcode sequence.
14. The method of claim 13, wherein the barcode sequence is indicative of a partition of origin.
15. The method of claim 13, wherein the barcode sequence is indicative of a cell of origin.
16. The method of claim 13, wherein the barcode sequence is indicative of a cell population of origin.
17. The method of claim 13, wherein the barcode sequence is indicative of an organism of origin.

18. The method of claim 1, wherein the cleaving occurs in open and closed chromatin compartments.
19. The method of claim 18, wherein at least 10% of the cleaving occurs in closed chromatin compartments.
20. The method of claim 18, wherein at least 20% of the cleaving occurs in closed chromatin compartments.
21. The method of claim 18, wherein at least 30% of the cleaving occurs in closed chromatin compartments.
22. The method of claim 1, wherein the stabilized sample comprises no more than 50,000 cells.
23. The method of claim 22, wherein the stabilized sample comprises at least 10,000 cells.
24. The method of claim 1, wherein the stabilized sample comprises stabilized nuclei.
25. The method of claim 24, wherein the stabilized sample comprises no more than 50,000 nuclei.
26. The method of claim 24, wherein the stabilized sample comprises at least 10,000 nuclei.
27. The method of claim 1, wherein the proximity-linked nucleic acid does not comprise an affinity tag.
28. The method of claim 3, wherein the circularized proximity-linked nucleic acid does not comprise an affinity tag.
29. The method of claim 3, wherein the circularized proximity-linked nucleic acid is greater than 250 base pairs in length.
30. The method of claim 3, wherein the circularizing does not circularize nucleic acids that are less than 250 base pairs in length.
31. The method of claim 27 or claim 28, wherein the proximity-linked nucleic acid and/or the circularized proximity-linked nucleic acid is isolated without use of affinity tags.