WHAT IS CLAIMED IS:

1. A method of preparing a sequencing library from a double-stranded target nucleic acid comprising:

(a) providing a plurality of transposomes, each transposome monomer comprising a transposase and a transposon nucleic acid, wherein the transposome is configured to nick only one strand of the double stranded target nucleic acid; and

(b) contacting the target nucleic acid with the transposomes such that the target nucleic acid is nicked at a plurality of sites of the target nucleic acid and single transposon nucleic acids are attached to at least one of the nicked target nucleic acids to generate transposed nucleic acids, thereby obtaining a library of modified nucleic acids for sequencing.

2. The method according to claim 1, wherein said method is a method of preparing a sequencing library having barcodes; wherein in step (a) each transposome comprises a transposase and a transposon nucleic acid comprising a recognition sequence; and

wherein step (b) comprises: (b) inserting the transposon nucleic acids into strands of the target nucleic acid, comprising:

(i) contacting the target nucleic acid with the transposomes such that the target nucleic acid is nicked at a plurality of sites and single transposon nucleic acids are attached to the nicked strands at one side of the nicked sites to generate transposed nucleic acids, and

(ii) ligating the attached single transposon nucleic acids to the nicked strands at the other side of the nicked sites, thereby obtaining a library of modified nucleic acids for sequencing.

3. A method for capturing contiguity information of a target DNA comprising:

(a) providing a plurality of transposomes, each transposome monomer comprising a transposase and a transposon nucleic acid, wherein the transposome is configured to nick only one strand of the double stranded target nucleic acid;

(b) contacting the target DNA with the transposomes such that the target DNA is nicked at a plurality of sites of the target nucleic acid;

(c) adding or inserting one or more recognition sequences to the target DNA sequence to generate treated target DNA;

(d) sequencing the treated target DNA; and

(e) capturing contiguity information by identifying the target DNA sequences or recognition sequences having a shared property.

4. A method of capturing contiguity information of a target DNA comprising:

(a) providing a plurality of transposomes, each transposome monomer comprising a transposase and a transposon nucleic acid comprising a recognition sequence, wherein the transposome is configured to nick only one strand of the double stranded target nucleic acid;

(b) inserting the transposon nucleic acids into strands of the target nucleic acid, comprising:

(i) contacting the target nucleic acid with the transposomes such that the target nucleic acid is nicked at a plurality of sites and single transposon nucleic acids are attached to the nicked strands at one side of the nicked sites, and

(ii) ligating the attached single transposon nucleic acids to the nicked strands at the other side of the nicked sites, thereby obtaining a modified nucleic acid;

(c) amplifying the modified nucleic acid, thereby obtaining a plurality of nucleic acids comprising inserted recognition sequences;

(d) sequencing the treated target DNA; and

(e) capturing contiguity information by identifying the target DNA sequences or recognition sequences having a shared property.

5. The method of claim 3 or 4, wherein the recognition sequence is a barcode, and wherein the barcode of at least one transposon nucleic acid is different; optionally wherein the recognition sequence is a barcode, and wherein the barcodes of the transposon nucleic acids are not the same.

6. The method of any one of the preceding claims, further comprising capturing the modified nucleic acids on a surface.

7. The method of claim 6, wherein the surface comprises a plurality of capture probes; optionally wherein

(i) the capture probes comprise nucleic acids and the method comprises hybridizing the modified nucleic acids with the capture probes; or

(ii) the modified nucleic acids and the capture probes each comprise an affinity moiety, for example biotin, avidin, or streptavidin; or

(iii) optionally, wherein the surface comprises at least about 100,000 captured nucleic acids per mm^2.

8. The method of any one of the preceding claims, wherein the transposomes that are contacted with the target nucleic acids in (b) are attached to a surface, thereby capturing the modified nucleic acids on the surface.

9. The method of any one of claims 6 to 8, comprising sequencing the captured nucleic acids on the surface.

10. The method of any one of claims 6 to 9, wherein the proximity of sequence information obtained from two captured nucleic acids in a linear representation of the target nucleic acid sequence is indicative of the proximity of the captured nucleic acids on the surface.

11. The method of claim 10, wherein captured nucleic acids in closer proximity to one another on the surface comprise sequences in closer proximity in the representation of the target nucleic acid sequence compared to captured nucleic acids in less close proximity.

12. The method of any one of claims 10 and 11, wherein the representation of the target nucleic acid sequence comprises a haplotype representation.

13. The method of any one of claims 1-12, wherein the transposome comprises a one-sided transposase activity; optionally (i) wherein the transposome comprises a monomer subunit lacking transposase activity; or (ii) wherein the transposome comprises covalently linked monomer subunits; or (iii) wherein the transposase lacks the ability to form dimers; and/or , (iv) wherein the quaternary structure of the transposase is monomeric.

14. The method of any one of claims 1-13, wherein the transposase is selected from the group consisting of Mu, Mu E392Q, Tn5, hyperactive Tn5, Tn5 variants, Vibhar, RAG, and Tn552.

15. The method of any one of claims 1-14, wherein the one or more transposon nucleic acids are non-functional; optionally (i) wherein the 3′ end of the non-functional transposon nucleic acid is selected from the group consisting of a dideoxy group, a spacer

group, an amine group, an alkyl group, an aryl group, a phosphate group, a thiol group, a reverse nucleotide, an azido group, a sulfate group, and a biotin group; or (ii) wherein the plurality of transposomes are prepared by contacting the transposases with functional transposon nucleic acids and non-functional transposon nucleic acids; or (iii) wherein the ratio of transposon nucleic acids comprising non-functional transposon nucleic acids to functional transposon nucleic acids is greater than or equal to 1:1.

16. The method of claim 3, further comprising:

(i) providing a DNA polymerase to the nicked target nucleic acid;

(ii) extending the 3' end of the target nucleic acid using the complementary strand as template;

(iii) optionally amplifying the extended nucleic acids; and

optionally, wherein the amplifying of the extended nucleic acids is with tailed amplification primers comprising a sequence selected from the group consisting of an anchor site, a sequencing primer site, an amplification primer site, a barcode, and a reporter tag.

17. The method of any one of claims 6 to 16, comprising amplifying the captured nucleic acids; optionally wherein the amplifying of the captured nucleic acids comprises bridge amplification.

18. The method of any one of claims 6 to 17, wherein the surface comprises a plurality of capture probes;

optionally wherein the capture probes comprise nucleic acids.

19. The method of any one of the preceding claims , wherein the transposon nucleic acid comprises a sequence selected from the group consisting of an anchor site, a barcode, a sequencing primer site, an amplification primer site, and a reporter tag.

20. The method of any one of claims 1-19, wherein at least one transposome comprises two transposon nucleic acids;

optionally wherein the two transposon nucleic acids have different sequences.

21. The method of any one of claims 1-20, wherein the plurality of transposomes comprise at least two different transposon nucleic acids.

22. The method of any one of claims 1-21, wherein the plurality of transposomes comprise at least one transposase having the ability to form a transposome but lacking the ability to transpose.

23. The method of any one of claims 1-22, wherein the target nucleic acid is selected from the group consisting of genomic DNA, fragments of genomic DNA, and cDNA.

24. The method of any one of claims 1-23, further comprising combinatorial barcoding, wherein the transposon comprises the first set of barcodes;

the first set of barcodes are introduced to the target nucleic acid during transposition to generate transposed target nucleic acids comprising first set of barcodes;

the transposed target nucleic acids are pooled to generate a first pool of transposed target nucleic acids;

a second set of barcodes are introduced to the first pool of transposed target nucleic acid to generate target nucleic acids comprising first and second sets of barcodes;

target nucleic acids comprising first and second sets of barcodes; are pooled to generate a second pool of transposed target nucleic acid;

optionally repeating the steps of introducing additional barcodes and pooling to generate a library of barcoded target nucleic acids.