What is claimed is:

1. A method for identifying methylation status of a nucleic acid in a biological sample, the method comprising:

(a) contacting the biological sample with a substrate;

(b) deaminating the nucleic acid in the biological sample;

(c) contacting the nucleic acid with a plurality of probes comprising a first probe and a second probe, wherein

the first probe comprises (i) a sequence complementary to at least a first sequence of the nucleic acid and (ii) a sequence complementary to a capture domain of a capture probe; and

the second probe comprises a sequence complementary to a second sequence of the nucleic acid;

(d) ligating the first probe and the second probe, thereby generating a ligation product;

(e) hybridizing the ligation product to the capture probe; and

(f) determining (i) the sequence of a spatial barcode of the capture probe or a complement thereof, and (ii) all or a portion of the sequence of the ligation product, or a complement thereof, and using the determined sequences of (i) and (ii) to identify the methylation status of the nucleic acid in the biological sample.

2. The method of claim 1, wherein the substrate comprises an array comprising a plurality of capture probes, wherein the capture probe is comprised in the plurality of capture probes, and wherein the capture probe comprises (i) the spatial barcode and (ii) the capture domain.

3. The method of claim 1, further comprising, between steps (d) and (e):

aligning the substrate with a second substrate comprising an array, such that at least a portion of the biological sample is aligned with at least a portion of the array, wherein the array comprises a plurality of capture probes and wherein a capture probe of the plurality of capture probes comprises (i) the spatial barcode and (ii) the capture domain; and

when the biological sample is aligned with at least a portion of the array, releasing the ligation product from the nucleic acid.

4. The method of claim 3, wherein the substrate does not comprise the array of capture probes.

5. The method of any one of claims 1-4, wherein the first probe and the second probe hybridize to the nucleic acid at sequences that are at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides apart.

6. A method for identifying a methylation status of a nucleic acid in a biological sample, the method comprising:

(a) contacting the biological sample with a substrate;

(b) providing one or more transposomes to the biological sample, wherein the one or more transposomes comprise one or more methylated adaptors, under conditions wherein the nucleic acid is fragmented and one or more methylated adaptors from the one or more transposomes is inserted into the nucleic acid , thereby generating a plurality of tagmented nucleic acid fragments, wherein a tagmented nucleic acid fragment of the plurality of tagmented nucleic acid fragments comprises the one or more methylated adaptors;

(c) ligating the tagmented nucleic acid fragment to a capture probe, thereby creating a ligation product;

(d) deaminating the ligation product; and

(e) determining (i) the sequence of a spatial barcode of the capture probe or a complement thereof, and (ii) all or part of the sequence of the ligation product, or a complement thereof, and using the determined sequences of (i) and (ii) to identify the methylation status of the nucleic acid in the biological sample.

7. The method of claim 6, wherein the substrate comprises an array comprising a plurality of capture probes, wherein the capture probe is comprised in the plurality of capture probes, wherein the capture probe comprises the spatial barcode, and wherein if the capture probe comprises one or more cytosines, the one or more cytosines are methylated cytosines.

8. The method of claim 6, further comprising:

aligning the substrate with a second substrate comprising the array, such that at least a portion of the biological sample is aligned with at least a portion of the array, wherein the array comprises a plurality of capture probes, wherein the capture probe is comprised in the plurality of capture probes, wherein the capture probe comprises the spatial barcode; and

when the biological sample is aligned with at least a portion of the array, releasing the tagmented nucleic acid fragment from the biological sample.

9. The method of claim 8, wherein the substrate does not comprise the array comprising a plurality of capture probes.

10. The method of any one of claims 6-9, wherein the one or more methylated adaptors are inserted into the nucleic acid using a transposase complexed with a transposon, wherein the transposase is a Tn5 transposase, or a functional derivative thereof, or a Tn7 transposase, or a functional derivative thereof.

11. The method of any one of claims 6-10, wherein the one or more methylated adaptors is at least about 10 nucleotides to about 50 nucleotides long.

12. The method of any one of claims 1-11, wherein the ligating comprises chemical ligation.

13. The method of any one of claims 1-11, wherein the ligating comprises enzymatic ligation using a ligase selected from a PBCV-1 DNA ligase, a *Chlorella* virus ligase, a single-stranded DNA ligase, or a T4 DNA ligase.

14. The method of any one of claims 1-13, further comprising contacting the biological sample with a reagent medium comprising a permeabilization reagent, optionally wherein the permeabilization reagent comprises a protease selected from proteinase K or pepsin.

15. The method of any one of claims 1-14, wherein the ligating utilizes a splint oligonucleotide.

16. The method of any one of claims 1-15, wherein the nucleic acid is DNA.

17. The method of claim 16, wherein the DNA is genomic DNA.

18. The method of any one of claims 1-17, wherein the biological sample is a fixed sample, a frozen sample, a fresh sample, or a fresh frozen sample.

19. The method of any one of claims 1-18, wherein the biological sample is a formalin fixed paraffin embedded (FFPE) sample.

20. The method of any one of claims 1-5, wherein the deaminating comprises contacting the biological sample with a composition comprising sodium bisulfite.

21. The method of any one of claims 1-5, wherein the deaminating comprises treating the biological sample with an enzyme.

22. The method of claim 21, wherein the enzyme is a cytidine deaminase or a demethylase.

23. The method of any one of claims 1-22, wherein the capture probe further comprises one or more functional domains, a unique molecular identifier, a cleavage domain, and combinations thereof.

24. The method of any one of claims 1-23, wherein the determining comprises sequencing (i) all or a part of the ligation product, or a complement thereof, and (ii) the spatial barcode, or a complement thereof.

25. The method of any one of claims 1-24, further comprising imaging the biological sample.