What is claimed is:

~~1. A method for identifying methylation status of an analyte in a biological sample, the method comprising:~~

~~(a) contacting the biological sample with an array comprising a plurality of capture probes, wherein a capture probe in the plurality of capture probes comprises (i) a spatial barcode and (ii) a capture domain comprising at least one methylated cytosine;~~

~~(b) deaminating the analyte in the biological sample;~~

~~(c) contacting the analyte 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 analyte and (ii) a sequence complementary to the capture domain; and~~

~~the second probe comprises a sequence complementary to at least a second sequence of the analyte;~~

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

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

~~(f) extending the capture probe using the ligation product as a template; thereby generating an extended capture probe; and~~

~~(g) determining (i) all or a portion of the sequence of the spatial barcode or the complement thereof, and (ii) all or a portion of the sequence of the extended capture probe, or a complement thereof, and using the determined sequences of (i) and (ii) to identify the methylation status of the analyte in the biological sample.~~

~~2. The method of claim 1, wherein the first oligonucleotide and the second oligonucleotide hybridize to the analyte at sequences that are at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more nucleotides apart.~~

~~3. The method of claim 1 or 2, further comprising extending the first oligonucleotide and/or the second oligonucleotide after step (c).~~

~~4. The method of claim 3, wherein the first probe and/or second probe is extended using a polymerase.~~

5. The method of any one of the preceding claims, further comprising releasing the ligation product from the analyte.

6. The method of claim 5, wherein the releasing occurs before hybridizing the ligation product to the capture probe.

7. The method of any one of the preceding claims, wherein the method further comprises, prior to step (b), contacting the biological sample with a permeabilization reagent.

8. The method of any one of the preceding claims, wherein the first probe and/or the second probe comprises a sequence that binds to a sequence on the analyte that does not have a CG dinucleotide.

9. The method of any one of the preceding claims, wherein the method further comprises washing the biological sample between step (b) and step (c).

10. A method for identifying a methylation status of DNA in a biological sample, the method comprising:

(a) providing one or more transposomes to the biological sample, wherein the transposomes comprise methylated adaptors, under conditions wherein the one or more methylated adaptors is inserted into the DNA, thereby generating tagmented DNA fragments comprising methylated adaptors;

(b) contacting the tagmented DNA fragments with an array comprising a plurality of capture probes, wherein a capture probe in the plurality of capture probes comprises a spatial barcode, wherein if the capture probe comprises one or more cytosines, wherein the one or more cytosines are methylated cytosines;

(c) ligating the sequence comprising the tagmented DNA fragments and the one or more methylated adaptors to the capture probe, thereby creating a ligation product;

(d) deaminating the ligation product; and

(e) determining (i) all or a portion of the sequence of the spatial barcode or the 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 DNA, or a portion thereof, in the biological sample.

~~11. The method of claim 10, wherein the ligating comprises adding a splint oligonucleotide comprises~~

~~(i) a sequence that binds specifically to a portion of the capture probe; and~~

~~(ii) a sequence that binds specifically to a portion of the ligation product.~~

~~12. The method of claim 11, wherein the splint oligonucleotide comprises a sequence that binds specifically to a portion of the one or more methylated adaptors.~~

~~13. The method of any one of claims 10-12, wherein the transposase enzyme is a Tn5 transposase enzyme, or a functional derivative thereof or a Tn7 transposase enzyme, or the functional derivative thereof.~~

~~14. The method of any one of claims 10-13, wherein the one or more methylated adaptors comprises a first methylated adaptor and a second methylated adaptor.~~

~~15. The method of any one of claims 10-14, further comprising incubating the ligation product with a terminal transferase and a plurality of deoxycytidine triphosphate (dCTP) molecules, thereby extending the ligation product at the 3' end.~~

~~16. The method of claim 15, further comprising amplifying the ligation product.~~

~~17. The method of claim 15 or 16, further comprising amplifying the ligation product using a primer sequence that is complementary to a poly-cysteine sequence at the 3' end of the ligation product.~~

~~18. The method of any one of the preceding claims, wherein the ligating comprises enzymatic ligation or chemical ligation.~~

~~19. The method of claim 18, wherein the enzymatic ligation utilizes a ligase.~~

~~20. The method of claim 19, wherein the ligase is one or more of a splintR ligase, a single stranded DNA ligase, or a T4 DNA ligase.~~

21. The method of any one of the preceding claims, further comprising a migration step wherein the analyte migrates to the substrate.

22. The method of claim 21, wherein the migration step is an active migration step comprising applying an electric field to the genomic DNA.

23. The method of claim 21, wherein the migration step is a passive migration step.

24. A method of identifying the methylation status of a nucleic acid in a biological sample on a first substrate, comprising:

(a) deaminating the nucleic acid;

(b) hybridizing a first probe and a second probe to the nucleic acid, 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 on an array; and

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

(c) ligating the first probe and the second probe to generate a ligation product;

(d) aligning the first substrate with the 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 a capture probe of the plurality of capture probes comprises: (i) a spatial barcode and (ii) the capture domain;

(e) when the biological sample is aligned with at least a portion of the array, (i) releasing the ligation product from the analyte and (ii) migrating the ligation product from the biological sample to the array; and

(f) capturing the ligation product with the capture domain.

25. The method of claim 24, further comprising determining (i) all or a portion of the sequence of the spatial barcode or the complement thereof and (ii) all or a portion of the sequence of the ligation product, or a complement thereof.

26. The method of claim 25, further comprising using the determined sequences of (i) and (ii) to identify the methylation status of the nucleic acid in the biological sample.

~~27. The method of any one of claims 24-26, wherein the first probe is at least 75%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to the nucleic acid.~~

~~28. The method of any one of claims 24-27, wherein the first probe is about 15 to about 120 nucleotides in length.~~

~~29. The method of any one of claims 24-28, wherein the first sequence is about 10 to about 60 nucleotides in length.~~

~~30. The method of any one of claims 24-29, wherein the second probe is at least 75%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% complementary to the nucleic acid.~~

~~31. The method of any one of claims 24-20, wherein the second probe is about 15 to about 120 nucleotides in length.~~

~~32. The method of any one of claims 24-31, wherein the second sequence is about 10 to about 60 nucleotides in length.~~

~~33. The method of any one of claims 24-32, wherein the first sequence and the second sequence are adjacent sequences.~~

~~34. The method of claim 29, wherein at least one deaminated nucleotide is located between the first sequence and the second sequence.~~

~~35. The method of claim 29, wherein at least two, at least three, at least four, at least five, or more deaminated nucleotide is located between the first sequence and the second sequence.~~

~~36. The method of claim 29 or 30, further comprising generating an extended first probe and/or an extended second probe using a polymerase, wherein the extended first probe or the extended second probe comprises a sequence complementary to a sequence between the first sequence and the second sequence.~~

37. The method of any one of claims 24-36, wherein at least one deaminated nucleotide is located in the first sequence.

38. The method of any one of claims 24-37, wherein the at least one deaminated nucleotide is located in the second sequence.

39. The method of any one of claims 24-38, wherein the releasing comprises heating the biological sample.

40. The method of any one of claims 24-39, wherein (e) further comprises contacting the biological sample with a reagent medium comprising a permeabilization reagent, optionally wherein the permeabilization reagent comprises a protease.

41. The method of any one of claims 24-35 or 37-40, wherein the ligating the first probe and the second probe comprises ligating via a ligase the first probe and the second probe.

42. The method of any one of claims 36-40, wherein the ligating the first probe and the second probe comprises ligating via a ligase:

(a) the first probe and the extended second probe; or

(b) the extended first probe and the second probe.

43. The method of claim 41 or 42, wherein the ligase is selected from a splintR ligase, a single stranded DNA ligase, or a T4 DNA ligase.

44. The method of any one of claims 24-43, wherein the first probe and the second probe are on a contiguous nucleic acid.

45. The method of any one of claims 24-44, wherein the ligating utilizes a splint oligonucleotide.

46. The method of claim 45, wherein the splint oligonucleotide comprises a first splint sequence that is substantially complementary to the first probe and a second splint sequence that is substantially complementary to the second probe.

47. The method of any one of claims 24-46, wherein the capturing the ligation product comprises hybridizing the sequence complementary to a capture domain to the capture domain.

48. The method of any one of claims 24-47, wherein the capturing the ligation product comprises ligating the ligation product to the capture probe.

49. The method of any one of claims 24-48, further comprising extending the capture probe using the ligation product as a template; thereby generating an extended capture probe.

50. A method of identifying a methylation status of a nucleic acid in a biological sample on a first substrate, the method comprising:

(a) ligating a methylated adaptor to a nucleic acid, generating an adapted nucleic acid fragment;

(b) deaminating the adapted nucleic acid fragment;

(c) aligning the first 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, wherein a capture probe of the plurality of capture probes comprises: (i) a spatial barcode and (ii) a capture domain;

(d) when the biological sample is aligned with at least a portion of the array, migrating the adapted nucleic acid fragment from the biological sample to the array; and

(e) capturing the adapted nucleic acid fragment with the capture domain.

51. The method of claim 50, further comprising determining (i) all or a portion of the sequence of the spatial barcode or the complement thereof, and (ii) all or a portion of the sequence of the ligation product, or a complement thereof.

52. The method of claim 51, further comprising using the determined sequences of (i) and (ii) to identify the methylation status of the nucleic acid, or a portion thereof, in the biological sample.

53. The method of any one of claims 50-52, wherein the methylated adaptor is ligated to the nucleic acid by tagmentation.

54. The method of any one of claims 50-53, wherein the methylated adaptor is ligated to the nucleic acid at a 5' end of the nucleic acid.

55. The method of any one of claims 50-54, wherein the methylated adaptor is ligated to the nucleic acid at a 3' end of the nucleic acid.

56. The method of any one of claims 50-55, wherein the methylated adaptor is at least about 10 nucleotides to about 50 nucleotides long.

57. The method of any one of claims 50-56, wherein the methylated adaptor comprises at least one, at least two, at least three, at least four, at least five, or more methylated cytosines.

58. The method of any one of claims 50-57, wherein the spatial barcode comprises at least one, at least two, at least three, at least four, at least five, or more methylated cytosines.

59. The method of any one of claims 50-58, wherein the ligating the methylated adaptor to the nucleic acid comprises attaching the one or more methylated adaptors to the 5' and/or 3' end of the nucleic acid using a transposase enzyme complexed with a transposon, wherein the transposase enzyme is a Tn5 transposase enzyme, or the functional derivative thereof.

60. The method of any one of claims 50-59, wherein the capturing the adapted nucleic acid fragment comprises hybridizing the adapted nucleic acid fragment with the capture domain.

61. The method of any one of claims 50-60, wherein the capturing the adapted nucleic acid fragment comprises ligating the adapted nucleic acid fragment with the capture domain, wherein the ligating comprises enzymatic ligation or chemical ligation.

62. The method of claim 61, wherein the ligating utilizes a splint oligonucleotide, optionally wherein the splint oligonucleotide comprises a first splint sequence that is substantially complementary to the adapted nucleic acid fragment and a second splint sequence that is substantially complementary to the capture probe.

~~63. The method of any one of claims 50-62, further comprising extending the capture probe using the adapted nucleic acid fragment as a template; thereby generating an extended capture probe.~~

~~64. The method of any one of claims 50-63, further comprising incubating the adapted nucleic acid fragment with a terminal transferase and a plurality of deoxycytidine triphosphate (dCTP) molecules, thereby generating an extended adapted nucleic acid fragment.~~

~~65. The method of claim 64, further comprising amplifying the extended adapted nucleic acid fragment.~~

~~66. The method of claim 64 or 65, further comprising amplifying the extended adapted nucleic acid fragment using a primer sequence that is complementary to a poly-cysteine sequence at the 3' end of the adapted nucleic acid fragment.~~

~~67. The method of any one of the preceding claims, wherein the biological sample is a cancer tissue sample.~~

~~68. The method of claim 67, wherein the biological sample is from a subject treated with a cancer therapy.~~

~~69. The method of any one of the preceding claims, wherein the nucleic acid is DNA.~~

~~70. The method of claim 69, wherein the DNA is genomic DNA.~~

~~71. The method of any one of the preceding claims, wherein the biological sample is a tissue sample, optionally wherein the tissue sample is a solid tissue sample, optionally wherein the tissue sample is a tissue section.~~

~~72. The method of any one of the preceding claims, wherein the biological sample is a fixed sample, a frozen sample, a fresh sample, or a fresh frozen sample.~~

~~73. The method of any one of the preceding claims, wherein the biological sample is a formalin fixed paraffin embedded (FFPE) sample.~~

~~74. The method of any one of the preceding claims, wherein the first substrate is a slide.~~

~~75. The method of any one of the preceding claims, wherein the first substrate is a glass slide.~~

~~76. The method of any one of the preceding claims, wherein the first substrate does not comprise an array of capture probes.~~

~~77. The method of any one of the preceding claims, wherein the deaminating comprises contacting the biological sample with a composition comprising sodium bisulfite.~~

~~78. The method of any one of the preceding claims, wherein the deaminating comprises treating the biological sample with an enzyme.~~

~~79. The method of claim 52, wherein the enzyme is a cytidine deaminase or a demethylase.~~

~~80. The method of any one of the preceding claims, wherein the second substrate is a glass slide.~~

~~81. The method of any one of the preceding claims, wherein a 5' end of the capture probe is attached to the second substrate.~~

~~82. The method of any one of the preceding claims, wherein the array is a bead array.~~

~~83. The method of 82, wherein a 5' end of the capture probe is attached to a bead of the bead array.~~

~~84. The method of any one of the preceding claims, wherein the capture probe further comprises a unique molecular identifier (UMI).~~

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

86. The method of any one of claims 24-85, wherein the migrating is active.

87. The method of any one of claims 24-85, wherein the migrating is passive.

88. The method of any one of the preceding claims, wherein the capture probe is extended using a polymerase.

89. The method of any one of the preceding claims, wherein the determining comprises sequencing (i) all or a part of the sequence of the nucleic acid, or a complement thereof, and (ii) all or a part of the sequence of the spatial barcode, or a complement thereof.

90. The method of any one of the preceding claims, wherein the methylation status comprises identifying that about 1% to about 100% of cytosines comprises a methyl group.

91. The method of any one of the preceding claims, further comprising imaging the biological sample.

92. The method of claim 91, wherein the imaging occurs prior to deaminating the biological sample.

93. A kit comprising comprising parts and instruction for performing the method of any one of the preceding claims.

94. The kit of claim 93, wherein the kit comprises a substrate comprising a plurality of capture probes, wherein a capture probe of the plurality of first capture probes comprises (i) a spatial barcode and (ii) a capture domain.

95. The kit of claim 93 or 94, wherein the kit comprises one or more enzymes.

~~96. The kit of claim 95, wherein the one or more enzyme is selected from the group consisting of a transposase, a ligase, a polymerase; a reverse transcriptase, a cytidine deaminase and a demethylase.~~

~~97. The kit of any one of claims 93-96, wherein the kit further comprises a transposome complex comprising a transposase, a transposon sequence, and/or an adaptor sequence.~~

~~98. A composition comprising reagents for performing the method of any one of the preceding claims.~~

~~99. The composition of claim 93, wherein the composition comprises a substrate comprising a plurality of capture probes, wherein a capture probe of the plurality of first capture probes comprises (i) a spatial barcode and (ii) a capture domain.~~

~~100. The composition of claim 98 or 99, wherein the composition comprises one or more enzyme.~~

~~101. The composition of claim 100, wherein the one or more enzyme is selected from the group consisting of a transposase, a ligase, a polymerase; a reverse transcriptase, a cytidine deaminase and a demethylase.~~

~~102. The composition of any one of claims 98-101, wherein the composition further comprises a transposome complex comprising a transposase, a transposon sequence, and/or an adaptor sequence.~~

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.