WHAT IS CLAIMED IS:

~~1. A method for determining the presence and/or abundance of an immune cell clonotype at a location in a biological sample, the method comprising:~~

~~(a) contacting a biological sample with an array comprising 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 that binds to a nucleic acid encoding an immune cell receptor of the immune cell clonotype; and~~

~~(b) determining (i) all or a portion of the sequence of the spatial barcode or a complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor or a complement thereof, and using the determined sequences of (i) and (ii) to determine the presence and/or abundance of the immune cell clonotype at a location in the biological sample.~~

~~2. The method of claim 1, wherein the immune cell clonotype is a T cell clonotype.~~

~~3. The method of claim 2, wherein the T cell clonotype is a T cell receptor alpha chain.~~

~~4. The method of claim 3, wherein the capture domain binds to a nucleic acid sequence encoding a constant region of the T cell receptor alpha chain.~~

~~5. The method of claim 3 or 4, wherein step (b) comprises determining a sequence encoding CDR3 of the T cell receptor alpha chain.~~

~~6. The method of claim 5, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor alpha chain.~~

~~7. The method of claim 5, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the T cell receptor alpha chain.~~

~~8. The method of claim 2, wherein the immune cell receptor is a T cell receptor beta chain.~~

~~9. The method of claim 8, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the T cell receptor beta chain.~~

~~10. The method of claim 8 or 9, wherein step (b) comprises determining a sequence encoding CDR3 of the T cell receptor beta chain.~~

~~11. The method of claim 10, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor beta chain.~~

~~12. The method of claim 10, wherein step (b) further comprises determining a sequence encoding a full length variable domain of the T cell receptor beta chain.~~

~~13. The method of claim 1, wherein the immune cell clonotype is a B cell clonotype.~~

~~14. The method of claim 13, wherein the B cell clonotype is an immunoglobulin kappa light chain.~~

~~15. The method of claim 14, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin kappa light chain.~~

~~16. The method of claim 14 or 15, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin kappa light chain.~~

~~17. The method of claim 16, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin kappa light chain.~~

~~18. The method of claim 16, wherein step (b) further comprises determining a sequence encoding a full length variable domain of the immunoglobulin kappa light chain.~~

~~19. The method of claim 13, wherein the B cell clonotype is an immunoglobulin lambda light chain.~~

~~20. The method of claim 19, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin lambda light chain.~~

~~21. The method of claim 19 or 20, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin lambda light chain.~~

~~22. The method of claim 21, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin lambda light chain.~~

~~23. The method of claim 21, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the immunoglobulin lambda light chain.~~

~~24. The method of claim 13, wherein the B cell clonotype is an immunoglobulin heavy chain.~~

~~25. The method of claim 24, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin heavy chain.~~

~~26. The method of claim 24 or 25, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin heavy chain.~~

~~27. The method of claim 26, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin heavy chain.~~

~~28. The method of claim 26, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the immunoglobulin heavy chain.~~

~~29. The method of claim 3 or 13, wherein the capture domain binds a poly(A) sequence of a nucleic acid encoding an immune cell clonotype.~~

~~30. The method of claim 29, wherein the capture domain binds to a nucleic acid sequence encoding a T cell clonotype.~~

~~31. The method of claim 30, wherein the T cell clonotype is a T cell receptor alpha chain, a T cell receptor beta chain, and combinations thereof.~~

~~32. The method of claim 29 or 30, wherein step (b) comprises determining: a sequence encoding CDR3 of the T cell receptor alpha chain, a sequence encoding CDR3 of the T cell receptor beta chain, and combinations thereof.~~

~~33. The method of claim 32, wherein step (b) further comprises determining: a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor alpha chain, a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor beta chain, and combinations thereof.~~

~~34. The method of claim 32, wherein step (b) further comprises determining: a sequence encoding a full-length variable domain of the T cell receptor alpha chain, a sequence encoding a full-length variable domain of the T cell receptor beta chain, and combinations thereof.~~

~~35. The method of claim 29, wherein the capture domain binds to a nucleic acid encoding a B cell clonotype.~~

~~36. The method of claim 35, wherein the B cell clonotype is an immunoglobulin kappa light chain, an immunoglobulin lambda light chain, an immunoglobulin heavy chain, and combinations thereof.~~

~~37. The method of claim 36, wherein step (b) comprises determining: a sequence encoding CDR3 of the immunoglobulin kappa light chain, a sequence encoding CDR3 of immunoglobulin lambda light chain, a sequence encoding CDR3 of the immunoglobulin heavy chain, and combinations thereof.~~

~~38. The method of claim 37, wherein step (b) further comprises determining: a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin kappa light chain, a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin lambda light chain, a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin heavy chain, and combinations thereof.~~

~~39. The method of claim 37, wherein step (b) further comprises determining: a sequence encoding a full-length variable domain of the immunoglobulin kappa light chain, a sequence encoding a full-length variable domain of the immunoglobulin lambda light chain, a sequence encoding a full-length variable domain of the immunoglobulin heavy chain, and combinations thereof.~~

~~40. The method of any one of claims 1-39, wherein step (b) comprises the capture probe using the nucleic acid encoding the immune cell receptor as a template, thereby generating an extended capture probe.~~

~~41. The method of claim 40, wherein step (b) comprises extending a 3' end of the capture probe.~~

~~42. The method of claim 40 or 41, wherein step (b) further comprises generating a second strand of nucleic acid that comprises (i) a sequence that is complementary to all or a portion of the spatial barcode, and (ii) a sequence that corresponds to all or a portion of the sequence of the nucleic acid encoding the immune cell receptor.~~

~~43. The method of any one of claims 1-42, wherein the capture probe further comprises a cleavage domain, a functional domain, a unique molecular identifier, or any combination thereof.~~

~~44. The method of any one of claims 1-43, wherein the capture probe further comprises a functional domain.~~

~~45. The method of claim 44, wherein step (b) further comprises generating a second strand of nucleic acid that comprises (i) a sequence that is complementary to all or a portion of the functional domain, (ii) a sequence that is complementary to all or a portion of the spatial barcode, and (iii) a sequence that corresponds to all or a portion of the sequence of the nucleic acid encoding the immune cell receptor.~~

~~46. The method of any one of claims 1-45, wherein the method further comprises enriching the nucleic acid encoding the immune cell receptor of the immune cell clonotype.~~

~~47. The method of claim 46, wherein enriching comprises hybridizing a plurality of hybridization probes to the nucleic acid encoding the immune cell receptor of the immune cell clonotype, wherein a hybridization probe comprises (i) a sequence complementary to a portion of the nucleic acid encoding the immune cell receptor and (ii) a binding moiety that interacts with a capture moiety.~~

~~48. The method of claim 47, wherein the binding moiety comprises biotin and the capture moiety comprises streptavidin.~~

~~49. The method of any one of claims 46-48, wherein enriching the nucleic acid encoding the immune cell receptor of the immune cell clonotype further comprises one or more blocking probes.~~

~~50. The method of claim 49, wherein the one or more blocking probes comprises a sequence having at least 80% identity to SEQ ID NO: 639.~~

~~51. The method of claim 49, wherein the one or more blocking probes comprises a sequence having at least 80% identity to SEQ ID NO: 640.~~

~~52. The method of any one of claims 1-51, wherein the method further comprises amplifying the nucleic acid encoding the immune cell receptor of the immune cell clonotype, or a complement thereof, using (i) a first primer comprising all or a portion of the functional domain, wherein the functional domain is 5' to the spatial barcode, and (ii) a second primer comprising a sequence that is substantially complementary to a portion of a sequence encoding a variable region of the immune cell receptor.~~

~~53. The method of claim 52, further comprising amplifying the nucleic acid encoding the immune cell receptor of the immune cell clonotype, or a complement thereof, using (i) the first primer comprising all or a portion of the functional domain, wherein the functional domain is 5' to the spatial barcode, and (ii) a third primer comprising a sequence that is substantially complementary to a portion of the nucleic acid sequence encoding a variable region of the immune cell receptor, wherein the third primer is 5' to the second primer.~~

54. The method of any one of claims 1-53, wherein the biological sample comprises a tissue sample.

55. The method of claim 54, wherein the tissue sample is a tissue section.

56. The method of claim 55, wherein the tissue section is a fixed tissue section.

57. The method of claim 56, wherein the fixed tissue section is a formalin-fixed paraffin-embedded tissue section.

58. The method of any one of claims 55-57, wherein the tissue section comprises a tumor region.

59. The method of any one of claims 1-58, wherein the nucleic acid encoding the immune cell receptor comprises RNA.

60. The method of claim 59, wherein the RNA is mRNA.

61. The method of any one of claims 1-60, wherein the nucleic acid encoding the immune cell receptor comprises DNA.

62. The method of claim 61, wherein the DNA is genomic DNA.

63. The method of any one of claims 1-62, wherein the method further comprises imaging the biological sample.

64. The method of any one of claims 1-63, wherein the determining in step (b) comprises sequencing (i) all or a portion of the sequence of the spatial barcode or a complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor or a complement thereof.

~~65. The method of any one of claims 1-64, wherein step (b) comprises determining the presence of the immune cell clonotype at a location in the biological sample.~~

~~66. The method of any one of claims 1-64, wherein step (b) comprises determining the abundance of the immune cell clonotype at a location in the biological sample.~~

~~67. The method of any one of claims 1-64, wherein step (b) comprises determining the presence and abundance of the immune cell clonotype at a location in the biological sample.~~

~~68. The method of any one of claims 1-64, wherein step (b) comprises determining the presence of two or more immune cell clonotypes at a location in the biological sample.~~

~~69. The method of any one of claims 1-64, wherein step (b) comprises determining the abundance of two or more immune cell clonotypes at a location in the biological sample.~~

~~70. The method of any one of claims 1-64, wherein step (b) comprises determining the presence and abundance of two or more immune cell clonotypes at a location in the biological sample.~~

~~71. The method of any one of claims 68-70, wherein the method further comprises comparing the two or more immune cell clonotypes.~~

~~72. The method of any one of claims 68-71, wherein the two or more immune cell clonotypes are each a B cell clonotype.~~

~~73. The method of any one of claims 68-71, wherein the two or more immune cell clonotypes are each a T cell clonotype.~~

~~74. The method of any one of claims 68-7151-54, wherein the two or more immune cell clonotypes comprise at least one T cell clonotype and at least one B cell clonotype.~~

~~75. A method for determining the presence and/or abundance of an immune cell receptor at a location in a biological sample, the method comprising:~~

(a) contacting a biological sample with an array comprising 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 that specifically binds to a nucleic acid encoding an immune cell receptor; and

(b) determining (i) all or a portion of the sequence of the spatial barcode or a complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor or a complement thereof, and using the determined sequences of (i) and (ii) to determine the presence and/or abundance of the immune cell receptor at a location in the biological sample.

76. The method of claim 75, wherein the immune cell receptor is a T cell receptor alpha chain.

77. The method of claim 76, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the T cell receptor alpha chain.

78. The method of claim 76 or 77, wherein step (b) comprises determining a sequence encoding CDR3 of the T cell receptor alpha chain.

79. The method of claim 78, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor alpha chain.

80. The method of claim 78, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the T cell receptor alpha chain.

81. The method of claim 75, wherein the immune cell receptor is a T cell receptor beta chain.

82. The method of claim 81, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the T cell receptor beta chain.

83. The method of claim 81 or 82, wherein step (b) comprises determining a sequence encoding CDR3 of the T cell receptor beta chain.

~~84. The method of claim 83, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor beta chain.~~

~~85. The method of claim 83, wherein step (b) further comprises determining a full-length variable domain of the T cell receptor beta chain.~~

~~86. The method of claim 75, wherein the immune cell receptor is an immunoglobulin kappa light chain.~~

~~87. The method of claim 86, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin kappa light chain.~~

~~88. The method of claim 86 or 87, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin kappa light chain.~~

~~89. The method of claim 88, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin kappa light chain.~~

~~90. The method of claim 88, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the immunoglobulin kappa light chain.~~

~~91. The method of claim 75, wherein the immune cell receptor is an immunoglobulin lambda light chain.~~

~~92. The method of claim 91, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin lambda light chain.~~

~~93. The method of claim 91 or 92, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin lambda light chain.~~

~~94. The method of claim 93, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin lambda light chain.~~

95. The method of claim 93, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the immunoglobulin lambda light chain.

96. The method of claim 75, wherein the immune cell receptor is an immunoglobulin heavy chain.

97. The method of claim 96, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin heavy chain.

98. The method of claim 96 or 97, wherein step (b) comprises determining a sequence encoding CDR3 of the immunoglobulin heavy chain.

99. The method of claim 98, wherein step (b) further comprises determining a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin heavy chain.

100. The method of claim 98, wherein step (b) further comprises determining a sequence encoding a full-length variable domain of the immunoglobulin heavy chain.

101. The method of claim 75, wherein the capture domain binds a poly(A) sequence of a nucleic acid encoding an immune cell receptor.

102. The method of claim 101, wherein the immune cell receptor is a T cell receptor alpha chain, a T cell receptor beta chain, and combinations thereof.

103. The method of claim 101, wherein step (b) comprises determining: a sequence encoding CDR3 of the T cell receptor alpha chain, a sequence encoding CDR3 of the T cell receptor beta chain, and combinations thereof.

104. The method of claim 103, wherein step (b) further comprises determining: a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor alpha chain, a sequence encoding one or both of CDR1 and CDR2 of the T cell receptor beta chain, and combinations thereof.

~~105. The method of claim 103, wherein step (b) further comprises determining: a sequence encoding a full-length variable domain of the T-cell receptor alpha chain, a sequence encoding a full-length variable domain of the T-cell receptor beta chain, and combinations thereof.~~

~~106. The method of claim 101, wherein the immune cell receptor is a B-cell receptor an immunoglobulin kappa light chain, an immunoglobulin lambda light chain, an immunoglobulin heavy chain, and combinations thereof.~~

~~107. The method of claim 106, wherein step (b) comprises determining: a sequence encoding CDR3 of the immunoglobulin kappa light chain, a sequence encoding CDR3 of immunoglobulin lambda light chain, a sequence encoding CDR3 of the immunoglobulin heavy chain, and combinations thereof.~~

~~108. The method of claim 107, wherein step (b) further comprises determining: a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin kappa light chain, a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin lambda light chain, a sequence encoding one or both of CDR1 and CDR2 of the immunoglobulin heavy chain, and combinations thereof.~~

~~109. The method of claim 107, wherein step (b) further comprises determining: a sequence encoding a full-length variable domain of the immunoglobulin kappa light chain, a sequence encoding a full-length variable domain of the immunoglobulin lambda light chain, a sequence encoding a full-length variable domain of the immunoglobulin heavy chain, and combinations thereof.~~

~~110. The method of any one of claims 75-109, wherein step (b) comprises extending an end of the capture probe using the nucleic acid encoding the immune cell receptor as a template, thereby generating an extended capture probe.~~

~~111. The method of claim 110, wherein step (b) comprises extending a 3' end of the capture probe.~~

~~112. The method of claim 110 or 111, wherein step (b) further comprises generating a second strand of nucleic acid that comprises (i) a sequence that is complementary to all or a portion of the spatial barcode, and (ii) a sequence that corresponds to all or a portion of the sequence of the nucleic acid encoding the immune cell receptor.~~

~~113. The method of any one of claims 75-112, where the capture probe further comprises a cleavage domain, a functional domain, a unique molecular identifier, or any combination thereof.~~

~~114. The method of any one of claims 75-87, wherein the capture probe further comprises a functional domain.~~

~~115. The method of claim 114, wherein step (b) further comprises generating a second strand of nucleic acid that comprises (i) a sequence that is complementary to all or a portion of the functional domain, (ii) a sequence that is complementary to all or a portion of the spatial barcode, and (iii) a sequence that corresponds to all or a portion of the sequence of the nucleic acid encoding the immune cell receptor.~~

~~116. The method of any one of claims 75-115, wherein the method further comprises enriching the nucleic acid encoding the immune cell receptor.~~

~~117. The method of claim 116, wherein enriching comprises hybridizing a plurality of hybridization probes to the nucleic acid encoding the immune cell receptor, wherein a hybridization probe comprises (i) a sequence complementary to a portion of the nucleic acid encoding the immune cell receptor and (ii) a binding moiety that interacts with a capture moiety.~~

~~118. The method of claim 117, wherein the binding moiety comprises biotin and the capture moiety comprises streptavidin.~~

~~119. The method of any one of claims 116-118, wherein enriching the nucleic acid encoding the immune cell receptor of the immune cell receptor further comprises one or more blocking probes.~~

120. The method of claim 119, wherein the one or more blocking probes comprises a sequence having at least 80% identity to SEQ ID NO: 639.

121. The method of claim 119, wherein the one or more blocking probes comprises a sequence having at least 80% identity to SEQ ID NO: 640.

122. The method of any one of claims 75-121, wherein the method further comprises amplifying the nucleic acid encoding an immune cell receptor, or a complement thereof, using (i) a first primer comprising all or a portion of the functional domain, wherein the functional domain is 5' to the spatial barcode in the second strand of nucleic acid, and (ii) a second primer comprising a sequence that is substantially complementary to a portion of a sequence encoding a variable region of the immune cell receptor.

123. The method of claim 122, further comprising amplifying the nucleic acid encoding the immune cell receptor, or a complement thereof, using (i) the first primer comprising all or a portion of the functional domain, wherein the functional domain is 5' to the spatial barcode, and (ii) a third primer comprising a sequence that is substantially complementary to a portion of the nucleic acid sequence encoding a variable region of the immune cell receptor, wherein the third primer is 5' to the second primer.

124. The method of any one of claims 75-123, wherein the biological sample comprises a tissue sample.

125. The method of claim 124, wherein the tissue sample is a tissue section.

126. The method of claim 125, wherein the tissue section is a fixed tissue section.

127. The method of claim 126, wherein the fixed tissue section is a formalin-fixed paraffin-embedded tissue section.

128. The method of any one of claims 125-127, wherein the tissue section comprises a tumor region.

~~129. The method of any one of claims 75-128, wherein the nucleic acid encoding the immune cell receptor comprises RNA.~~

~~130. The method of claim 129, wherein the RNA is mRNA.~~

~~131. The method of any one of claims 75-130, wherein the nucleic acid encoding the immune cell receptor comprises DNA.~~

~~132. The method of claim 131, wherein the DNA is genomic DNA.~~

~~133. The method of any one of claims 75-132, wherein the method further comprises, prior to step (b), contacting the biological sample with ribosomal RNA depletion probes and mitochondrial RNA depletion probes.~~

~~134. The method of any one of claims 75-133, wherein the method further comprises imaging the biological sample.~~

~~135. The method of any one of claims 75-134, wherein the determining in step (b) comprises sequencing (i) all or a portion of the sequence of the spatial barcode or a complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor or a complement thereof.~~

~~136. The method of any one of claims 75-135, wherein step (b) comprises determining the presence of the immune cell receptor at a location in the biological sample.~~

~~137. The method of any one of claims 75-135, wherein step (b) comprises determining the abundance of the immune cell receptor at a location in the biological sample.~~

~~138. The method of any one of claims 75-135, wherein step (b) comprises determining the presence and abundance of the immune cell receptor at a location in the biological sample.~~

~~139. The method of any one of claims 75-135, wherein step (b) comprises determining the presence of two or more immune cell receptors at a location in the biological sample.~~

~~140. The method of any one of claims 75-135, wherein step (b) comprises determining the abundance of two or more immune cell receptors at a location in the biological sample.~~

~~141. The method of any one of claims 75-135, wherein step (b) comprises determining the presence and abundance of two or more immune cell receptors at a location in the biological sample.~~

~~142. The method of any one of claims 139-141, wherein the method further comprises comparing the two or more immune cell receptors.~~

~~143. The method of any one of claims 139-142, wherein the two or more immune cell clonotypes are each an immune cell receptor of a B cell.~~

~~144. The method of any one of claims 139-142, wherein the two or more immune cell clonotypes are each an immune cell receptor of a T cell.~~

~~145. The method of any one of claims 139-142, wherein the two or more immune cell clonotypes comprise at least one immune cell receptor of a T cell and at least one immune cell receptor from a B cell.~~

~~146. An array comprising 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 that binds to a nucleic acid encoding an immune cell receptor of an immune cell clonotype.~~

~~147. The array of claim 146, wherein the immune cell clonotype is a T cell clonotype.~~

~~148. The array of claim 147, wherein the immune cell receptor is a T cell receptor alpha chain.~~

~~149. The array of claim 148, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the T cell receptor alpha chain.~~

~~150. The array of claim 147, wherein the immune cell receptor is a T cell receptor beta chain.~~

~~151. The array of claim 150, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the T cell receptor beta chain.~~

~~152. The array of claim 146, wherein the immune cell clonotype is a B cell clonotype.~~

~~153. The array of claim 152, wherein the immune cell receptor is an immunoglobulin kappa light chain.~~

~~154. The array of claim 153, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin kappa light chain.~~

~~155. The array of claim 152, wherein the immune cell receptor is an immunoglobulin lambda light chain.~~

~~156. The array of claim 155, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin lambda light chain.~~

~~157. The array of claim 152, wherein the immune cell receptor is an immunoglobulin heavy chain.~~

~~158. The array of claim 157, wherein the capture domain binds specifically to a nucleic acid sequence encoding a constant region of the immunoglobulin heavy chain.~~

~~159. The array of any one of claims 146-158, where the capture probe further comprises a cleavage domain, a functional domain, a unique molecular identifier, or any combination thereof.~~

~~160. A kit comprising:~~

~~an array of any one of claims 146-159;~~

~~one or more hybridization probes, wherein a hybridization probe comprises (i) a sequence substantially complementary to a nucleic acid encoding an immune cell receptor and (ii) a binding moiety that interacts with a capturing moiety; and~~

~~one or more blocking probes.~~

1. A method for determining the presence of an immune cell clonotype at a location 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 of the plurality of capture probes comprises (i) a spatial barcode and (ii) a capture domain that hybridizes to a nucleic acid encoding an immune cell receptor of the immune cell clonotype;

(b) extending the capture probe using the nucleic acid encoding the immune cell receptor as a template to generate an extended capture probe;

(c) hybridizing one or more probes to the extended capture probe, or a complement thereof, in a portion encoding a constant region of the immune cell receptor of the immune cell clonotype,

(d) enriching the extended capture probe or the complement thereof; and

(e) determining (i) the sequence of the spatial barcode or a complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor of the immune cell clonotype or a complement thereof, and using the determined sequences of (i) and (ii) to determine the presence of the immune cell clonotype at a location in the biological sample.

2. The method of claim 1, wherein the capture probe further comprises a cleavage domain, one or more functional domains, a unique molecular identifier, and combinations thereof.

3. The method of claim 1, wherein the capture domain comprises a poly(T) sequence.

4. The method of claim 1, wherein the one or more probes comprises a binding moiety capable of binding a capture moiety.

5. The method of claim 4, wherein the enriching step is performed via an interaction between the binding moiety in the one or more probes and the capture moiety.

6. The method of any one of claims 1-5, wherein the immune cell clonotype is a T cell clonotype, the immune cell receptor of the immune cell clonotype comprises a T cell receptor alpha chain, and the one or more probes hybridizes to a nucleic acid sequence encoding a constant region of the T cell receptor alpha chain, or a complement thereof.

7. The method of claim 6, wherein step (e) comprises determining a sequence encoding one or more of CDR1, CDR2, and CDR3 of the T cell receptor alpha chain and, optionally, determining a sequence encoding a full-length variable domain of the T cell receptor alpha chain.

8. The method of any one of claims 1-5, wherein the immune cell clonotype is a T cell clonotype, the immune cell receptor of the immune cell clonotype comprises a T cell receptor beta chain, and the one or more probes hybridizes to a nucleic acid sequence encoding a constant region of the T cell receptor beta chain, or a complement thereof.

9. The method of claim 8, wherein step (e) comprises determining a sequence encoding one or more of CDR1, CDR2, and CDR3 of the T cell receptor beta chain, and optionally, determining a sequence encoding a full-length variable domain of the T cell receptor beta chain.

10. The method of any one of claims 1-5, wherein the immune cell clonotype is a B cell clonotype, the immune cell receptor of the immune cell clonotype comprises an immunoglobulin kappa light chain, and the one or more probes hybridizes to a nucleic acid sequence encoding a constant region of the immunoglobulin kappa light chain, or a complement thereof.

11. The method of claim 10, wherein step (e) comprises determining a sequence encoding one or more of CDR1, CDR2, and CDR3 of the immunoglobulin kappa light chain, and optionally, determining a sequence encoding a full-length variable domain of the immunoglobulin kappa light chain.

12. The method of any one of claims 1-5, wherein the immune cell clonotype is a B cell clonotype, the immune cell receptor of the immune cell clonotype comprises an immunoglobulin lambda light chain, and the one or more probes hybridizes to a nucleic acid

sequence encoding a constant region of the immunoglobulin lambda light chain, or a complement thereof.

13. The method of claim 12, wherein step (e) comprises determining a sequence encoding one or more of CDR1, CDR2, and CDR3 of the immunoglobulin lambda light chain, and optionally, determining a sequence encoding full-length variable domain of the immunoglobulin lambda light chain.

14. The method of any one of claims 1-5, wherein the immune cell clonotype is a B cell clonotype, the immune cell receptor of the immune cell clonotype comprises an immunoglobulin heavy chain, and the one or more probes hybridizes to a nucleic acid sequence encoding a constant region of the immunoglobulin heavy chain, or a complement thereof.

15. The method of claim 14, wherein step (e) comprises determining a sequence encoding one or more of CDR1, CDR2, and CDR3 of the immunoglobulin heavy chain, and optionally, determining a sequence encoding a full-length variable domain of the immunoglobulin heavy chain.

16. The method of claim 4, wherein the binding moiety comprises biotin and the capture moiety comprises streptavidin.

17. The method of any one of claims 1-5, further comprising generating the complement of the extended capture probe using the extended capture probe as a template, wherein the complement of the extended capture probe comprises (i) a sequence that is complementary to the spatial barcode, and (ii) a sequence that corresponds to all or a portion of the sequence of the nucleic acid encoding the immune cell receptor of the immune cell clonotype.

18. The method of any one of claim 1-5, wherein the biological sample comprises a tissue sample, optionally wherein the tissue sample is a tissue section, optionally, wherein the tissue section is a fresh-frozen tissue section.

19. The method of any one of claims 1-5, wherein the nucleic acid encoding the immune cell receptor of the immune cell clonotype comprises DNA or mRNA.

20. The method of any one of claims 1-5, wherein the method further comprises imaging the biological sample.

21. The method of any one of claims 1-5, wherein step (e) comprises sequencing the extended capture probe or the complement thereof to determine (i) the sequence of the spatial barcode, or the complement thereof, and (ii) all or a portion of the sequence of the nucleic acid encoding the immune cell receptor of the immune cell clonotype or the complement thereof.

22. The method of claim 21, wherein the sequencing comprises long read sequencing.

23. The method of any one of claims 1-5, wherein the method further comprises after step (d), performing an enrichment polymerase chain reaction using i) a first primer complementary to an adaptor domain of the capture probe, and ii) a second primer complementary to a portion of a nucleic acid sequence encoding a variable region of the immune cell receptor of the immune cell clonotype.

24. The method of claim 23, wherein the second primer is complementary to a nucleic acid sequence 5' to the sequence encoding CDR3 of the immune cell receptor of the immune cell clonotype.

25. The method of claim 23, wherein the immune cell clonotype is a T cell clonotype, and the immune cell receptor is a T cell receptor.

26. The method of any one of claims 1-5, wherein the method comprises determining the presence of two or more immune cell clonotypes at a location in the biological sample, and optionally, wherein the method further comprises comparing the two or more immune cell clonotypes.

27. The method of claim 17, wherein the step of generating the complement of the extended capture probe comprises use of a template switch oligonucleotide.

28. The method of any one of claims 1-5, wherein the extending in step (b) generates an extended capture probe comprising a sequence encoding a CDR3, or a complement thereof, of the immune cell receptor of the immune cell clonotype.