What is claimed is:

1. A nucleic acid array for detecting spatial information of a nucleic acid in a sample, which comprises a solid support with multiple kinds of carrier sequences attached to its surface, in which each kind of carrier sequence occupies a different position in the array, said each kind of carrier sequence comprises a plurality of copies of the carrier sequence, and the carrier sequence in the direction from 5' to 3' comprises a positioning sequence and a first immobilization sequence, wherein,

the positioning sequence has a unique nucleotide sequence corresponding to the position of the kind of carrier sequence on the array;

the first immobilization sequence allows annealing to its complementary nucleotide sequence and initiating an extension reaction;

wherein the multiple copies of carrier sequence are an amplification product formed by amplification using a complementary sequence of the carrier sequence as a template;

and wherein said each kind of carrier sequence comprising the same positioning sequence occupies an area having a diameter of less than 1 micrometer.

2. The nucleic acid array according to claim 1, wherein the nucleic acid array further comprises a first nucleic acid molecule, the first nucleic acid molecule in the direction from 5' to 3' comprises: a complement of the first immobilization sequence and a complement of the positioning sequence, and the first nucleic acid molecule hybridizes to the first immobilization sequence and the positioning sequence of the carrier sequence to form a double strand;

and wherein each copy of each kind of carrier sequence comprises a first nucleic acid molecule hybridized therewith.

3. The nucleic acid array according to claim 2, wherein the nucleic acid array further comprises a second nucleic acid molecule, the second nucleic acid molecule is ligated to the first nucleic acid molecule, and the second nucleic acid molecule comprises a capture sequence;

the capture sequence is capable of hybridizing with the whole or part of a nucleic acid to be captured, and comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and, the capture sequence has a free 3' end to enable the second nucleic acid molecule to function as an extension primer;

and wherein each first nucleic acid molecule is ligated to the second nucleic acid molecule.

4. The nucleic acid array according to claim 2, wherein each carrier sequence further comprises a second immobilization sequence at its 5' end, and the second immobilization sequence allows annealing to its complementary nucleotide sequence;

and wherein the second immobilization sequence allows annealing to its complementary nucleotide sequence and initiating an extension reaction.

5. The nucleic acid array according to claim 4, wherein the nucleic acid array further comprises a second nucleic acid molecule, and the second nucleic acid molecule in the direction from 5' to 3' comprises a complement of the second immobilization sequence and a capture sequence;

the complement of second immobilization sequence hybridizes to the second immobilization sequence of the carrier sequence to form a double strand;

the capture sequence is capable of hybridizing with the whole or part of the nucleic acid to be captured, and comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and, the capture sequence has a free 3' end to enable the second nucleic acid molecule to function as an extension primer;

and wherein each copy of each kind of carrier sequence comprises a second nucleic acid molecule hybridized therewith.

6. The nucleic acid array according to any one of claims 1 to 5, wherein the amplification is selected from rolling circle amplification (RCA), bridge PCR amplification, multiple strand displacement amplification (MDA) or emulsion PCR amplification.

7. The nucleic acid array according to any one of claims 1 to 5, wherein the multiple copies of carrier sequence are a DNA nanoball (DNB) formed by a concatemer of the carrier sequence; wherein the multiple copies of carrier sequence are a DNB formed by rolling circle amplification using a complementary sequence of the carrier sequence as a template.

8. The nucleic acid array according to any one of claims 1 to 5, wherein the multiple copies of carrier sequence are a DNA cluster formed by a clone population of the carrier sequence.

9. The nucleic acid array according to claim 8, wherein:

(i) the multiple copies of carrier sequence are a DNA cluster formed by bridge PCR amplification using a complementary sequence of the carrier sequence as a template;

(ii) the multiple copies of carrier sequence are a DNA cluster formed by emulsion PCR amplification using a complementary sequence of the carrier sequence as a template; or,

(iii) the multiple copies of carrier sequence are a DNA cluster formed by multiple strand displacement amplification using a complementary sequence of the carrier sequence as a template.

10. The nucleic acid array according to claim 2, wherein the first nucleic acid molecule further comprises a unique molecular identifier (UMI) sequence, and the UMI sequence is located at the 5' end of the complement of first immobilization sequence;

the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5 nucleotides N, each N is independently any one of A, C, G and T;

and wherein the UMI sequence contained in each first nucleic acid molecule is different from each other.

11. The nucleic acid array according to claim 3 or 5, wherein the second nucleic acid molecule further comprises a UMI sequence, and the UMI sequence is located at the 5' end of the capture sequence;

the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5 nucleotides N, each N is independently any one of A, C, G and T;

and wherein the UMI sequence contained in each second nucleic acid molecule is different from each other.

12. The nucleic acid array according to any one of claims 1 to 11, wherein the solid support is a sequencing chip.

13. The nucleic acid array according to claim 3 or 5, wherein the oligonucleotide sequence capable of capturing mRNA comprises a poly-T oligonucleotide sequence.

14. The nucleic acid array according to claim 1, wherein the carrier sequence further comprises a capture sequence template located upstream of the positioning sequence, the capture sequence template comprises a complementary sequence of the capture sequence, and the capture sequence is capable of hybridizing with the whole or part of the nucleic acid to be captured, which comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid;

and, the first immobilization sequence of the carrier sequence also comprises a cleavage site, and the cleavage is selected from enzymatic cleavage with nicking enzyme, enzymatic cleavage with USER enzyme, photocleavage, chemical cleavage or CRISPR-based cleavage;

and, the nucleic acid array further comprises a first nucleic acid molecule, and the first nucleic acid molecule in the direction from 5' to 3' comprises: a binding region, a cleavage region, and a carrier sequence complementary region,

the binding region comprises a linker capable of ligating to the surface of the solid support;

the cleavage region comprises a cleavage site;

the carrier sequence complementary region comprises a sequence that is complementary to the carrier sequence, and in the direction from 5' to 3', comprises: a complement of the first immobilization sequence, a complement of the positioning sequence, and a capture sequence; and, the capture sequence has a free 3' end to enable the first nucleic acid molecule to function as an extension primer;

and, the carrier sequence complementary region of the first nucleic acid molecule hybridizes to the carrier sequence to form a double strand;

and wherein each copy of each kind of carrier sequence comprises a first nucleic acid molecule hybridized therewith.

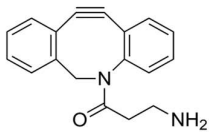
15. The nucleic acid array according to claim 14, wherein the carrier sequence further comprises a complement of UMI sequence located downstream of the capture sequence template and upstream of the first immobilization sequence, the complement of UMI sequence is complementary to the UMI sequence, the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5nucleotides N, and each N is independently any one of A, C, G and T;

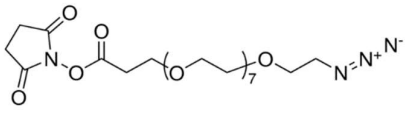
and, the carrier sequence complementary region of the first nucleic acid molecule further comprises the UMI sequence located upstream of the capture sequence and downstream of the complement of first immobilization sequence;

and wherein each copy of each kind of carrier sequence (i.e., carrier sequences comprising the same positioning sequence) comprises a complement of UMI sequence different from each other.

16. The nucleic acid array according to claim 14 or 15, wherein the linker of the first nucleic acid molecule is a linking group capable of coupling with an activating group, and the surface of the solid support is modified by the activating group.

17. The nucleic acid array according to claim 16, wherein the linker comprises -SH, -DBCO or -NHS.

18. The nucleic acid array according to claim 16, wherein the linker is 

(DBCO), and 

(Azido-dPEG®8-NHS ester) is attached to the surface of the solid support.

19. The nucleic acid array according to any one of claims 14 to 18, wherein the cleavage site contained in the cleavage region of the first nucleic acid molecule is a site where controlled cleavage is performed by a chemical, enzymatic, or photochemical method.

20. The nucleic acid array according to claim 19, wherein the cleavage region of the first nucleic acid molecule is different from the cleavage site contained in the first immobilization sequence of the carrier sequence.

21. The nucleic acid array according to any one of claims 14 to 20, wherein the solid support is a sequencing chip.

22. The nucleic acid array according to any one of claims 14 to 21, wherein the oligonucleotide sequence capable of capturing mRNA comprises a poly-T oligonucleotide sequence.

23. A kit, which comprises: (i) the nucleic acid array according to any one of claims 1 to 13, wherein the nucleic acid array does not comprise a second nucleic acid molecule; and, (ii) a second nucleic acid molecule, wherein the second nucleic acid molecule in the direction from 5' to 3' comprises an immobilization region and a capture sequence;

the capture sequence is capable of hybridizing with the whole or part of the nucleic acid to be captured, and comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and, the capture sequence has a free 3' end to enable the second nucleic acid molecule to function as an extension primer.

24. The kit according to claim 23, wherein the kit comprises the nucleic acid array according to claim 2, and the immobilization region of the second nucleic acid molecule comprises a double-stranded nucleic acid sequence.

25. The kit according to claim 23, wherein the kit comprises the nucleic acid array according to claim 4, and the immobilization region of the second nucleic acid molecule comprises a complement of second immobilization sequence.

26. The kit according to any one of claims 23 to 25, wherein the first nucleic acid molecule further comprises a unique molecular identifier (UMI) sequence, and the UMI sequence is located at the 5' end of the complement of first immobilization sequence, or the second nucleic acid molecule further comprises a UMI sequence, and the UMI sequence is located at the 5' end of the capture sequence;

and wherein the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5 nucleotides N, each N is independently any one of A, C, G and T.

27. A method for generating a nucleic acid array for detecting spatial information of a nucleic acid in a biological sample, which comprises the following steps:

(1) providing multiple kinds of carrier sequences, each kind of carrier sequence comprises a plurality of copies of the carrier sequence, and the carrier sequence in the direction from 5' to 3' comprises a positioning sequence and a first immobilization sequence,

the positioning sequence has a unique nucleotide sequence corresponding to the position of the kind of carrier sequence on the array;

the first immobilization sequence allows annealing to its complementary nucleotide sequence and initiating an extension reaction;

(2) ligating the multiple kinds of carrier sequences to a surface of a solid support;

(3) providing a first primer, and perform a primer extension reaction by using the carrier sequence as a template, so that a region of the first immobilization sequence and the positioning sequence of the carrier sequence forms a double strand, wherein the strand that hybridizes to the carrier sequence is a first nucleic acid molecule, the first nucleic acid molecule in the direction from 5' to 3' comprises a complementary sequence of the first immobilization sequence and a complementary sequence of the positioning sequence; wherein, the first primer comprises a first immobilization sequence complementary region at its 3' end, the first immobilization sequence complementary region comprises a complementary sequence of the first immobilization sequence or a fragment thereof, and has a free 3' end;

and wherein in step (1), the multiple kinds of carrier sequences are provided by the following steps:

(i) providing multiple kinds of carrier sequence templates, the carrier sequence template comprising a complementary sequence of the carrier sequence;

(ii) perform a nucleic acid amplification reaction by using each kind of carrier sequence template as a template, to obtain an amplification product of each kind of carrier sequence template, the amplification product comprising a plurality of copies of the carrier sequence;

and wherein said each kind of carrier sequence comprising the same positioning sequence occupies an area having a diameter of less than 1 micrometer.

28. The method according to claim 27, wherein rolling circle amplification is performed to obtain a DNB formed by a concatemer of the carrier sequence.

29. The method according to claim 27, wherein bridge PCR amplification, emulsion PCR amplification or multiple strand displacement amplification is performed to obtain a DNA cluster formed by a clone population of the carrier sequence.

30. The method according to any one of claims 27-29, wherein the method further comprises the following steps:

(4) providing a second nucleic acid molecule, the second nucleic acid molecule comprising a capture sequence;

the capture sequence is capable of hybridizing with the whole or part of the nucleic acid to be captured, which comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and, the capture sequence has a free 3' end to enable the second nucleic acid molecule to function as an extension primer,

(5) ligating the second nucleic acid molecule to the first nucleic acid molecule.

31. The method according to claim 30, wherein in step (5), using a ligase to ligate the second nucleic acid molecule to the first nucleic acid molecule.

32. The method according to claim 30 or 31, wherein the second nucleic acid molecule in the direction from 5' to 3' comprises an immobilization region and a capture sequence, and the immobilization region comprises a double-stranded DNA sequence.

33. The method according to claim 30 or 31, wherein each carrier sequence further comprises a second immobilization sequence at its 5' end, and the second immobilization sequence allows annealing to its complementary nucleotide sequence; the method further comprises the following steps:

(4) providing a second nucleic acid molecule, the second nucleic acid molecule in the direction from 5' to 3' comprising a complement of second immobilization sequence and a capture sequence;

the complement of second immobilization sequence allows hybridization to its complementary nucleotide sequence;

the capture sequence is capable of hybridizing with the whole or part of the nucleic acid to be captured, and comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and, the capture sequence has a free 3' end to enable the second nucleic acid molecule to function as an extension primer;

(5) hybridizing the complement of second immobilization sequence with the second immobilization sequence under a condition that allow annealing, thereby ligating the second nucleic acid molecule to the carrier sequence.

34. The method according to claim 33, further comprising:

(6) ligating the first nucleic acid molecule and the second nucleic acid molecule that are hybridized to the carrier sequence respectively.

35. The method according to claim 34, wherein using a ligase to ligate the second nucleic acid molecule to the first nucleic acid molecule.

36. The method according to any one of claims 30 to 35, wherein, in step (3), the first primer further comprises a unique molecular identifier (UMI) sequence at the 5' end of its first immobilization sequence complementary region, so that the first nucleic acid molecule comprises the UMI sequence at the 5' end of its complement of first immobilization sequence; or, in step (4), the second nucleic acid molecule further comprises a UMI sequence, and the UMI sequence is located at the 5' end of the capture sequence;

and wherein the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5 nucleotides N, each N is independently any one of A, C, G and T.

37. The method according to any one of claims 27-29, wherein:

in step (1), the carrier sequence further comprises a capture sequence template located upstream of the positioning sequence, the capture sequence template comprises a complementary sequence of the capture sequence, and the capture sequence can hybridize to the whole or part of the nucleic acid to be captured, which comprises: (a) an oligonucleotide sequence capable of capturing mRNA; (b) a random or degenerate oligonucleotide sequence; or, (c) a specific sequence for a specific target nucleic acid; and the first immobilization sequence of the carrier sequence also comprises a cleavage site, and the cleavage is selected from enzymatic cleavage with nicking

enzyme, enzymatic cleavage with USER enzyme, photocleavage, chemical cleavage or CRISPR-based cleavage;

in step (3), a region of the first immobilization sequence, the positioning sequence and the capture sequence template of the carrier sequence forms a double strand, so that the first nucleic acid molecule in the direction from 5' to 3' comprises a complement of first immobilization sequence, a complement of positioning sequence and a capture sequence; wherein,

the first primer in the direction from 5' to 3' comprises a binding region, an cleavage region, and a first immobilization sequence complementary region, the binding region comprises a linker capable of ligating to the surface of the solid support, and the cleavage region comprises a cleavage site;

and, the method further comprises the following steps:

(4) ligating the first primer to the surface of the solid support; wherein, steps (3) and (4) are performed in any order.

38. The method according to claim 37, wherein each kind of carrier sequence is a DNB formed by a concatemer of the multiple copies of carrier sequence.

39. The method according to claim 37, which further comprising:

(5) performing cleavage at the cleavage site contained in the first immobilization sequence of the carrier sequence to digest the carrier sequence, so that the extension product in step (3) is separated from the template where such extension product is formed (i.e., carrier sequence), and the first nucleic acid molecule is therefore ligated to the surface of the solid support.

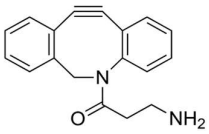
40. The method according to any one of claims 37-39, wherein, in step (1), the cleavage site contained in the first immobilization sequence is a cleavage site of nicking enzyme.

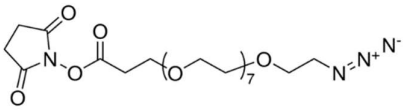
41. The method according to any one of claims 37 to 40, wherein, in step (1), the carrier sequence further comprises a complement of UMI sequence located downstream of the capture sequence template and upstream of the first immobilization sequence, the complement of UMI sequence is complementary to a UMI sequence, and the UMI sequence is a nucleotide sequence consisting of at least 1, at least 2, at least 3, at least 4, or at least 5 nucleotides N, each N is independently any one of A, C, G and T;

and, in step (3), a region of the first immobilization sequence, the positioning sequence, the capture sequence template, and the complement of UMI sequence of the carrier sequence forms a double strand, so that the first nucleic acid molecule in the direction from 5' to 3' comprises the complement of first immobilization sequence, the complement of positioning sequence and the capture sequence, and the UMI sequence located upstream of the capture sequence and downstream of the complement of first immobilization sequence.

42. The method according to any one of claims 37 to 41, wherein the linker of the first primer is a linking group capable of coupling with an activating group, and the surface of the solid support is modified by the activating group.

43. The method according to claim 42, wherein the linker comprises -SH, -DBCO or -NHS.

44. The method according to claim 42, wherein the linker is 

(DBCO), and 

(Azido-dPEG®8-NHS ester) is attached to the surface of the solid support.

45. The method according to any one of claims 37 to 44, wherein the cleavage site contained in the cleavage region of the first primer is a site where controlled cleavage is performed by a chemical, enzymatic, or photochemical method;

and wherein the cleavage region of the first primer is different from the cleavage site contained in the first immobilization sequence of the carrier sequence.

46. The method according to any one of claims 30, 33, 37, wherein the oligonucleotide sequence capable of capturing mRNA comprises a poly-T oligonucleotide sequence.

47. The method according to any one of claims 27 to 46, wherein the solid support is a sequencing chip.

48. The method according to any one of claims 27 to 47, wherein, in step (3), while performing an extension reaction, the carrier sequence is sequenced to obtain the sequence information of the positioning sequence contained in the carrier sequence.

49. The method according to any one of claims 27 to 48, wherein, before step (3), a step of sequencing the carrier sequence is comprised.

50. A nucleic acid array prepared by the method according to any one of claims 30 to 36;

wherein the nucleic acid array is as defined in any one of claims 3 and 5-13.

51. A nucleic acid array prepared by the method according to any one of claims 37 to 45.

wherein the nucleic acid array is as defined in any one of claims 14 to 22.

52. A method for detecting spatial information of a nucleic acid in a sample, which comprises the following steps:

(1) providing the nucleic acid array according to claim 3 or 5, or obtaining a nucleic acid array by the method according to any one of claims 30 to 36; wherein,

the nucleic acid array comprises multiple kinds of carrier sequences attached to a surface of a solid support, each kind of carrier sequence occupies a different position in the array, and said each kind of carrier sequence comprises a plurality of copies of the carrier sequence;

each carrier sequence comprises a first nucleic acid molecule hybridized therewith, and the first nucleic acid molecule is ligated to a second nucleic acid molecule, or each carrier sequence comprises a first nucleic acid molecule and a second nucleic acid molecule that are hybridized therewith;

the first nucleic acid molecule comprises a complement of positioning sequence corresponding to the position of the kind of carrier sequence on the array,

the second nucleic acid molecule comprises a capture sequence capable of capturing the nucleic acid in the sample;

and wherein said each kind of carrier sequence comprising the same positioning sequence occupies an area having a diameter of less than 1 micrometer;

(2) contacting the nucleic acid array with a sample to be tested under a condition that allows annealing, so that the nucleic acid in the sample to be tested anneals to the capture sequence of the second nucleic acid molecule, and thus the position of the nucleic acid is correlated with the position of the carrier sequence on the nucleic acid array;

(3) performing (i), (ii) or (iii):

(i) when the first nucleic acid molecule and the second nucleic acid molecule are not ligated to each other, ligating the first nucleic acid molecule and the second nucleic acid molecule that are hybridized to each carrier sequence; and performing one or both of (i-a) and (i-b):

(i-a) performing a primer extension reaction by using the ligated first and second nucleic acid molecules as a primer, and using the captured nucleic acid molecule as a template under a condition that allows the primer extension, so as to produce an extension product, in which the strand that hybridizes to the captured nucleic acid molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag; and,

(i-b) performing a primer extension reaction by using the captured nucleic acid molecule as a primer, and using the ligated first and second nucleic acid molecules as a template under a condition that allows the primer extension, so as to produce an extended captured nucleic acid molecule, in which the extended captured nucleic acid has the positioning sequence as a spatial information tag;

or, (ii) when the first nucleic acid molecule and the second nucleic acid molecule are not ligated to each other, performing a primer extension reaction by using the second nucleic acid molecule as a primer and using the captured nucleic acid molecule as a template under a condition that allows the primer extension, to produce an extended second nucleic acid molecule, in which the extended second nucleic acid molecule comprises a complementary sequence of the captured nucleic acid; ligating the first nucleic acid molecule and the extended second nucleic acid molecule that are hybridized to each carrier sequence, in which the extended second nucleic acid molecule which is ligated to the first nucleic acid molecule has the complement of positioning contained in the first nucleic acid molecule as a spatial information tag;

or, (iii) when the first nucleic acid molecule and the second nucleic acid molecule are ligated to each other, performing one or both of (iii-a) and (iii-b):

(iii-a) performing a primer extension reaction by using the ligated first and second nucleic acid molecules as a primer, and using the captured nucleic acid molecule as a template under a condition that allows the primer extension, to produce an extension product, in which the strand

that hybridizes to the captured nucleic acid molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag; and,

(iii-b) performing a primer extension reaction by using the captured nucleic acid molecule as a primer, and using the ligated first and second connected nucleic acid molecules as a template under a condition that allows the primer extension, to produce an extended captured nucleic acid molecule, in which the extended captured nucleic acid molecule has the positioning sequence as a spatial information tag;

(4) releasing at least part of the nucleic acid molecules labeled with spatial information tags from the surface of the array, wherein the part comprises the positioning sequence or its complementary strand and the captured nucleic acid molecule or its complementary strand; and

(5) directly or indirectly analyzing the sequence of the nucleic acid molecule released in step (4);

wherein the spatial information of the nucleic acid comprises the location, distribution or expression of the nucleic acid.

53. The method according to claim 52, which is used to detect a transcriptome in a sample, wherein:

(a) in step (3)(i), generating a cDNA molecule from the captured RNA molecule by using the ligated first and second nucleic acid molecules as a reverse transcription primer, the cDNA molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag; or, in step (3)(ii), generating a cDNA molecule from the captured RNA molecule by using the second nucleic acid molecule as a reverse transcription primer, ligating the first nucleic acid molecule and the cDNA molecule that hybridizes to each carrier sequence, to generate a cDNA molecule having the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag; or, in step (3)(iii), generating a cDNA molecule from the captured RNA molecule by using the ligated first and second nucleic acid molecules as a reverse transcription primer, the cDNA molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag;

and,

(b) in step (4), releasing at least part of the cDNA molecules or their amplicons from the surface of the array, wherein the released nucleic acid molecule may be the first or second strand

of the cDNA molecule or an amplicon thereof, and wherein the part comprises the positioning sequence or its complementary strand;

and wherein in step (1), the capture sequence comprises an oligonucleotide sequence capable of capturing mRNA.

54. A method for detecting spatial information of a nucleic acid in a sample, which comprises the following steps:

(1) providing the nucleic acid array according to any one of claims 14 to 22, or obtaining a nucleic acid array by the method according to any one of claims 37 to 45; wherein the nucleic acid array comprises a solid support with multiple kinds of carrier sequences attached to its surface, each kind of carrier sequence occupies a different position in the array, and said each kind of carrier sequence comprises a plurality of copies of the carrier sequence;

each carrier sequence comprises a first nucleic acid molecule hybridized therewith, and the first nucleic acid molecule comprises a complement of positioning sequence corresponding to the position of the kind of carrier sequence on the array and a capture sequence capable of capturing the nucleic acid in the sample;

and wherein said each kind of carrier sequence comprising the same positioning sequence occupies an area having a diameter of less than 1 micrometer;(2) contacting the nucleic acid array with the sample to be tested under a condition that allows annealing, so that the nucleic acid in the sample to be tested anneals to the capture sequence of the first nucleic acid molecule, and thus the position of the nucleic acid is correlated with the position of the first nucleic acid molecule on the nucleic acid array;

(3) performing a primer extension reaction by using the first nucleic acid molecule as a primer and using the captured nucleic acid molecule as a template under a condition that allows the primer extension, to produce an extension product, in which the strand that hybridizes to the captured nucleic acid molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag;

(4) releasing at least part of the nucleic acid molecules labeled with the spatial information tags from the surface of the array, wherein the part comprises the positioning sequence or its complementary strand and the captured nucleic acid molecule or its complementary strand; and

(5) directly or indirectly analyzing the sequence of the nucleic acid molecule released in step (4);

and wherein the spatial information of the nucleic acid comprises the location, distribution or expression of the nucleic acid.

55. The method according to claim 54, in which the method is used to detect a transcriptome in a sample, wherein:

in step (3), generating a cDNA molecule from the captured RNA molecule by using the first nucleic acid molecule as an RT primer, the cDNA molecule has the complement of positioning sequence contained in the first nucleic acid molecule as a spatial information tag;

in step (4), releasing at least part of the cDNA molecules or their amplicons from the surface of the array, wherein the released nucleic acid molecule may be the first or second strand of the cDNA molecule or an amplicon thereof, and wherein the part comprises the positioning sequence or its complementary strand;

and wherein in step (1), the capture sequence comprises an oligonucleotide sequence capable of capturing mRNA.

56. The method according to any one of claims 52-55, wherein the sample is a tissue sample.

57. The method according to any one of claims 52-55, wherein the sample is a formalin-fixed paraffin-embedded (FFPE) tissue or deep-frozen tissue.

58. The method according to any one of claims 52 to 57, wherein the multiple copies of the carrier sequence is a DNB formed by a concatemer of the carrier sequence, or the multiple copies of the carrier sequence is a DNA cluster formed by a clone population of the carrier sequence.

59. The method according to any one of claims 52 to 58, in step (5), the sequence analysis comprises sequencing or a sequence-specific PCR reaction.

60. The method according to any one of claims 52 to 59, in which the method further comprises step (6): correlating the sequence analysis information obtained in step (5) to an image of the sample, wherein the sample is imaged before or after step (3);

and wherein the imaging of the sample uses light, bright field, dark field, phase contrast, fluorescence, reflection, interference, confocal microscopy or a combination thereof.

61. The method according to any one of claims 52 to 60, wherein before or after the nucleic acid molecule labeled with spatial information tag or the cDNA molecule labeled with spatial information tag is released from the surface of the array, the complementary strand or the second strand cDNA is generated;

and wherein the synthesis of the complementary strand or the second strand uses a random primer and a strand displacement polymerase.

62. The method according to any one of claims 52 to 61, wherein before the sequence analysis, the method further comprises a step of amplifying the nucleic acid molecule or cDNA molecule labeled with the spatial information tag;

and wherein the amplification step is performed after the nucleic acid molecule or cDNA molecule labeled with the spatial information tag is released from the array, or the amplification step is performed in situ on the array;

and wherein the amplification step comprises PCR.

63. The method according to any one of claims 52 to 62, wherein, before the sequence analysis, the method further comprises a step of purifying the released nucleic acid molecule.

64. The method according to any one of claims 52 to 63, wherein before step (4), the method further comprises a step of washing the array to remove a residue of the sample.

65. The method according to any one of claims 52 to 64, wherein in step (4), the nucleic acid molecule is released from the surface of the array by the following method: (i) nucleic acid cleavage; (ii) denaturation; or (iii) physical method.