

What is claimed is:

1. A method for detecting at least one target nucleic acid in a sample comprising:
 - (1) contacting the sample with at least one probe capable of recognizing and binding a first specific region of the at least one target nucleic acid, wherein the at least one probe comprises:
 - a target binding domain and a barcode domain
 - wherein the target binding domain comprises 20-60 nucleotides and is capable of recognizing and binding the first specific region of the target nucleic acid and wherein the target binding domain comprises a known nucleotide sequence;
 - wherein the barcode domain comprises a first attachment region comprising a nucleic acid sequence capable of being bound by a first complementary nucleic acid molecule, a first complementary nucleic acid molecule of a first reporter complex or a first hybridizing nucleic acid molecule, an at least second attachment region comprising a nucleic acid sequence capable of being bound by an at least second complementary nucleic acid molecule, an at least second complementary nucleic acid molecule of an at least second reporter complex or an at least second hybridizing nucleic acid molecule and an at least third attachment region comprising a nucleic acid sequence capable of being bound by an at least third complementary nucleic acid molecule, an at least third reporter complex or an at least third hybridizing nucleic acid molecule;
 - wherein the sequence of the first attachment region is different from the sequence of the at least second attachment region, and
 - wherein the sequence of the at least third attachment region is different from the sequence of another attachment region;
 - (2) binding to the first attachment region a first complementary nucleic acid molecule comprising a first detectable label or a first complementary nucleic acid molecule of a first reporter complex comprising a first detectable label, thereby associating a detectable label with the first attachment region;
 - (3) detecting the first detectable label associated with the first attachment region;
 - (4) removing the first detectable label or first complementary nucleic acid molecule;
 - (5) binding to the at least second attachment region an at least second complementary nucleic acid molecule comprising a second detectable label or an at least second complementary nucleic acid molecule of an at least second reporter complex comprising a second detectable

label, thereby associating a detectable label with the at least second attachment region; and

(6) detecting the second detectable label associated with the at least second attachment region;

(7) removing the second detectable label or second complementary nucleic acid molecule;

(8) binding to the at least third attachment region and at least third complementary nucleic acid molecule comprising a third detectable label or an at least third complementary nucleic acid molecule of an at least third reporter complex comprising a third detectable label, thereby associating a detectable label with the at least third attachment region; and

(9) detecting the third detectable label associated with the at least third attachment region;

wherein the linear or sequential order of the first detectable label associated with the first attachment region, the second detectable label associated with the at least second attachment region, and the third detectable label associated with the at least third attachment region identifies the specific region of the at least one target nucleic acid, thereby detecting the at least one target nucleic acid in the sample.

2. The method of claim 1, wherein the target binding domain comprises 35-50 nucleotides.

3. The method of claim 1 or claim 2, wherein the barcode domain comprises an at least fourth, at least fifth, at least sixth or at least seventh attachment region comprising a nucleic acid sequence capable of being bound by an at least fourth complementary nucleic acid molecule, an at least fourth reporter complex or an at least fourth hybridizing nucleic acid molecule;

wherein the sequence of the at least fourth attachment region is different from the sequence of another attachment region.

4. The method of claim 3, wherein steps of:

(a) removing the respective detectable label or complementary nucleic acid molecule;

(b) binding to the respective attachment region a complementary nucleic acid molecule comprising a detectable label or a complementary nucleic acid molecule of a reporter complex comprising a detectable label, thereby associating a detectable label with the respective attachment

region; and

(c) detecting the respective detectable label associated with the attachment region; are repeated until each attachment region in the barcode domain has been sequentially bound by a complementary nucleic acid molecule comprising a detectable label and the detectable label of the sequentially bound complementary nucleic acid molecule has been detected,

wherein the linear or sequential order of the detectable labels associated with each attachment region identifies the specific region of the at least one target nucleic acid, thereby detecting the at least one target nucleic acid in the sample.

5. The method of claim 1, wherein removal of the first detectable label in step (4) comprises contacting the first complementary nucleic acid molecule or the first complementary nucleic acid molecule of an at least first reporter complex with a force to a location of the first complementary nucleic acid molecule sufficient to release the first detectable label.

6. The method of any one of claims 1 to 5, wherein at least one of the first complementary nucleic acid molecule, first complementary nucleic acid molecule of a first reporter complex, at least second complementary nucleic acid molecule, at least second complementary nucleic acid molecule of an at least second reporter complex, at least third complementary nucleic acid molecule or at least third complementary nucleic acid molecule of an at least third reporter complex comprises at least one cleavable linker.

7. The method of claim 6 wherein the at least one cleavable linker is independently selected from the group photo-cleavable, chemically cleavable and enzymatically cleavable.

8. The method of claim 5, wherein the force is light.

9. The method of any one of claims 1 to 8, further comprising washing the probe from the at least one target nucleic acid.

10. The method of claim 9 further comprising:

(i) contacting the sample with at least a second probe capable of recognizing and binding

a second specific region of the at least one target nucleic acid, wherein the second specific region is different from the first specific region of the at least one target nucleic acid;

(ii) contacting the sample with an at least second copy of the first probe capable of recognizing and binding the first specific region of the at least one target nucleic acid; or

(iii) contacting the sample with an at least third probe capable of recognizing and binding a first specific region of an at least second target nucleic acid, wherein the at least second target nucleic acid is different from the at least one target nucleic acid;

wherein the probe comprises:

a target binding domain and a barcode domain

wherein the target binding domain comprises 20-60 nucleotides; and

wherein the barcode domain comprises a first attachment region comprising a nucleic acid sequence capable of being bound by a first complementary nucleic acid molecule, a first complementary nucleic acid molecule of a first reporter complex or a first hybridizing nucleic acid molecule, an at least second attachment region comprising a nucleic acid sequence capable of being bound by an at least second complementary nucleic acid molecule, an at least second complementary nucleic acid molecule of an at least second reporter complex or an at least second hybridizing nucleic acid molecule and an at least third attachment region comprising a nucleic acid sequence capable of being bound by an at least third complementary nucleic acid molecule, an at least third reporter complex or an at least third hybridizing nucleic acid molecule.

11. The method of claim 10 further comprising repeating steps (1) to (9) of claim 1 with the at least second probe, the at least second copy of the first probe, or the at least third probe.

12. The method of claim 1, wherein the target nucleic acid is first immobilized to a substrate prior to contact by a probe, by at least binding a first position of the target nucleic acid with a first capture probe that comprises a first affinity binding reagent that selectively binds to the substrate, wherein the first capture probe binds the target nucleic acid at a different position on the target nucleic acid than the at least one probe binds to the target nucleic acid.

13. The method of any one of claims 1 to 12, wherein each reporter complex comprising a detectable label comprises a complementary nucleic acid molecule directly linked to a primary

nucleic acid molecule.

14. The method of any one of claims 1 to 12, wherein each reporter complex comprising a detectable label comprises a complementary nucleic acid molecule indirectly linked to a primary nucleic acid molecule via a cleavable linker.

15. The method of claim 14, wherein the cleavable linker is independently selected from the group photo-cleavable, chemically cleavable and enzymatically cleavable.

16. The method of claim 13, wherein each primary nucleic acid molecule is hybridized to at least one, at least two, at least three, at least four, at least five or at least six secondary nucleic acid molecules.

17. The method of claim 16, wherein the each secondary nucleic acid molecule independently comprises a cleavable linker.

18. The method of claim 17, wherein the cleavable linker is independently selected from the group photo-cleavable, chemically cleavable and enzymatically cleavable.

19. The method of claim 16, wherein the secondary nucleic acid molecule or molecules comprise at least one detectable label.

20. The method of claim 16, wherein each secondary nucleic acid molecule is hybridized to at least one, at least two, at least three, at least four, at least five, at least six or at least seven tertiary nucleic acid molecules comprising at least one detectable label.