

WHAT IS CLAIMED IS:

1. A target reporter construct (TRC) for detecting a target nucleic acid, the TRC being a closed, partially single-stranded nucleic acid comprising:
 - (a) a target sequence complementary to the target nucleic acid;
 - (b) a bridge sequence forming a double-stranded portion of the TRC; and
 - (c) an accessory sequence comprising a multifunctional probe sequence.
2. The TRC of claim 1, wherein the TRC comprises DNA, RNA, or a combination thereof.
3. The TRC of claim 2, wherein the TRC comprises standard canonical bases, modified bases, non-natural bases, or any combination of the bases thereof.
4. The TRC of claim 3, wherein the target nucleic acid is single-stranded DNA (ssDNA), double-stranded DNA (dsDNA), or single-stranded RNA (ssRNA).
5. The TRC of claim 4, wherein the ssRNA is microRNA (miRNA).
6. The TRC of claim 4, wherein the ssRNA is a non-coding RNA (ncRNA).
7. The TRC of claim 6, wherein the ncRNA is small interfering RNA (siRNA), piwi-interacting RNA (piRNA), miRNA, long non-coding RNA (lncRNA), or small nucleolar RNA (snoRNA).
8. The TRC of claim 1, wherein the target sequence is further defined as a toehold switch, wherein the toehold switch is a sequence capable of uniquely hybridizing to the target nucleic acid.
9. The TRC of claim 8, wherein the toehold switch comprises a double-stranded switch stem and a single-stranded toehold.
10. The TRC of claim 9, wherein the toehold is between 5 and 10 nucleotides in length.
11. The TRC of claim 10, wherein the toehold is 7, 8, or 9 nucleotides in length.
12. The TRC of claim 8, wherein the toehold switch and the bridge sequence overlap.

13. The TRC of claim 8, wherein the target sequence or toehold switch is structurally independent from the bridge sequence.
14. The TRC of claim 13, wherein the toehold switch is within 5-10 nucleotides of the bridge sequence.
15. The TRC of claim 1, further comprising a second target sequence complementary to a second target nucleic acid.
16. The TRC of claim 1, wherein the bridge sequence comprises a palindromic sequence.
17. The TRC of claim 1, wherein the bridge sequence is between the target sequence and accessory sequence.
18. The TRC of claim 1, wherein the bridge sequence comprises a low complexity, repetitive sequence.
19. The TRC of claim 1, wherein the TRC comprises two or more bridge sequences.
20. The TRC of claim 19, wherein the two or more bridge sequence are identical in sequence.
21. The TRC of claim 19, wherein the two or more bridge sequences comprise different sequences.
22. The TRC of claim 1, wherein the accessory sequence further comprises at least a second probe sequence.
23. The TRC of claim 22, wherein the second probe sequence is distinct from the first probe sequence.
24. The TRC of claim 23, wherein the first probe sequence and distinct second probe sequence form a unique multiplex probe signature.
25. The TRC of claim 24, wherein the unique multiplex probe signature further comprises a third, fourth, or fifth probe sequence.

26. The TRC of claim 1, wherein the TRC forms a loop structure under hybridization conditions.
27. The TRC of claim 26, wherein the loop structure is a hairpin structure, a dumbbell structure, or a multi-loop structure.
28. The TRC of claim 1, wherein the multifunctional probe sequence comprises a binding sequence.
29. The TRC of claim 28, wherein the binding sequence facilitates localization to an oligonucleotide array.
30. The TRC of claim 1, wherein the TRC is between 50 and 100 nucleotides in length.
31. The TRC of claim 1, wherein the TRC is between 100 and 500 nucleotides in length.
32. A replicated TRC comprising concatenated monomer repeats of a TRC according to any one of claims 1-30.
33. The replicated TRC of claim 32, wherein the replicated TRC is produced from rolling circle replication (RCR) and/or rolling circle amplification (RCA).
34. A replicated nanosphere comprising a replicated TRC of claim 32, wherein the replicated TRC has undergone intramolecular hybridization between the bridge sequences within the replicated TRC.
35. A method of detecting a target nucleic acid comprising:
 - (a) obtaining target reporter constructs (TRCs) according to any one of claims 1-30;
 - (b) contacting the TRCs with a population of target nucleic acids, wherein the target nucleic acids within the population hybridize to the complementary target sequence of a target-specific TRC;
 - (c) performing rolling circle replication (RCR), thereby obtaining replicated TRCs;
 - (d) introducing at least one detectable moiety, wherein the at least one detectable moiety binds the probe sequence of the replicated TRC; and

- (e) detecting the at least one detectable moiety, thereby detecting the target nucleic acid.
36. The method of claim 35, wherein performing RCR comprises introducing a strand-displacing polymerase.
37. The method of claim 36, wherein the strand-displacing polymerase is a DNA polymerase or RNA polymerase
38. The method of claim 36, wherein the DNA polymerase is ϕ 29, *Bst*, or *Bsu*.
39. The method of claim 35, wherein step (b) and step (c) are performed in a single tube.
40. The method of claim 35, wherein RCR is performed for 45 minutes to 90 minutes.
41. The method of claim 35, wherein the target nucleic acids have a length greater than the length of the TRC, thereby producing a 3' overhang or a 5' overhang.
42. The method of claim 41, further comprising introducing an exonuclease.
43. The method of claim 42, wherein the exonuclease is exonuclease T.
44. The method of claim 42, wherein the exonuclease removes a 3' overhang of the target nucleic acid hybridized to the TRC, thereby presenting a 3'-OH group.
45. The method of claim 35, wherein obtaining replicated TRCs comprises hybridizing the bridge of at least one of the replicated TRCs within the population to the bridge of at least a second replicated TRC within the population.
46. The method of claim 35, wherein the replicated TRCs comprise at least two replicated TRCs interconnected at the bridge.
47. The method of claim 35, wherein the replicated TRCs comprises at least 100, 1,000, 5,000, or 50,000 replicated TRCs interconnected at the bridge.
48. The method of claim 35, wherein the population of target nucleic acids comprises pathogenic nucleic acids.

49. The method of claim 48, wherein the pathogenic nucleic acids are human immunodeficiency virus (HIV), herpes simplex virus (HSV-1), human papillomavirus (HPV), and/or Epstein-Barr virus (EBV) pathogenic nucleic acids.
50. The method of claim 48, wherein the target sequence for the pathogenic nucleic acids comprises a length of 50-100 nucleotides.
51. The method of claim 35, wherein the population of target nucleic acids comprise one or more miRNAs.
52. The method of claim 51, wherein the one or more miRNAs are tumor-associated miRNAs.
53. The method of claim 52, wherein the tumor-associated miRNAs are selected from the group consisting of miR-let7, miR-10b, miR-21, miR-25, miR-106b, miR-11, miR-196a, miR-210, miR-212, and miR-221.
54. The method of claim 35, wherein the population of target nucleic acids comprise diabetes-associated miRNAs.
55. The method of claim 54, wherein the diabetes-associated miRNAs are selected from the group consisting of miR146a, miR-195, miR-320, miR29, miR192, miR-377, miR-126, miR-203, and miR-503.
56. The method of claim 35, wherein TRCs comprise TRCs with identical target sequences.
57. The method of claim 35, wherein TRCs comprise subsets of TRCs with different target sequences.
58. The method of claim 35, wherein TRCs comprise TRCs with multiple target sequences for a viral pathogen.
59. The method of claim 35, wherein TRCs comprise TRCs with target sequences for more than one viral pathogen.

- 60. The method of claim 35, wherein the population of TRCs comprises TRCs with target sequences for HIV, HSV-1, and/or EBV.
- 61. The method of claim 35, further comprising applying the replicated TRCs of step (c) to an array prior to step (d).
- 62. The method of claim 61, wherein the array is a grid-patterned array.
- 63. The method of claim 62, wherein the grid-patterned array is functionalized with chemical or biological moieties to direct replicated TRC positioning.
- 64. The method of claim 62, wherein the grid-patterned array is silanized by an aminosilane, epoxy silane, isothiocyanate, aminophenyl, mercaptosilane, aldehyde or epoxy.
- 65. The method of claim 62, wherein the grid-patterned array is silanized by an aminosilane.
- 66. The method of claim 35, wherein the detectable moiety is a fluorophore, chromophore, or radioisotope.
- 67. The method of claim 35, wherein the detectable moiety is a fluorophore.
- 68. The method of claim 35, wherein the detectable moiety is soluble or insoluble.
- 69. The method of claim 35, wherein the detectable moiety is an intercalating dye or pH sensitive dye.
- 70. The method of claim 35, wherein the detectable moiety comprises modified nucleotides.
- 71. The method of claim 70, wherein the modified nucleotides are fluorescently labeled nucleotides.
- 72. The method of claim 70, wherein detecting comprises detecting the presence of modified nucleotides that have been incorporated into the replicated TRC.

73. The method of claim 35, wherein detecting the at least one detectable moiety comprises normalizing to a control replicated TRC.
74. The method of claim 35, wherein step (d) comprises introducing 2, 3, or 4 distinct detectable moieties.
75. The method of claim 74, wherein step (e) comprises detecting the 2, 3, or 4 distinct detectable moieties.
76. The method of claim 75, wherein detecting the 2, 3, or 4 distinct detectable moieties is further defined as detecting the unique multiplex probe signature of a replicated TRC.
77. The method of claim 75, wherein detecting is performed using an epifluorescence microscope.
78. The method of claim 75, wherein detecting is performed using colorimetric analysis.