molecules into individual physical containers. The approach is practical, and after labeling, a simple detector device such as a microarray with complementary probe sequences to the labels can be used to identify and count the number of labels present. In addition, when stochastic labels are attached to DNA molecules that are prepared for DNA sequencing readouts, the labeling sequence can serve as discreet counting tags for absolute quantitation, or as unique identifiers to distinguish each originally tagged template from its amplified daughter molecules (Kinde et al. Proc Natl Acad Sci USA 108: 9530-9535 (2011)).

SUMMARY OF THE INVENTION

[0006] In one aspect, there is provided a digital reverse transcription method comprising:

a. contacting a sample comprising a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labeled-RNA molecule, wherein:

i. the plurality of RNA molecules comprise at least 2 mRNA molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. an oligonucleotide tag of the plurality of oligonucleotide tags comprises a unique identifier region.

b. conducting a first strand synthesis reaction by contacting the labeled-RNA molecules with a reverse transcriptase enzyme to produce a labeled-cDNA molecule;

c. conducting a polymerase chain reaction on the labeled-cDNA molecule of step (b) to produce a double-stranded labeled-cDNA molecule;

d. conducting a nested PCR reaction on the double-stranded labeled-cDNA molecule; and

e. detecting the double-stranded-labeled-cDNA molecule by hybridizing at least a portion of the double-stranded-labeled-cDNA molecule to a solid support.

[0006a] In another aspect, there is provided a method comprising:

a. contacting an original sample comprising a plurality of nucleic acid molecules with a plurality of oligonucleotide tags to produce an original labeled sample comprising a plurality of labeled-nucleic acid molecules;

b. treating the original labeled sample with a uracil DNA glycosylase (UDG), thereby generating a treated labeled sample;

c. amplifying the treated labeled sample by using one or more labeled-nucleic acid molecules from the treated labeled sample as a template parent molecule, thereby producing one

or more samples comprising clonally replicated molecules originating from the template parent molecule; and

d. determining a count of a first molecule from the original sample by determining a number of different clonally replicated molecules comprising the first molecule from a first sample of the one or more samples.

[0006b] In another aspect, there is provided a reverse transcription method comprising:

a. hybridizing a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labelled-RNA molecule, wherein:

i. the plurality of RNA molecules comprises at least 2 mRNA molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. an oligonucleotide tag of the plurality of oligonucleotide tags comprises an oligodT sequence and a unique identifier region;

b. conducting a first strand synthesis reaction by contacting the labelled-RNA molecule with a reverse transcriptase enzyme to produce a labelled-cDNA molecule;

c. amplifying the labelled-cDNA molecule by conducting a polymerase chain reaction on the labelled-cDNA molecule to produce an amplified double-stranded DNA molecule; and

d. detecting the amplified double-stranded DNA molecule by hybridizing at least a portion of the double-stranded amplified DNA molecule to a solid support.

[0006c] In some embodiments is a digital reverse transcription method comprising: a) contacting a sample comprising a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labeled-RNA molecule, wherein: the plurality of RNA molecules comprise at least 2 mRNA molecules of different sequences; the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and the plurality of oligonucleotide tags comprises an oligodT sequence; b)conducting a first strand synthesis reaction by contacting the labeled-RNA molecules with a reverse transcriptase enzyme to produce a labeled-cDNA molecule; and c) detecting the labeled-cDNA molecule by hybridizing the labeled-cDNA molecule to a solid support.

[0007] In some embodiments is a stochastic label-based hybridization chain reaction

method comprising stochastically labeling one or more nucleic acid molecules with a plurality of hairpin oligonucleotide tags, wherein the hairpin oligonucleotide tag comprises an overhang; and the one or more nucleic acid molecules act as initiators for a hybridization chain reaction.

[0008] At least a portion of the hairpin oligonucleotide tag may hybridize to at least a portion of the one or more nucleic acid molecules. The hairpin oligonucleotide tag may comprise an oligodT sequence. The one or more nucleic acid molecules may comprise one or more adapters. At least a portion of the hairpin oligonucleotide tag may hybridize to at least a portion of the one or more adapters. At least one hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags may comprise one or more labels. At least one hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags may comprise two or more labels.

[0009] Each hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags may comprise one or more labels. Each hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags may comprise two or more labels. In some instances, the hairpin oligonucleotide tag does not comprise a label.

What is claimed is:

1. A digital reverse transcription method comprising:

a. contacting a sample comprising a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labeled-RNA molecule, wherein:

i. the plurality of RNA molecules comprise at least 2 mRNA molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. the plurality of oligonucleotide tags comprises an oligodT sequence;

b. conducting a first strand synthesis reaction by contacting the labeled-RNA molecules with a reverse transcriptase enzyme to produce a labeled-cDNA molecule; and

c. detecting the labeled-cDNA molecule by hybridizing the labeled-cDNA molecule to a solid support.

2. The method of claim 1, wherein the oligonucleotide tag further comprises a unique identifier region.

3. The method of claim 2, wherein the unique identifier region is at least one nucleotide in length.

4. The method of claim 1, wherein the oligonucleotide tag further comprises a universal primer binding site.

5. The method of claim 1, wherein the oligonucleotide tag is at least one nucleotide in length.

6. The method of claim 1, wherein the solid support is an array.

7. The method of claim 1, wherein the solid support is an addressable array.

8. The method of claim 1, wherein the solid support is an Affymetrix 3K tag array, Arrayjet non-contact printed array, or Applied Microarrays Inc (AMI) array.

9. The method of claim 1, wherein the solid support is a bead.

10. The method of claim 1, further comprising conducting a polymerase chain reaction on the labeled-cDNA molecule of step (b) to produce a double-stranded labeled-cDNA molecule.

11. The method of claim 10, wherein conducting the polymerase chain reaction comprises annealing a first target specific primer to the labeled-cDNA molecule.

12. The method of claim 10, wherein conducting the polymerase chain reaction further comprises annealing a universal primer to the universal primer binding site of the oligonucleotide tag.

13. The method of claim 10, wherein the polymerase chain reaction comprises absolute PCR, HD-PCR, Next Gen PCR, digital RTA, or any combination thereof.

14. The method of claim 10, further comprising conducting a nested PCR reaction on the double-stranded labeled-cDNA molecule.

15. The method of claim 14, wherein conducting the nested PCR reaction comprises denaturing the double-stranded labeled cDNA molecule to produce a denatured single-stranded labeled-cDNA molecule.

16. The method of claim 14, wherein conducting the nested PCR reaction further comprises annealing a second target specific primer to the denatured single-stranded labeled-cDNA molecule.

17. The method of claim 14, wherein conducting the nested PCR reaction further comprises annealing a universal primer to the universal primer binding site of the oligonucleotide tag.

18. The method of claim 1, further comprising conducting a sequencing reaction to determine the sequence of at least a portion of the oligonucleotide tag, at least a portion of the labeled-cDNA molecule, a complement thereof, a reverse complement thereof, or any combination thereof.

19. The method of claim 1, wherein detecting the labeled-cDNA molecules comprises an array detector, fluorescent reader, non-fluorescent detector, CR reader, or scanner.

20. The method of claim 19, wherein the array detector is a flatbed scanner.

21. The method of claim 19, wherein the fluorescent reader is a Sensovation, AG fluorescent reader.

22. The method of claim 1, wherein detecting the labeled-cDNA molecules comprises detecting the labeled-cDNA molecules hybridized to the solid support.

23. The method of claim 1, further comprising conducting a hybridization chain reaction.

24. The method of claim 1, wherein the oligonucleotide tag comprises one or more secondary structures.

25. The method of claim 24, wherein the one or more secondary structures is a hairpin.

26. The method of claim 1, wherein the oligonucleotide tag is linear.

27. A kit comprising:

a. a plurality of oligonucleotide tags, wherein the oligonucleotide tag of the plurality of oligonucleotide tags comprises:

i. a target specific region; and

ii. a unique identifier region;

b. an enzyme.

28. The kit of claim 27, wherein the enzyme is a reverse transcriptase enzyme.

29. The kit of claim 27, wherein the enzyme is a ligase.

30. The kit of claim 27, wherein the enzyme is a polymerase.

31. The kit of claim 27, wherein the enzyme is an RNase.

32. The kit of claim 27, wherein the enzyme is a DNase.

33. The kit of claim 27, wherein the enzyme is an endonuclease.

34. The kit of claim 27, wherein the oligonucleotide tag is at least 25 nucleotides in length.

35. The kit of claim 27, wherein the unique identifier region is at least 10 nucleotides in length.

36. The kit of claim 27, wherein the target specific region is at least 10 nucleotides in length.

37. The kit of claim 27, wherein the target specific region comprises an oligodT sequence.

38. The kit of claim 27, wherein the oligonucleotide tag further comprises a universal primer binding site.

39. The kit of claim 27, further comprising a support.

40. The kit of claim 39, wherein the support is a semi-solid support.

41. The kit of claim 39, wherein the support is a solid support.

42. The kit of claim 41, wherein the solid support is an array.

43. The kit of claim 39, wherein the support is an addressable array.

44. The kit of claim 39, wherein the support is an Affymetrix 3K tag array, Arrayjet non-contact printed array, or Applied Microarrays Inc (AMI) array.

45. The kit of claim 39, the support is a bead.

46. The kit of claim 27, further comprising a primer.

47. The kit of claim 46, wherein the primer is a universal primer.

48. The kit of claim 46, wherein the primer binds to the oligonucleotide tag.

49. The kit of claim 46, wherein the primer binds to the universal primer binding site of the oligonucleotide tag.

50. The kit of claim 27, further comprising a control oligo.

51. The kit of claim 50, wherein the control oligo comprises at least 15 nucleotides.

52. The kit of claim 50, wherein the control oligo is a bright hybridization control oligo.

53. The kit of claim 50, wherein the control oligo is a spike-in template control.

54. The kit of claim 27, wherein the oligonucleotide tag further comprises a label.

55. The kit of claim 46, wherein the primer further comprises a label.

56. The kit of claim 50, wherein the control oligo further comprises a label.

57. The kit of any of claims 54-56, wherein the label is a dye label.

58. The kit of any of claims 54-56, wherein the label is a Cy3 dye.

59. The kit of any of claims 54-56, wherein the label is a Tye563 dye.

60. The kit of claim 27, further comprising a buffer.

61. The kit of claim 27, further comprising a carrier.

62. The kit of claim 27, further comprising a detergent.

63. The kit of claim 27, further comprising a thermal cycler.

64. The kit of claim 27, further comprising a sequencer.

65. The kit of claim 27, further comprising a hybridization chamber.

66. The kit of claim 27, further comprising a detector.

67. The kit of claim 27, further comprising an array detector, fluorescent reader, non-fluorescent detector, CR reader, or scanner.

68. The kit of claim 67, wherein the fluorescent reader is a Sensovation or AG fluorescent reader.

69. The kit of claim 67, wherein the scanner is a flatbed scanner.

70. The kit of claim 27, further comprising a computer.

71. The kit of claim 70, wherein the computer comprises a memory device.

72. The kit of claim 71, wherein the memory device is capable of storing data.

73. The kit of claim 27, further comprising a software program.

74. The kit of claim 27, further comprising a computer-readable program.

75. A cell analysis method comprising:

a. contacting a sample comprising a plurality of molecules with a plurality of oligonucleotide tags to produce a labeled-molecule, wherein:

i. the plurality of molecules comprise at least 2 molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. the sample is from at least one cell; and

b. detecting the labeled-molecule by hybridizing the labeled-molecule to a solid support.

76. A clonal amplification method comprising:

a. stochastically labeling a plurality of molecules with a plurality of oligonucleotide tags to produce a labeled-molecule, wherein:

i. the plurality of molecules comprise at least 2 molecules of different sequences; and

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of

different sequences;

b. amplifying the labeled-molecules to produce a labeled-amplicon; and

c. detecting the labeled-amplicon.

77. The method of any of claims 75-76, wherein the oligonucleotide tag further comprises a unique identifier region.

78. The method of claim 77, wherein the unique identifier region is at least 10 nucleotides in length.

79. The method of claim 77, wherein the unique identifier region is cannot hybridize to the molecule.

80. The method of any of claims 75-76, wherein the oligonucleotide tag further comprises a universal primer binding site.

81. The method of any of claims 75-76, wherein the oligonucleotide tag is at least 20 nucleotides in length.

82. The method of any of claims 75-76, wherein the oligonucleotide tag further comprises a target specific region.

83. The method of claim 82, wherein the target specific region comprises an oligodT sequence.

84. The method of claim 82, wherein the target specific region is at least 10 nucleotides in length.

85. The method of any of claims 75-76, wherein the solid support is an array.

86. The method of any of claims 75-76, wherein the solid support is an addressable array.

87. The method of any of claims 75-76, wherein the solid support is an Affymetrix 3K tag array, Arrayjet non-contact printed array, or Applied Microarrays Inc (AMI) array.

88. The method of any of claims 75-76, wherein the solid support is a bead.

89. The method of any of claims 75-76, further comprising conducting a first strand synthesis reaction to produce a labeled-cDNA molecule.

90. The method of claim 75, further comprising conducting a polymerase chain reaction on the labeled-molecule or any product thereof to produce a double-stranded labeled-molecule.

91. The method of claim 76, wherein amplifying the labeled-molecule comprises conducting a polymerase chain reaction.

92. The method of any of claims 90-91, wherein conducting the polymerase chain reaction comprises annealing a first target specific primer to the labeled-molecule or any product thereof.

93. The method of any of claims 90-91, wherein conducting the polymerase chain reaction further comprises annealing a universal primer to the universal primer binding site of the oligonucleotide tag.

94. The method of any of claims 90-91, wherein the polymerase chain reaction comprises absolute PCR, HD-PCR, Next Gen PCR, digital RTA, or any combination thereof.

95. The method of any of claims 75-76, further comprising conducting a nested PCR reaction on the double-stranded labeled-cDNA molecule.

96. The method of claim 95, wherein conducting the nested PCR reaction comprises denaturing the labeled-molecule or any product thereof to produce a denatured single-stranded labeled- molecule or any product thereof.

97. The method of any of claims 95-96, wherein conducting the nested PCR reaction further comprises annealing a second target specific primer to the denatured single-stranded labeled- molecule or any product thereof.

98. The method of any of claims 95-96, wherein conducting the nested PCR reaction further comprises annealing a universal primer to the universal primer binding site of the oligonucleotide tag.

99. The method of any of claims 75-76, further comprising conducting a sequencing reaction to determine the sequence of at least a portion of the oligonucleotide tag, at least a portion of the labeled-molecule, a product thereof, a complement thereof, a reverse complement thereof, or any combination thereof.

100. The method of any of claims 75-76, wherein detecting the labeled-molecules or any products thereof comprises an array detector, fluorescent reader, non-fluorescent detector, CR reader, or scanner.

101. The method of claim 100, wherein the fluorescent reader is a Sensovation, or a AG fluorescent reader.

102. The method of claim 100, wherein the scanner is a flatbed scanner.

103. The method of any of claims 75-76, wherein detecting the labeled-molecules or any products thereof comprises detecting the labeled- molecules hybridized to the solid support.

104. The method of any of claims 75-76, wherein the molecule is a nucleic acid molecule.

105. The method of claim 104, wherein the nucleic acid molecule is a DNA molecule.

106. The method of claim 104, wherein the nucleic acid molecule is an RNA molecule.

107. The method of any of claims 75-76, wherein the molecule is a peptide.

108. The method of claim 107, wherein the peptide is a polypeptide.

109. The method of claim 76, wherein the plurality of molecules is from a cell.

110. The method of claim 75, wherein the sample is from a single cell.

111. The method of claim 75, wherein the sample is from less than about 100 cells.

112. The method of claim 75, wherein the sample is from less than about 50 cells.

113. The method of claim 75, wherein the sample is from less than about 20 cells.

114. The method of claim 75, wherein the sample is from less than about 10 cells.

115. The method of claim 75, wherein the sample is from less than about 5 cells.

116. The method of claim 75, wherein the cell is a mammalian cell.

117. The method of claim 75, wherein the cell is a human cell.

118. The method of claim 75, wherein the cell is from a subject suffering from a disease or condition.

119. The method of claim 118, wherein the disease or condition is cancer.

120. The method of claim 118, wherein the disease or condition is a pathogenic infection.

121. The method of claim 118, wherein the disease or condition is a genetic disorder.

122. The method of any of claims 109-110, wherein the cell is from a healthy subject.

123. The method of any of claims 109-110, wherein the cell is a diseased cell.

124. The method of claim 123, wherein the diseased cell is a cancerous cell.

125. The method of any of claims 109-110, wherein the cell is a healthy cell.

126. The method of claim 125, wherein the cell is not a diseased or infected cell.

127. The method of any of claims 1 and 75-76, wherein labeled-molecules are produced by stochastic labeling.

128. A stochastic label-based hybridization chain reaction method, comprising stochastically labeling one or more nucleic acid molecules with a plurality of hairpin oligonucleotide tags, wherein:

(a) the hairpin oligonucleotide tag comprises an overhang; and

(b) the one or more nucleic acid molecules act as initiators for a hybridization chain reaction.

129. The method of claim 128, wherein at least a portion of the hairpin oligonucleotide tag hybridizes to at least a portion of the one or more nucleic acid molecules.

130. The method of claim 128, wherein the hairpin oligonucleotide tag comprises an oligodT sequence.

131. The method of claim 128, wherein the one or more nucleic acid molecules comprise one or more adapters.

132. The method of claim 131, wherein at least a portion of the hairpin oligonucleotide tag hybridizes to at least a portion of the one or more adapters.

133. The method of claim 128, wherein at least one hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags comprises one or more labels.

134. The method of claim 128, wherein at least one hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags comprises two or more labels.

135. The method of claim 128, wherein each hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags comprises one or more labels.

136. The method of claim 128, wherein each hairpin oligonucleotide tag of the plurality of hairpin oligonucleotide tags comprises two or more labels.

137. The method of claim 128, wherein the hairpin oligonucleotide tag does not comprise a label.

138. The method of claim 128, wherein the plurality of hairpin oligonucleotide tags comprises one or more hairpin oligonucleotide tags with a 3' overhang, hairpin oligonucleotide tags with a 3' overhang, or a combination thereof.

139. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is one or more nucleotides in length.

140. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is two or more nucleotides in length.

141. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is three or more nucleotides in length.

142. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is four or more nucleotides in length.

143. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is five or more nucleotides in length.

144. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is six or more nucleotides in length.

145. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is seven or more nucleotides in length.

146. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is eight or more nucleotides in length.

147. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is nine or more nucleotides in length.

148. The method of claim 128, wherein the stem portion of the hairpin oligonucleotide tag is ten or more nucleotides in length.

149. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is one or more nucleotides in length.

150. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is two or more nucleotides in length.

151. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is three or more nucleotides in length.

152. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is four or more nucleotides in length.

153. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is five or more nucleotides in length.

154. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is six or more nucleotides in length.

155. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is seven or more nucleotides in length.

156. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is eight or more nucleotides in length.

157. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is nine or more nucleotides in length.

158. The method of claim 128, wherein the loop portion of the hairpin oligonucleotide tag is ten or more nucleotides in length.

159. The method of claim 128, wherein the hairpin oligonucleotide tag comprises a unique identifier region.

160. The method of claim 159, wherein the unique identifier region is in the loop portion of the hairpin oligonucleotide tag.

161. The method of claim 159, wherein the unique identifier region is in the stem portion of the hairpin oligonucleotide tag.

162. The method of claim 159, wherein the unique identifier region is in the overhang portion of the hairpin oligonucleotide tag.

163. The method of claim 133, wherein the label comprises a unique identifier region.

What is claimed is:

1. A digital reverse transcription method comprising:

a. contacting a sample comprising a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labeled-RNA molecule, wherein:

i. the plurality of RNA molecules comprise at least 2 mRNA molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. an oligonucleotide tag of the plurality of oligonucleotide tags comprises a unique identifier region.

b. conducting a first strand synthesis reaction by contacting the labeled-RNA molecules with a reverse transcriptase enzyme to produce a labeled-cDNA molecule;

c. conducting a polymerase chain reaction on the labeled-cDNA molecule of step (b) to produce a double-stranded labeled-cDNA molecule;

d. conducting a nested PCR reaction on the double-stranded labeled-cDNA molecule; and

e. detecting the double-stranded-labeled-cDNA molecule by hybridizing at least a portion of the double-stranded-labeled-cDNA molecule to a solid support.

2. The method of claim 1, wherein an oligonucleotide tag of the plurality of oligonucleotide tags comprises an oligodT sequence.

3. The method of claim 1, wherein an oligonucleotide tag of the plurality of oligonucleotide tags comprises a universal primer binding site.

4. The method of claim 1, wherein the solid support is an array.

5. The method of claim 1, wherein the solid support is an addressable array.

6. The method of claim 1, wherein the solid support is a bead

7. The method of claim 1, wherein conducting the polymerase chain reaction comprises annealing a first target specific primer to the labeled-cDNA molecule.

8. The method of claim 1, wherein conducting the polymerase chain reaction further comprises annealing a universal primer to a universal primer binding site of the oligonucleotide tag.

9. The method of claim 1, wherein the polymerase chain reaction comprises absolute PCR, HD-PCR, Next Gen PCR, digital RTA, or any combination thereof.

10. The method of claim 1, wherein conducting the nested PCR reaction comprises denaturing the double-stranded labeled cDNA molecule to produce a denatured single-stranded labeled-cDNA molecule.

11. The method of claim 1, wherein conducting the nested PCR reaction further comprises annealing a second target specific primer to the denatured single-stranded labeled-cDNA molecule.

12. The method of claim 1, wherein conducting the nested PCR reaction further comprises annealing a universal primer to a universal primer binding site of the oligonucleotide tag.

13. The method of claim 1, further comprising conducting a sequencing reaction to determine the sequence of at least a portion of the oligonucleotide tag, at least a portion of the labeled-cDNA molecule, a complement thereof, a reverse complement thereof, or any combination thereof.

14. The method of claim 1, wherein detecting the labeled-cDNA molecules comprises use of an array detector, fluorescent reader, non-fluorescent detector, CR reader, or scanner.

15. The method of claim 14, wherein the array detector is a flatbed scanner.

16. The method of claim 1, wherein detecting the labeled-cDNA molecules comprises detecting the labeled-cDNA molecules hybridized to the solid support.

17. The method of claim 1, further comprising conducting a hybridization chain reaction.

18. The method of claim 1, wherein the oligonucleotide tag comprises one or more secondary structures.

19. The method of claim 18, wherein the one or more secondary structures is a hairpin.

20. The method of claim 1, wherein the oligonucleotide tag is linear.

21. The method of claim 1, wherein producing the double-stranded-labeled-cDNA molecule comprises use of a primer.

22. The method of claim 21, wherein the primer comprises an oligodU sequence.

23. The method of claim 21, wherein the primer comprises a target-specific sequence.

24. The method of claim 21, further comprising treating the sample with a uracil DNA glycosylase (UDG).

25. The method of claim 21, wherein the primer further comprises a unique identifier region.

26. The method of claim 1, wherein conducting the nested PCR reaction comprises the use of a polymerase.

27. The method of claim 26, wherein the polymerase is a Pfu DNA polymerase.

28. The method of claim 26, wherein the polymerase cannot amplify dimerized oligonucleotide tags.

29. The method of claim 26, wherein the polymerase cannot amplify templates containing one or more uracils.

30. A clonal amplification method comprising:

a. stochastically labeling a plurality of molecules with a plurality of oligonucleotide tags to produce a labeled-molecule, wherein:

i. the plurality of molecules comprise at least 2 molecules of different sequences; and

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences;

b. amplifying the labeled-molecules to produce a labeled-amplicon, wherein amplifying the labeled-molecules comprises HD-PCR and/or nested-PCR; and

c. detecting the labeled-amplicon.

31. A stochastic label-based hybridization chain reaction method, comprising stochastically labeling one or more nucleic acid molecules with a plurality of hairpin oligonucleotide tags, wherein:

a. the hairpin oligonucleotide tag comprises an overhang; and

b. the one or more nucleic acid molecules act as initiators for a hybridization chain reaction.

32. A method comprising:

a. contacting an original sample comprising a plurality of nucleic acid molecules with a plurality of oligonucleotide tags to produce an original labeled sample comprising a plurality of labeled-nucleic acid molecules;

b. treating the original labeled sample with a uracil DNA glycosylase (UDG), thereby generating a treated labeled sample;

c. amplifying the treated labeled sample by using one or more labeled-nucleic acid molecules from the treated labeled sample as a template parent molecule, thereby producing one or more samples comprising clonally replicated molecules originating from the template parent molecule; and

d. determining a count of a first molecule from the original sample by determining a number of different clonally replicated molecules comprising the first molecule from a first sample of the one or more samples.

33. The method of claim 32, wherein producing the one or more samples of step (c) comprises producing two or more samples comprising clonally replicated molecules originating from the template parent molecule.

34. The method of claim 33, wherein the two or more samples are produced at two or more times.

35. The method of claim 33, wherein producing the two or more samples comprises amplifying the plurality of labeled-nucleic acid molecules from the treated sample two or more times.

36. The method of claim 33, wherein producing the two or more samples comprises repeatedly amplifying the plurality of labeled-nucleic acid molecules from the treated sample.

37. The method of claim 36, wherein repeatedly amplifying the plurality of labeled-nucleic acid molecules from the treated sample comprises amplifying the plurality of labeled-nucleic acid molecules at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 times.

38. The method of claim 33, wherein producing the two or more samples comprises amplifying the clonally replicated molecules from the first sample.

39. The method of claim 38, wherein producing the two or more samples comprises amplifying the clonally replicated molecules from the first sample two or more times.

40. The method of claim 38, wherein generating the two or more clonal samples comprises repeatedly amplifying the amplicons from a first clonal sample.

41. The method of claim 40, wherein repeatedly amplifying the clonally replicated molecules from the first sample comprises amplifying the clonally replicated molecules at least 2, 3, 4, 5, 6, 7, 8, 9, or 10 times.

42. The method of claim 1, wherein the plurality of nucleic acid molecules comprise a plurality of RNA molecules.

43. The method of claim 42, further comprising conducting a first strand synthesis reaction by contacting the plurality of labeled-nucleic acid molecules with a reverse transcriptase enzyme to produce a labeled-cDNA molecule.

44. The method of claim 43, wherein conducting the first strand synthesis reaction occurs prior to producing the one or more samples comprising the clonally replicated molecules.

45. The method of claim 44, wherein the clonally replicated molecules comprise a copy of the labeled-cDNA molecule.

46. The method of claim 45, further comprising detecting one or more clonally replicated molecules from the one or more samples.

47. The method of claim 46, wherein detecting the one or more clonally replicated molecules comprises hybridizing the one or more clonally replicated molecules to a solid support.

48. The method of claim 32, further comprising detecting one or more clonally replicated molecules from the one or more samples.

49. The method of claim 48, wherein detecting the one or more clonally replicated molecules comprises hybridizing the one or more clonally replicated molecules to a solid support.

50. The method of claim 32, further comprising conducting a nested PCR reaction on the one more clonally replicated molecules from the one or more samples.

51. The method of claim 32, wherein the original sample is from one or more cells.

52. The method of claim 32, wherein an oligonucleotide tag of the plurality of oligonucleotide tags comprises a unique identifier region.

53. The method of claim 32, wherein an oligonucleotide tag of the plurality of oligonucleotide tags comprises a universal primer binding site.

54. A reverse transcription method comprising:

a. hybridizing a plurality of RNA molecules with a plurality of oligonucleotide tags to produce a labelled-RNA molecule, wherein:

i. the plurality of RNA molecules comprises at least 2 mRNA molecules of different sequences;

ii. the plurality of oligonucleotide tags comprises at least 2 oligonucleotide tags of different sequences; and

iii. an oligonucleotide tag of the plurality of oligonucleotide tags comprises an oligodT sequence and a unique identifier region;

b. conducting a first strand synthesis reaction by contacting the labelled-RNA molecule with a reverse transcriptase enzyme to produce a labelled-cDNA molecule;

c. amplifying the labelled-cDNA molecule by conducting a polymerase chain reaction on the labelled-cDNA molecule to produce an amplified double-stranded DNA molecule; and

d. detecting the amplified double-stranded DNA molecule by hybridizing at least a portion of the double-stranded amplified DNA molecule to a solid support.

55. The method of claim 54, wherein the oligonucleotide tag of the plurality of oligonucleotide tags further comprises a universal primer binding site.

56. The method of claim 54, wherein the solid support is an array.

57. The method of claim 54, wherein the solid support is an addressable array.

58. The method of claim 54, wherein the solid support is a bead.

59. The method of claim 54, wherein conducting the polymerase chain reaction comprises annealing a first target specific primer to the labelled-cDNA molecule.

60. The method of claim 59, wherein conducting the polymerase chain reaction further comprises annealing a universal primer to a universal primer binding site of the oligonucleotide tag.