

WHAT IS CLAIMED IS:

1. A method of identifying the origin of a nucleic acid sample comprising the steps of
 - (a) forming a reaction mixture comprising a nucleic acid sample comprising nucleic acid molecules from a single cell and a set of barcodes;
 - (b) incorporating the set of barcodes into the nucleic acid molecules of the sample; and
 - (c) identifying the set of barcodes incorporated into the nucleic acid molecules of the single cell thereby identifying the origin of the nucleic acid sample.
2. The method of claim 1, wherein forming the reaction mixture comprises contacting the single cell with the set of barcodes and lysing the cell to provide the nucleic acid sample from the single cell.
3. The method of claim 1, wherein forming the reaction mixture comprises providing cells in a suspension buffer and contacting the suspension buffer comprising the cells with a barcoding buffer comprising the set of barcodes under conditions to form the reaction mixture comprising the single cell and the set of barcodes.
4. The method of any one of claims 1-3, wherein the set of barcodes comprises one or more 5' nucleic acid constructs each construct comprising a unique 5' barcode and one or more 3' nucleic acid constructs each construct comprising a unique 3' barcode.
5. The method of claim 4, wherein forming the reaction mixture comprises providing a cells in a suspension buffer, and contacting the suspension buffer with a barcoding buffer comprising the 5' and 3' nucleic acid constructs under conditions to form the reaction mixture comprising the single cell and at least one 5' nucleic acid construct and at least one 3' nucleic acid construct.
6. The method of claim 4, wherein forming the reaction mixture comprises providing a cells in a suspension buffer, and contacting the suspension buffer with a first barcoding buffer comprising the 5' nucleic acid constructs and a second barcoding buffer comprising the 3'

nucleic acid constructs under conditions to form the reaction mixture comprising the single cell and at least one 5' nucleic acid construct and at least one 3' nucleic acid construct.

7. The method of any one of claims 4-6, wherein the constructs further comprise a unique molecular identifier (UMI) sequence.

8. The method of any one of claims 4-7, wherein each 5' nucleic acid construct is provided in multiple copies attached to a solid surface.

9. The method of any one of claims 4-8, wherein each 3' nucleic acid construct is provided in multiple copies attached to a solid surface

10. The method of claim 8 or 9, wherein the solid surface is a bead, microbead, microparticle, microsphere, nanoparticle, nanobead, or hydrogel.

11. The method of any one of claims 4-10, wherein the reaction mixture comprises the nucleic acid sample from the single cell, at least one bead comprising multiple copies of the 5' nucleic acid constructs, and at least one bead comprising multiple copies of the 3' nucleic acid construct.

12. The method of any one of claims 4-11, wherein each 5' and 3' nucleic acid construct further comprises a photocleavable linker or a restriction enzyme site.

13. The method of any one of claims 4-11, wherein each 5' nucleic acid construct further comprises a photocleavable linker and each 3' nucleic acid construct further comprises a restriction enzyme site.

14. The method of any one of claims 4-11, wherein each 5' nucleic acid construct further comprises a restriction enzyme site and each 3' nucleic acid construct further comprises a photocleavable linker.

15. The method of claim 13 or 14, wherein the method further comprises contacting the reaction mixture with a restriction enzyme and exposing the reaction mixture to UV light to release the 5' and 3' nucleic acid constructs from the solid surface.
16. The method of claim 12, wherein the 5' and 3' nucleic acid constructs further comprise a restriction enzyme site and the method further comprises contacting the reaction mixture with a restriction enzyme to release the 5' and 3' nucleic acid constructs from the solid surface.
17. The method of claim 12, wherein the 5' and 3' nucleic acid constructs further comprise a photocleavable linker and the method further comprises exposing the reaction mixture to UV light to release the 5' and 3' nucleic acid constructs from the solid surface.
18. The method of any one of claims 4-17, wherein the 5' nucleic acid construct is a double stranded nucleic acid construct comprising a promoter and wherein the 5' nucleic acid construct serves as a template to produce multiple copies of the 5' nucleic acid construct.
19. The method of any one of claims 1-18, wherein the set of barcodes comprises 1, 2, 3, 4, 5, 6, 7, or 8 5' nucleic acid constructs and 1, 2, 3, 4, 5, 6, 7, or 8 3' nucleic acid constructs.
20. The method of any one of claims 1-19, wherein the combination of 5' and 3' barcodes in the nucleic acid sample identifies the origin of the nucleic acid sample.
21. The method of any one of claims 1-20, wherein the 3' nucleic acid constructs further comprise a binding sequence.
22. The method of claim 21, wherein the binding sequence comprises a poly-T sequence.
23. The method of claim 22, wherein the poly-T sequence binds to the poly-A sequences on the nucleic acid molecules of the sample.

24. The method of any one of claims 1-23, wherein the barcodes on the 3' nucleic acid constructs are incorporated by reverse transcription.
25. The method of claim 24, wherein the reverse transcription produces nucleic acid molecules comprising the 3' barcode sequence.
26. The method of claim 25, wherein the reverse transcriptase enzyme adds two to five cysteine residues to the end of the nucleic acid molecules in the sample.
27. The method of claim 26, wherein the two to five cysteine residues provides a binding sequence complementary to a binding sequence on the 5' nucleic acid constructs.
28. The method of claim 27, wherein the binding sequence on the 5' nucleic acid constructs comprises a poly-G sequence.
29. The method of claim 28, wherein the binding sequence on the 5' nucleic acid constructs binds to poly-C sequences on the nucleic acid molecules of the sample.
30. The method of any one of claims 1-29, wherein the 5' nucleic acid construct is incorporated into the nucleic acid sample using a reverse transcriptase enzyme.
31. The method of any one of claims 24-30, wherein the reverse transcriptase is an M-MLV enzyme.
32. The method of claim 31, wherein the reverse transcriptase is MMLV H- reverse transcriptase.
33. The method of any one of claims 1-32, wherein the nucleic acid sample is further amplified to produce multiple copies of the plurality of nucleic acid sequences each sequence comprising a 5' barcode and a 3' barcode.

34. The method of any one of claims 1-33, wherein the nucleic acid molecules comprise mRNAs.
35. The method of claim 34, wherein the mRNAs comprise at least 1, 3, 10, 30, 100, 300, 1,000, 3,000, 10,000, 30,000, 100,000, 300,000, or 1,000,000 mRNAs.
36. The method of any one of claims 1-35, wherein the barcodes in the nucleic acid sample are identified by sequencing.
37. The method of any one of claims 1-3, wherein the set of barcodes comprises at least two 5' nucleic acid constructs each construct comprising a unique 5' barcode.
38. The method of any one of claims 1-3, wherein the set of barcodes comprises at least two 3' nucleic acid constructs each construct comprising a unique 3' barcode.
39. The method of claim 1, wherein one or more of the nucleic acid molecules comprises two or more unique barcodes.
40. The method of claim 39, wherein the unique barcodes are located at the 5' end, the '3' end or both the 5' and 3' end of the nucleic acid molecules.
41. The method of any one of claims 1-40, wherein the method comprises forming a plurality of reaction mixtures.
42. The method of claim 41, wherein two or more unique barcodes are present in 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of the reaction mixtures.
43. The method of claim 41, wherein forming the plurality of reaction mixtures comprises adding the set of barcodes to the plurality of reaction mixtures at a lambda greater than 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2.0, 3.0, 4.0 or 5.0.
44. The method of any one of claims 1-40, wherein the reaction mixture is a droplet.
45. A method of identifying the origin of a nucleic acid sample comprising the steps of:

- (a) providing a set of 3' nucleic acid constructs each construct comprising a unique 3' barcode sequence, a binding sequence, and a barcode association sequence;
- (b) providing a nucleic acid sample comprising nucleic acid molecules from a single cell;
- (c) contacting the nucleic acid sample with the set of 3' nucleic acid constructs;
- (d) separating the 3' barcode sequence and binding sequence from the barcode association sequence;
- (e) incorporating into the nucleic acid molecules the 3' barcode sequences from the 3' nucleic acid constructs; and
- (f) identifying the set of 3' barcode sequences using the barcode association sequences thereby identifying the origin of the nucleic acid sample from the single cell.

46. The method of claim 45, wherein the set of 3' nucleic acid constructs comprises 2, 3, 4, 5, 6, 7, or 8 3' nucleic acid constructs.

47. The method of claim 45 or 46, wherein the 3' nucleic acid constructs further comprise unique molecular identifier (UMI) sequences.

48. The method of any one of claims 45-47, wherein the 3' nucleic acid construct is capable of forming a hairpin.

49. The method of any one of claims 45-48, wherein the 3' barcode sequence and binding sequence are separated from the barcode association segment by a restriction enzyme sequence or photocleavable linker.

50. The method of any one of claims 45-49, wherein multiple copies of the 3' nucleic acid constructs are attached to a solid surface.

51. The method of claim 50, wherein the solid surface is a bead, microbead, microparticle, microsphere, nanoparticle, nanobead or hydrogel.

52. The method of claim 51, a restriction enzyme releases the 3' barcode sequence from the solid surface and separates the binding sequence from the barcode association segment.
53. The method of claim 51, wherein UV light releases the 3' barcode sequence from the solid surface and separates the binding sequence from the barcode association segment.
54. The method of any one of claims 45-53, wherein the binding sequence on the 3' nucleic acid constructs comprises a poly-T sequence.
55. The method of claim 54, wherein the binding sequence of the 3' nucleic acid constructs binds to the poly-A sequences on the nucleic acid molecules of the sample.
56. The method of any one of claims 45-55, wherein the barcode sequences on the 3' nucleic acid constructs are incorporated by reverse transcription.
57. The method of claim 56, wherein the reverse transcription produces nucleic acid molecules comprising the 3' barcode sequence.
58. The method of any one of claims 45-57, wherein the barcode association segment comprises a priming sequence.
59. The method of claim 58, wherein the priming sequence is a palindromic sequence.
60. The method of claim 58, wherein the priming sequence of one barcode association segment is capable of binding the priming sequence of any other barcode association segment in the nucleic acid sample.
61. The method of claim 59, wherein the barcode association segments that have contacted each other are extended by a DNA polymerase to incorporate both barcode association segments into a single nucleic acid.

62. The method of any one of claims 45-61, wherein the method further comprises identifying the barcode sequences incorporated into the nucleic acid molecules.
63. The method of claim 62, wherein the barcode sequences in the nucleic acid sample are identified by sequencing.
64. The method of claim 62 , wherein the barcode association segments are identified by sequencing.