

CLAIMS**WHAT IS CLAIMED IS:**

1. A method for analyzing a single cell process in a cell sample, comprising:
 - (a) providing a plurality of analyte carriers, a plurality of control beads, and a plurality of barcode beads;
 - (b) generating a plurality of partitions comprising a first partition and a second partition, wherein (i) said first partition comprises an analyte carrier from said plurality of analyte carriers and a first barcode bead from said plurality of barcode beads, wherein said analyte carrier comprises a template nucleic acid molecule, and wherein said first barcode bead comprises a first nucleic acid barcode molecule comprising a first barcode sequence, and (ii) said second partition comprises a control bead from said plurality of control beads and a second barcode bead from said plurality of barcode beads, wherein said second barcode bead comprises a second nucleic acid barcode molecule comprising a second barcode sequence, wherein said second barcode sequence is different than said first barcode sequence, and wherein said control bead comprises a nucleic acid molecule comprising a known sequence;
 - (c) using (i) said template nucleic acid molecule and said first nucleic acid barcode molecule to generate a barcoded template nucleic acid molecule and (ii) said nucleic acid molecule comprising said known sequence and said second nucleic acid barcode molecule to generate a barcoded nucleic acid molecule comprising said known sequence; and
 - (d) sequencing said barcoded template nucleic acid molecule, or derivative thereof, and said barcoded nucleic acid molecule, or derivative thereof wherein (i) a sequence of said barcoded template nucleic acid molecule identifies said analyte carrier, and (ii) a sequence of said barcoded nucleic acid molecule identifies said control bead.
2. The method of claim 1, further comprising identifying said known sequence to analyze said single cell process.
3. The method of any one of claims 1-2, further comprising providing a plurality of second control beads, wherein said plurality of partitions comprises a third partition, wherein said third partition comprises a third barcode bead from said plurality of barcode beads and a second control bead from said plurality of second control beads, wherein said third barcode bead comprises a third nucleic acid barcode molecule comprising a third barcode sequence, wherein

said third barcode sequence is different than said first barcode sequence and said second barcode sequence, and wherein said second control bead comprises a second nucleic acid molecule comprising a second known sequence, wherein said second known sequence is different from said known sequence.

4. The method of any one of claims 1-3, further comprising generating a second barcoded nucleic acid molecule comprising said second known sequence, wherein a sequence of said second barcoded nucleic acid molecule identifies said second known sequence.
5. The method of any one of claims 1-4, further comprising processing said known sequence and said second known sequence to analyze said single cell process.
6. The method of any one of claims 1-5, wherein said processing comprises comparing a frequency of said known sequence and a frequency of said second known sequence to analyze said single cell process.
7. The method of any one of claims 1-6, wherein said processing further comprising determining a doublet rate.
8. The method of claim 3, wherein said second control bead has a size within 40% deviation from an average size of said analyte carrier.
9. The method of any one of claims 3 or 8, wherein said second control bead has a size within 25% deviation from said average size of said analyte carrier.
10. The method of any one of claims 3 or 8-9, wherein said second control bead has a size within 10% deviation from said average size of said analyte carrier.
11. The method of any one of claims 3 or 8-10, wherein said second control bead has a size within 5% deviation from said average size of said analyte carrier.
12. The method of claim 3, wherein said size of said second control bead has a size within 40% deviation from an average size of said control bead.
13. The method of any one of claims 3 or 12, wherein said second control bead has a size within 25% deviation from said average size of said control bead.
14. The method of any one of claims 3 or 12-13, wherein said second control bead has a size within 10% deviation from said average size of said control bead.
15. The method of any one of claims 3 or 12-14, wherein said second control bead has a size within 5% deviation from said average size of said control bead.
16. The method of any one of claims 1-3, wherein said known sequence is derived from a first species and said second known nucleic acid sequence is derived from a second species.
17. The method of any one of claims 1-16, wherein said first species is a human and wherein said second species is a mouse.

18. The method of any one of claims 1-17, wherein said control bead has a size within 40% deviation from an average size of said analyte carrier.
19. The method of any one of claims 1-18, wherein said control bead has a size within 25% deviation from said average size of said analyte carrier.
20. The method of any one of claims 1-19, wherein said control bead has a size within 10% deviation from said average size of said analyte carrier.
21. The method of any one of claims 1-20, wherein said control bead has a size within 5% deviation from said average size of said analyte carrier.
22. The method of any one of claims 1-21, wherein said control bead has a size between from about 15 micrometers to about 35 micrometers.
23. The method of any one of claims 1-21, wherein said control bead has a size between from about 35 micrometers to about 60 micrometers.
24. The method of any one of claims 1-23, wherein a given bead from said plurality of barcode beads comprises a plurality of nucleic acid barcode molecules comprising a common barcode sequence.
25. The method of any one of claims 1-24, wherein said common barcode sequence is different from common barcode sequences of other beads of said plurality of beads.
26. The method of any one of claims 1-25, further comprising, prior to (b), mixing analyte carriers from said plurality of analyte carriers with control beads of said plurality of control beads.
27. The method of any one of claims 1-26, further comprising, prior to (b), mixing analyte carriers from said plurality of analyte carriers with control beads of said plurality of control beads and control beads of said second plurality of control beads.
28. The method of any one of claims 1-27, wherein said control beads from said plurality of control beads is present in said mixture at a first concentration, wherein said control beads from said second plurality of control beads is present in said mixture at a second concentration, and wherein said first concentration and said second concentration are known.
29. The method of any one of claims 1-28, wherein a ratio of said first concentration to said second concentration is at least about 1:0.001.
30. The method of any one of claims 1-28, wherein a ratio of a concentration of said analyte carriers in said mixture to said first concentration is known.
31. The method of claim 30, wherein said ratio is about 0.001:1.
32. The method of any one of claims 1-31, wherein said control bead comprises a plurality of unique nucleic acid molecules with known nucleic acid sequences that vary in length, concentration, and/or GC content.

33. The method of any one of claims 1-32, wherein said plurality of unique nucleic acid molecules is a plurality of DNA molecules.
34. The method of any one of claims 1-32, wherein said plurality of unique nucleic acid molecules is a plurality of RNA molecules.
35. The method of any one of claims 1-34, wherein (i) said control bead comprises a first plurality of unique nucleic acid molecules with known nucleic acid sequences that vary in length, concentration, and/or GC content, and wherein (ii) said second control bead comprises a second plurality of unique nucleic acid molecules with known nucleic acid sequences that vary in length, concentration, and/or GC content, wherein said first plurality of unique nucleic acid molecules and said second plurality of unique nucleic acid molecules are different.
36. The method of claim 35, wherein said first plurality of unique nucleic acid molecules and said second plurality of unique nucleic acid molecules are both a plurality of DNA molecules.
37. The method of claim 35, wherein said first plurality of unique nucleic acid molecules and said second plurality of unique nucleic acid molecules are both a plurality of RNA molecules.
38. The method of claim 35, wherein a given bead from said plurality of barcode beads comprises a plurality of nucleic acid barcode molecules, wherein each of said plurality of nucleic acid barcode molecules comprises an identifier sequence, wherein said identifier sequence is different from identifier sequences associated with other nucleic acid barcode molecules in said plurality of nucleic acid barcode molecules.
39. The method of any one of claims 35-38, further comprising identifying a first set of identifiers associated with said first plurality of unique nucleic acid molecules and a second set of identifiers associated with said second plurality of unique nucleic acid molecules.
40. The method of claim 39, further comprising processing said first set of identifiers and said second set of identifiers to determine an identifier purity for said single cell process.
41. The method of any one of claims 1-40, wherein a given bead from said plurality of barcode beads comprises a plurality of nucleic acid barcode molecules releasably attached thereto.
42. The method of any one of claims 1-41, wherein said first nucleic acid barcode molecule and said second nucleic acid barcode molecule is released from said first barcode bead and said second barcode bead.
43. The method of any one of claims 1-42, wherein said plurality of barcode beads is a plurality of gel beads.
44. The method of any one of claims 1-43, wherein said nucleic acid molecule comprising the known sequence is releasably attached to said control bead.
45. The method of any one of claims 1-44, wherein the control bead is a gel bead.

46. The method of any one of claims 1-45, wherein said control bead comprises a first functional group, and said nucleic acid molecule comprising the known sequence comprises a second functional group.
47. The method of any one of claims 1-46, wherein said nucleic acid molecule comprising the known sequence is attached to said control bead by reacting said first functional group with said second functional group.
48. The method of any one of claims 46-47, wherein said first functional group is an alkyne, a *trans*-cyclooctene, an avidin, or any combination thereof.
49. The method of any one of claims 46-48, wherein said first functional group is an alkyne.
50. The method of any one of claims 46-49, wherein said second functional group is an azide, a tetrazine, a biotin, or a combination thereof.
51. The method of any one of claims 46-50, wherein said second functional group is an azide.
52. The method of any one of claim 46-51, wherein said first functional group reacts with said second functional group in a click reaction.
53. The method of any one of claim 46-52, wherein said click reaction is a copper-catalyzed azide-alkyne cycloaddition reaction, an inverse-electron demand Diels-Alder reaction, or an avidin-biotin interaction.
54. The method of any one of claim 46-53, wherein said click reaction is a copper-catalyzed azide-alkyne cycloaddition reaction.
55. The method of any one of claims 46-47, wherein said first functional group is a carboxylic acid, and said second functional group is an amine.
56. The method of claim 55, wherein said first functional group reacts with said second functional group via an amide bond formation reaction.
57. The method of any one of claims 55-56, wherein said amide bond formation reaction further comprises 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC), N-hydroxysuccinimide (NHS), or a combination thereof.
58. The method of any one of claims 1-57, wherein said nucleic acid molecule comprising the known sequence is releasably attached to said control bead.
59. The method of any one of claims 1-58, wherein said nucleic acid molecule comprising the known sequence is released from said control bead.
60. The method of any one of claims 1-59, wherein said nucleic acid molecule comprising the known sequence is within said control bead.
61. The method of any one of claims 1-60, wherein said known sequence is synthetic.

62. The method of any one of claims 1-60, wherein said known sequence is derived from a biological sample.
63. The method of any one of claims 1-62, wherein said control bead comprises a protein-DNA complex and said nucleic acid molecule comprising the known sequence is part of said protein-DNA complex.
64. The method of any one of claims 1-63, wherein said known sequence comprises defined protein binding sites.
65. The method of any one of claims 1-64, wherein said single cell process comprises ATAC-seq.
66. The method of any one of claims 1-65, wherein said plurality of analyte carriers is a plurality of cells.
67. The method of any one of claims 1-65, wherein said plurality of analyte carriers is a plurality of nuclei.
68. The method of any one of claims 1-65, wherein said plurality of analyte carriers is a plurality of cell beads.
69. The method of any one of claims 1-68, wherein said plurality of partitions is a plurality of droplets.
70. The method of any one of claims 1-68, wherein said plurality of partitions is a plurality of wells.
71. A kit for analyzing a cellular sample comprising analyte carriers, comprising:
- (a) a set of control beads, wherein at least a subset of said set of control beads comprise (i) identical nucleic acid molecules each comprising a known nucleic acid sequence, and (ii) has a characteristic corresponding to within 70% deviation from an average value of said characteristic of said analyte carriers; and
 - (b) an index comprising said known nucleic acid sequence.
72. The kit of claim 71, wherein said characteristic is selected from a group consisting of size, shape, density, conductivity, hardness, deformability, and hydrophobicity.
73. The kit of any one of claims 71-72, wherein said index comprises a concentration of said known nucleic acid sequence.
74. The kit of any one of claims 71-73, wherein a subset of said set of control beads comprises additional identical nucleic acid molecules that are different than said identical nucleic acid molecules, each of which additional nucleic acid molecules comprises an additional known nucleic acid sequence.
75. The kit of any one of claims 73-74, wherein said index comprises said additional known nucleic acid sequence.

76. The kit of any one of claims 73-75, wherein said index comprises a concentration of said additional known nucleic acid sequence.
77. The kit of any one of claims 71-76, wherein said known nucleic acid sequence and said additional known nucleic acid sequence vary in length, concentration, and/or GC content.
78. The kit of any one of claims 71-77, wherein said set of control beads comprises a first subset of control beads and a second subset of control beads.
79. The kit of any one of claims 71-78, wherein said first subset of control beads comprises a first set of nucleic acid molecules comprising a first set of known sequences, and said second subset of control beads comprises a second set of nucleic acid molecules comprising a second set of known sequences.
80. The kit of claim 79, wherein said first set of known sequences comprises 96 different known sequences and said second set of known sequences comprises 96 different known sequences.
81. The kit of any one of claims 79-80, wherein said 96 different known sequences of said first set of known sequences are different then said 96 different known sequences of said second set of known sequences.
82. The kit of any one of claims 78-81, wherein said first subset of control beads and said second subset of control beads are present in a ratio.
83. The kit of claim 82, wherein said ratio is at least about 1:0.001, 1:0.01, 1:0.1, 1:0.2, 1:0.3, 1:0.4, 1:0.5, 1:0.6, 1:0.7, 1:0.8, 1:0.9, 1:1, 1:1.1, 1:1.2, 1:1.3, 1:1.4, 1:1.5, 1:1.6, 1:1.7, 1:1.8, 1:1.9, 1:2, 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:20, 1:30, 1:40, 1:50, 1:60, 1:70, 1:80, 1:90, 1:100, or 1:1000.
84. The kit of claim 82, wherein said ratio is at most about 1:1000, 1:100, 1:90, 1:80, 1:70, 1:60, 1:50, 1:40, 1:30, 1:20, 1:10, 1:9, 1:8, 1:7, 1:6, 1:5, 1:4, 1:3, 1:2, 1:1.9, 1:1.8, 1:1.7, 1:1.6, 1:1.5, 1:1.4, 1:1.3, 1:1.2, 1:1.1, 1:1, 1:0.9, 1:0.8, 1:0.7, 1:0.6, 1:0.5, 1:0.4, 1:0.3, 1:0.2, 1:0.1, 1:0.01, or 1:0.001.
85. The kit of claim 82, wherein said ratio is about 1:2.