[0007] An aspect of the present disclosure provides a method for processing or analyzing a metabolite from a cell. The method comprises: (a) generating a partition comprising (i) the metabolite, (ii) one or more beads (e.g., a single bead, a plurality of beads) comprising a plurality of nucleic acid cell barcode molecules each comprising a cell barcode sequence and a capture sequence, which cell barcode sequence uniquely corresponds to the cell, and (iii) a molecular complex that is capable of coupling to the metabolite, where the molecular complex comprises a molecular complex capture sequence and a molecular complex identifier sequence, where the molecular complex capture sequence is inaccessible to the capture sequence in the absence of the metabolite coupled to the molecular complex; (b) in the partition, providing conditions sufficient for the metabolite to couple to the molecular complex to (i) render the molecular complex capture sequence accessible to the capture sequence of a given nucleic acid cell barcode molecule of the plurality of nucleic acid cell barcode molecules and (ii) permit the capture sequence to couple to the molecular complex capture sequence; and (c) with the capture sequence coupled to the molecular complex capture sequence, using the given nucleic acid cell barcode molecule and the molecular complex to synthesize a nucleic acid molecule comprising (1) a first nucleic acid sequence corresponding to the molecular complex identifier sequence, and (2) a second nucleic acid sequence corresponding to the cell barcode sequence, where the first nucleic acid sequence and the second nucleic acid sequence permit the metabolite to be identified as corresponding to the cell. In some cases, a corresponding sequence may be a complementary sequence.

[0007a] Another aspect of the present disclosure provides a method for processing or analyzing a metabolite from a cell, comprising: (a) generating a partition comprising (i) said metabolite, (ii) a bead comprising a plurality of nucleic acid cell barcode molecules each comprising a cell barcode sequence and a capture sequence, which cell barcode sequence uniquely corresponds to said cell, and (iii) a molecular complex that is capable of coupling to said metabolite, wherein said molecular complex comprises a molecular complex capture sequence and a molecular complex identifier sequence, wherein said molecular complex capture sequence is inaccessible to said capture sequence in the absence of said metabolite coupled to said molecular complex; (b) in said partition, providing conditions sufficient for said metabolite to couple to said molecular complex to (i) render said molecular complex capture sequence accessible to said capture sequence of a given nucleic acid cell barcode molecule of said plurality of nucleic acid cell barcode molecules and (ii) permit said capture sequence to couple to said molecular complex capture sequence; and (c) with said capture sequence coupled to said molecular complex capture sequence, using said given nucleic acid cell barcode molecule and said molecular complex to synthesize a nucleic acid molecule comprising (1) a first nucleic acid

sequence corresponding to said molecular complex identifier sequence, and (2) a second nucleic acid sequence corresponding to said cell barcode sequence, wherein said first nucleic acid sequence and said second nucleic acid sequence permit said metabolite to be identified as corresponding to said cell.

[0008] In some embodiments, the method further comprises sequencing at least a portion of the nucleic acid molecule or a derivative thereof, to identify the molecular complex identifier sequence and the cell barcode sequence. In some embodiments, the method further comprises using the molecular complex identifier sequence and the cell barcode sequence to identify the metabolite as originating from the cell. In some embodiments, the molecular complex is a riboswitch. In some embodiments, the partition comprises the cell. In some embodiments, the method further comprises, after (a), releasing the metabolite from the cell.

[0009] In some embodiments, the method further comprises, prior to (c), releasing the nucleic acid cell barcode molecule from the bead. In some embodiments, the nucleic acid cell barcode molecule is released from the bead upon exposure to a chemical stimulus in the partition. In some embodiments, (c) is performed in the partition. In some embodiments, the method further comprises releasing or recovering the nucleic acid molecule or a derivative thereof from the partition. In some embodiments, in (c), the nucleic acid molecule is synthesized using one or more of a nucleic acid amplification reaction, a reverse transcription reaction and a template switching reaction.

CLAIMS

WHAT IS CLAIMED IS:

1. A method for processing or analyzing a metabolite from a cell, comprising:

(a) generating a partition comprising (i) said metabolite, (ii) a bead comprising a plurality of nucleic acid cell barcode molecules each comprising a cell barcode sequence and a capture sequence, which cell barcode sequence uniquely corresponds to said cell, and (iii) a riboswitch that is capable of coupling to said metabolite, wherein said riboswitch comprises a riboswitch capture sequence and a riboswitch identifier sequence, wherein said riboswitch capture sequence is inaccessible to said capture sequence in the absence of said metabolite coupled to said riboswitch;

(b) in said partition, providing conditions sufficient for said metabolite to couple to said riboswitch to (i) render said riboswitch capture sequence accessible to said capture sequence of a given nucleic acid cell barcode molecule of said plurality of nucleic acid cell barcode molecules and (ii) permit said capture sequence to couple to said riboswitch capture sequence; and

(c) with said capture sequence coupled to said riboswitch capture sequence, using said given nucleic acid cell barcode molecule and said riboswitch to synthesize a nucleic acid molecule comprising (1) a first nucleic acid sequence corresponding to said riboswitch identifier sequence, and (2) a second nucleic acid sequence corresponding to said cell barcode sequence, wherein said first nucleic acid sequence and said second nucleic acid sequence permit said metabolite to be identified as corresponding to said cell.

2. The method of claim 1, further comprising sequencing at least a portion of a sequence of said nucleic acid molecule, to identify said riboswitch identifier sequence and said cell barcode sequence.

3. The method of claim 2, further comprising using said riboswitch identifier sequence and said cell barcode sequence to identify said metabolite as originating from said cell.

4. The method of claim 1, wherein said partition comprises said cell.

5. The method of claim 4, further comprising, after (a), releasing said metabolite from said cell.

6. The method of claim 1, further comprising, prior to (c), releasing said plurality of nucleic acid cell barcode molecules from said bead.

7. The method of claim 6, wherein said nucleic acid cell barcode molecule is released from said bead upon exposure to a chemical stimulus in said partition.

8. The method of claim 1, wherein (c) is performed in said partition.

9. The method of claim 8, further comprising releasing or recovering a sequence of said nucleic acid molecule from said partition.

10. The method of claim 1, wherein in (c), said nucleic acid molecule is synthesized using one or more reactions selected from the group consisting of a nucleic acid amplification reaction, a reverse transcription reaction and a template switching reaction.

11. The method of claim 1, further comprising subjecting said nucleic acid molecule to one or more additional reactions.

12. The method of claim 11, wherein said one or more additional reactions comprise a primer extension reaction.

13. The method of claim 11, wherein said one or more additional reactions comprise addition of one or more functional sequences to said nucleic acid molecule, wherein said one or more functional sequences are configured to permit coupling of a sequence of said nucleic acid molecule to a flow cell of a sequencer.

14. The method of claim 1, wherein said bead is a gel bead.

15. The method of claim 1, wherein while said nucleic acid molecule is synthesized, said nucleic acid cell barcode molecule is attached to said bead.

16. The method of claim 1, wherein said partition comprises an additional riboswitch that is capable of coupling to an additional metabolite that is different than said metabolite of (a).

17. The method of claim 16, wherein said bead comprises an additional plurality of nucleic acid cell barcode molecules each comprising said cell barcode sequence and an additional capture sequence capable of coupling to an additional riboswitch capture sequence of said additional riboswitch when said additional metabolite is coupled to said additional riboswitch.

18. The method of claim 17, further comprising:

in said partition, providing conditions sufficient for said additional metabolite to couple to said additional riboswitch to (iii) render said additional riboswitch capture sequence accessible to said additional capture sequence of a given additional nucleic acid cell barcode molecule of said additional plurality of nucleic acid cell barcode molecules and (iv) permit said additional capture sequence to couple to said additional riboswitch capture sequence; and

with said additional capture sequence coupled to said additional riboswitch capture sequence, using said given additional nucleic acid cell barcode molecule and said additional riboswitch to synthesize an additional nucleic acid molecule comprising (3) a third nucleic acid sequence corresponding to said additional riboswitch identifier sequence, and (4) a fourth additional nucleic acid sequence corresponding to said cell barcode sequence, wherein said third nucleic acid sequence and said fourth nucleic acid sequence permit said additional metabolite to be identified as corresponding to said cell.

19. The method of claim 1, wherein said plurality of nucleic acid cell barcode molecules comprises at least 100,000 nucleic acid cell barcode molecules.

20. The method of claim 1, wherein said partition is a droplet among a plurality of droplets.

21. The method of claim 1, wherein said partition is a well among a plurality of wells.

22. The method of claim 1, wherein said metabolite is selected from the group consisting of adenosine triphosphate (ATP), adenosine diphosphate (ADP), adenosine monophosphate (AMP), guanosine triphosphate (GTP), guanosine diphosphate (GDP), guanosine monophosphate (GMP), ribose, glucose, mannose, glycerol, phosphatidyl choline, phosphoryl choline, glyceryl phosphoryl choline, phosphatidyl serine, phosphatidyl ethanolamine, diglyceride, nicotinamide adenine dinucleotide phosphate, nicotinamide adenine dinucleotide, glycine, glutamine, aspartic acid, citrate, glycerine, acetone, acetoacetic acid and lysine.

23. The method of claim 1, wherein each of said plurality of nucleic acid cell barcode molecules comprises an identifier sequence separate from said cell barcode sequence, and wherein said identifier sequence is different for each nucleic acid cell barcode molecule of said at least said subset of said plurality of nucleic acid cell barcode molecules.

24. The method of claim 1, wherein, in (a), each of said plurality of nucleic acid cell barcode molecules comprises said cell barcode sequence, wherein said bead is from a plurality of beads, and wherein said cell barcode sequence is different from cell barcode sequences of nucleic acid cell barcode molecules of other beads of said plurality of beads.

25. The method of claim 1, wherein said bead comprises a plurality of additional nucleic acid cell barcode molecules each comprising said cell barcode sequence and a binding sequence, which binding sequence is capable of coupling to an additional nucleic acid molecule different from said riboswitch.

26. The method of claim 25, wherein said additional nucleic acid molecule is selected from the group consisting of a ribonucleic acid molecule (RNA) of said cell, a deoxyribonucleic acid

molecule (DNA) of said cell, and an editing nucleic acid molecule capable of participating in a gene editing reaction.

27. The method of claim 25, further comprising, prior to (a), exposing a protein of said cell to an antibody coupled to said additional nucleic acid molecule, wherein said antibody binds to said protein.

28. The method of claim 25, wherein said partition comprises said additional nucleic acid molecule, and said method further comprises, permitting a given additional nucleic acid cell barcode molecule of said additional plurality of nucleic acid cell barcode molecules to bind to said additional nucleic acid molecule via said binding sequence.

29. The method of claim 28, further comprising, using said additional nucleic acid molecule and said given additional nucleic acid cell barcode molecule of said additional plurality of nucleic acid cell barcode molecules to synthesize a reporter nucleic acid molecule comprising (3) a third nucleic acid sequence corresponding to a sequence of said reporter nucleic acid molecule, and (4) a fourth nucleic acid sequence corresponding to said cell barcode sequence.

30. The method of claim 29, further comprising sequencing at least a portion of a sequence of said reporter nucleic acid molecule, to identify said additional nucleic acid molecule as associated with said cell.