CLAIMS

1. A single-cell transcriptome sequencing method comprising:

preparing a single-cell suspension with a test cell sample and then fixing cells with a fixative solution; and

synthesizing a first cDNA strand using by performing an in-situ reverse transcription reaction on RNA of the fixed single cell using a reverse transcription primer.

2. The method of claim 1, wherein the reverse transcription primer is a random reverse transcription primer, a reverse transcription primer designed for a target RNA sequence, or a mixture of the random reverse transcription primer and the reverse transcription primer designed for the target RNA sequence.

3. The method of claim 1, further comprising adding a capture adapter to an end of the first cDNA strand obtained by the in-situ reverse transcription reaction, wherein the capture adapter is sequence-complementary to a complementary strand of the capture adapter on a coding bead, and the capture adapter is a random fragment of a known sequence.

4. The method of claim 3, further comprising embedding the single cell and the single coding bead into a single chamber after adding the capture adapter, to separate the single cell and synthesize a second cDNA strand in the single chamber.

5. The method of claim 4, further comprising amplifying double-stranded cDNA via PCR, constructing a library and performing sequencing, after the second cDNA strand is synthesized.

6. The method of claim 3, wherein a single-stranded DNA on the coding bead used in the method comprises a complementary fragment of an upstream amplification primer, a barcode, a UMI, and a complementary strand of the capture adapter.

7. The method of claim 3, wherein the separation of the single cells is completed by a microfluidic chip or a microwell used in the method.

8. The method of claim 1, wherein the fixative solution is a simple fixative solution or a mixed fixative solution.

9. The method of claim 1, for use in whole-transcriptome sequencing of a single cell, a single nucleus, or a single microorganism.

10. The method of claim 3, wherein the capture adapter is a Poly(dA) fragment, a Poly(dT) fragment, a Poly(dG) fragment, or a Poly(dC) fragment.

11. The method of claim 6, wherein the barcode comprises one or more barcodes.

12. The method of claim 11, wherein the barcode comprises three barcodes.

13.The method of claim 8, wherein the simple fixative solution comprises paraformaldehyde, formaldehyde, formalin, methanol, acetone, ethanol, acetic acid, picric acid, chromic acid, potassium dichromate, or mercury bichloride.

14. The method of claim 8, wherein the mixed fixative solution comprises acetic acid-alcohol mixture, formalin-acetic acid-alcohol solution, or Bouin's fixative solution.

15. The method of claim 9, for use in fields of microbiology, basic medicine, clinical medicine, agronomy, cell biology, immunology, developmental biology, pathology, neurobiology and neurodevelopment, genetics, stem cells, tumors, reproductive health, metagenomics, microecology, or new drug development.