CLAIMS

1. A method of simultaneously preparing RNA and DNA libraries in a single compartment from a sample, comprising:

providing a sample comprising DNA and RNA, wherein the RNA comprises a 3' polyA tail;

tagmenting the DNA with a 3' polyA tail using transposomes with polyA transposons;

contacting the sample in a single compartment with a polyT capture probe configured to hybridize to the 3' polyA tail of the RNA and the DNA, wherein the capture probe comprises a first common sequence (CS1);

hybridizing the capture probe to the RNA and to the DNA, thereby simultaneously capturing DNA and RNA;

converting the RNA to cDNA; and

simultaneously generating a cDNA library and a gDNA library.

2. The method of Claim 1, wherein the capture probe is immobilized on a solid support.

3. The method of Claim 1, wherein the capture probe further comprises a substrate recognition sequence.

4. The method of Claim 1, wherein the sample is a population of cells, a single cell, a population of cell nuclei, or a cell nucleus.

5. The method of Claim 2, wherein the solid support is a substrate, an etched surface, a well, a covered well, a sealed well, an array, a flowcell device, a microfluidic channel, a bead, a magnetic bead, a column, a droplet, or a microparticle.

6. The method of Claim 1, further comprising performing DNA analysis, RNA analysis, protein analysis, tagmentation, nucleic acid amplification, nucleic acid sequencing, assay for transposase accessible chromatic using sequencing (ATAC-seq), contiguity-preserving transposition (CPT-seq), single cell combinatorial indexed sequencing (SCI-seq), or single cell genome amplification, or any combination thereof.

7. The method of Claim 1, further comprising simultaneously analyzing in the single compartment a protein, wherein the protein is tagged.

8. The method of Claim 1, wherein the sample comprises a cell, and wherein the cell is fixed with a fixative.

9. The method of Claim 8, wherein the fixative comprises an alcohol, optionally including methanol, ethanol, an aldehyde, or a para-formaldehyde.

10. The method of Claim 1, wherein the CS1 is used for downstream amplification, molecular indexing, or molecular demultiplexing.

11. The method of Claim 1, wherein the RNA is converted to cDNA by reverse transcriptase.

12. The method of Claim 1, further comprising purifying the cDNA and gDNA from a cell nucleus using column purification.

13. The method of Claim 1, further comprising tagmenting the cDNA and the DNA to incorporate a second common sequence (CS2) configured to generate full-length RNA , and to incorporate molecular indexes.

14. The method of Claim 13, wherein the full-length RNA is generated using template switching activity of reverse transcriptase and a template switching oligonucleotide (TSO).