What is claimed is:

1. A method of preparing a sequencing library comprising nucleic acids from a plurality of single cells, the method comprising:

(a) providing isolated nuclei from a plurality of cells;

(b) subjecting the isolated nuclei to a chemical treatment to generate nucleosome-depleted nuclei, while maintaining integrity of the isolated nuclei;

(c) distributing subsets of the nucleosome-depleted nuclei into a first plurality of compartments and contacting each subset with a transposome complex, wherein the transposome complex in each compartment comprises a transposase and a first index sequence that is different from first index sequences in the other compartments;

(d) fragmenting nucleic acids in the subsets of nucleosome-depleted nuclei into a plurality of nucleic acid fragments and incorporating the first index sequences into at least one strand of the nucleic acid fragments to generate indexed nuclei comprising indexed nucleic acid fragments, wherein the indexed nucleic acid fragments remain attached to the transposases;

(e) combining the indexed nuclei to generate pooled indexed nuclei;

(f) distributing subsets of the pooled indexed nuclei into a second plurality of compartments;

(g) incorporating into the indexed nucleic acid fragments in each compartment a second index sequence to generate dual-index fragments, wherein the second index sequence in each compartment is different from second index sequences in the other compartments;

(h) combining the dual-index fragments, thereby producing a sequencing library comprising whole genome nucleic acids from the plurality of single cells.

2. The method of claim 1, wherein the chemical treatment comprises a treatment with a chaotropic agent capable of disrupting nucleic acid-protein interactions.

3. The method of claim 2, wherein the chaotropic agent comprises lithium 3,5-diiodosalicylic acid.

4. The method of claim 3, wherein the chemical treatment comprises a treatment with a detergent capable of disrupting nucleic acid-protein interactions.

5. The method of any one of claims 2 to 4, wherein the detergent comprises sodium dodecyl sulfate (SDS).

6. The method of claim 5, wherein the nuclei are treated with the cross-linking agent prior to step (b).

7. The method of claim 6, wherein the cross-linking agent is formaldehyde.

8. The method of claim 7, wherein the concentration of formaldehyde ranges from about 0.2% to about 2%.

9. The method of claim 7, wherein the concentration of formaldehyde is no greater than about 1.5%.

10. The method of claim 7, wherein the cross-linking by formaldehyde is reversed after step (f) and prior to step (g).

11. The method of claim 10, wherein the reversal of the cross-linking comprises incubation at about 55°C to about 72°C.

12. The method of any one of claims 10 or 11, wherein the transposases are disassociated from the indexed nucleic acid fragments prior to the reversal of the cross-linking.

13. The method of claim 12, wherein the transposases are disassociated from the indexed nucleic acid fragments using sodium dodecyl sulfate (SDS).

14. The method of claim 1, wherein the nuclei are treated with a restriction enzyme prior to step (d).

15. The method of claim 14, wherein the nuclei are treated with a ligase after treatment with the restriction enzyme.

16. The method of claim 1, wherein the distributing in steps (c) and (f) is performed by fluorescence-activated nuclei sorting.

17. The method of claim 1, wherein the subsets of the nucleosome-depleted nuclei comprise approximately equal numbers of nuclei.

18. The method of claim 17, wherein the subsets of the nucleosome-depleted nuclei comprise from 1 to about 2000 nuclei.

19. The method of claim 1, wherein the first plurality of compartments is a multi-well plate.

20. The method of claim 19, wherein the multi-well plate is a 96-well plate or a 384-well plate.

21. The method of claim 1, wherein the subsets of the pooled indexed nuclei comprise approximately equal numbers of nuclei.

22. The method of claim 21, wherein the subsets of the pooled indexed nuclei comprise from 1 to about 25 nuclei.

23. The method of claim 1, wherein the subsets of the pooled indexed nuclei include at least 10 times fewer nuclei than the subsets of the nucleosome-depleted nuclei.

24. The method of claim 1, wherein the subsets of the pooled indexed nuclei include at least 100 times fewer nuclei than the subsets of the nucleosome-depleted nuclei.

25. The method of claim 1, wherein the second plurality of compartments is a multi-well plate.

26. The method of claim 25, wherein the multi-well plate is a 96-well plate or a 384-well plate.

27. The method of claim 1, wherein step (c) comprises adding the transposome complex to the compartments after the subsets of nucleosome-depleted nuclei are distributed.

28. The method of claim 1, wherein each of the transposome complexes comprises a transposon, each of the transposons comprising a transferred strand.

29. The method of claim 28, wherein the transferred strand comprises the first index sequence and a first universal sequence.

30. The method of claim 29, wherein the incorporation of the second index sequence in step (g) comprises contacting the indexed nucleic acid fragments in each compartment with a first universal primer and a second universal primer, each comprising an index sequence and each comprising a sequence identical to or complementary to a portion of the first universal sequence, and performing an exponential amplification reaction.

31. The method of claim 30, wherein the index sequence of the first universal primer is the reverse complement of the index sequence of the second universal primer.

32. The method of claim 30, wherein the index sequence of the first universal primer is different from the reverse complement of the index sequence of the second universal primer.

33. The method of claim 30, wherein the first universal primer further comprises a first capture sequence and a first anchor sequence complementary to a universal sequence at the 3' end of the dual-index fragments.

34. The method of any one of claims 30 to 33, wherein the first capture sequence comprises the P5 primer sequence.

35. The method of claim 30, wherein the second universal primer further comprises a second capture sequence and a second anchor sequence complementary to a universal sequence at the 5' end of the dual-index fragments.

36. The method of claim 35, wherein the second capture sequence comprises the reverse complement of the P7 primer sequence.

37. The method of claim 30, wherein the exponential amplification reaction comprises a polymerase chain reaction (PCR).

38. The method of claim 37, wherein the PCR comprises 15 to 30 cycles.

39. The method of claim 1, further comprising an enrichment of dual-index fragments using a plurality of capture oligonucleotides having specificity for the dual-index fragments.

40. The method of claim 39, wherein the capture oligonucleotides are immobilized on a surface of a solid substrate.

41. The method of any one of claims 39 to 40, wherein the capture oligonucleotides comprise a first member of a universal binding pair, and wherein a second member of the binding pair is immobilized on a surface of a solid substrate.

42. The method of claim 1, further comprising sequencing of the dual-index fragments to determine the nucleotide sequence of nucleic acids from the plurality of single cells.

43. The method of claim 42, further comprising:

providing a surface comprising a plurality of amplification sites, wherein the amplification sites comprise at least two populations of attached single stranded capture oligonucleotides having a free 3' end, and

contacting the surface comprising amplification sites with the dual-index fragments under conditions suitable to produce a plurality of amplification sites that each comprise a clonal population of amplicons from an individual dual-index fragment.

44. The method of claim 43, wherein the number of the dual-index fragments exceeds the number of amplification sites, wherein the dual-index fragments have fluidic access to the amplification sites, and wherein each of the amplification sites comprises a capacity for several dual-index fragments in the sequencing library.

45. The method of any one of claims 43 to 44, wherein the contacting comprises simultaneously (i) transporting the dual-index fragments to the amplification sites at an average transport rate, and (ii) amplifying the dual-index fragments that are at the amplification sites at an average amplification rate, wherein the average amplification rate exceeds the average transport rate.

46. A composition comprising chemically treated nucleosome-depleted isolated nuclei, wherein the isolated nuclei comprise indexed nucleic acid fragments.

47. The composition of claim 46, wherein the isolated nuclei comprise non-natural cross-links.

48. The composition of claim 46, wherein the composition comprises indexed nucleic acid fragments that terminate in a cleaved restriction site comprising an overhang.

49. The composition of any one of claims 46 to 48, wherein the isolated nuclei comprise rearranged genomic DNA.

50. A multi-well plate, wherein a well of the multi-well plate comprises the composition of any one of claims 46-49.