CLAIMS

What is claimed is:

1. A method for detecting accessible chromatin, comprising:
   a) obtaining a transposase complex comprising a transposase bound to at least one nucleic acid adapter, wherein said transposase or said at least one nucleic acid adapter comprises a detectable label;
   b) contacting chromatin with said transposase complex under conditions suitable for transposase binding to accessible regions in said chromatin; and
   c) detecting said detectable label.

2. The method of claim 1,
   wherein said at least one nucleic acid adapter comprises (i) a recognition sequence for said transposase and (ii) said detectable label, and
   wherein contacting said chromatin with said transposase complex is performed under conditions suitable for transposition, thereby joining said at least one nucleic acid adapter with said chromatin at accessible regions in said chromatin.

3. The method of claim 1,
   wherein said transposase comprises said detectable label and is bound to at least one nucleic acid adapter comprising a recognition sequence for said transposase; and
   wherein contacting said chromatin with said transposase complex is performed under conditions suitable for binding of said transposase to accessible regions in said chromatin.

4. The method of claim 2 or 3, wherein said at least one nucleic acid adapter comprises i) a first oligonucleotide comprising the nucleotide sequence of SEQ ID NO:1 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO:1, and ii) a second oligonucleotide comprising a sequence sufficiently complementary to and capable of hybridizing with a portion of said first oligonucleotide such that said at

least one nucleic acid adapter comprises at least a portion that is double-stranded, wherein said double stranded portion comprises said recognition sequence for said transposase.

5. The method of any prior claim, wherein said at least one nucleic acid adapter comprises (i) a first nucleic acid adapter comprising a first oligonucleotide comprising the nucleotide sequence of SEQ ID NO: l or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: l and a second oligonucleotide comprising the nucleotide sequence of SEQ ID NO:2 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO:2, and (ii) a second nucleic acid adapter comprising a third oligonucleotide comprising the nucleotide sequence of SEQ ID NO: l or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: l and a fourth oligonucleotide comprising the nucleotide sequence of SEQ ID NO:3 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: 3.

6. The method of any prior claim, wherein said detectable label is a fluorophore, a metal particle, a magnetic particle, an isotopic label, a chemiluminescent label, a ligand, a mass tag, a quantum dot or a hapten.

7. The method of claim 6, wherein said fluorophore is an ATTO fluorescent dye.

8. The method of any prior claim, wherein said detecting comprises performing fluorescence imaging or flow cytometry.

9. The method of any of claim 1-7, wherein said detecting comprises performing electron microscopy.

10. The method of any of claims 1-7, wherein said detecting comprises performing mass cytometry.

11. The method of any prior claim, further comprising identifying regulatory elements, a transcription factor binding site, or a nucleosome binding site in said accessible chromatin.

12. The method of any prior claim, further comprising mapping positions of sites that said at least one nucleic acid adapter inserts into said accessible chromatin.

13. The method of any prior claim, further comprising sequencing DNA at sites where said at least one nucleic acid inserts into said accessible chromatin.

14. The method of any prior claim, wherein said method is performed on chromatin *in situ* inside a cell, wherein said cell is a living cell or a fixed cell.

15. The method of claim 14, wherein said cell is a permeabilized cell.

16. The method of any of claims 1-13, wherein said method is performed on isolated chromatin.

17. The method of any prior claim, further comprising sorting cells based on labeling of their accessible chromatin by said detectable label.

18. The method of any prior claim, further comprising generating tagged nucleic acid fragments from said chromatin.

19. The method of claim 18, further comprising amplifying said tagged nucleic acid fragments.

20. The method of claim 18, further comprising sequencing said tagged nucleic acid fragments or a derivative thereof.

21. The method of any prior claim, wherein said transposase is a MuA transposase.

22. The method of any prior claim, wherein said transposase is a Tn transposase.

23. The method of claim 22, wherein said Tn transposase is a Tn5 transposase.

24. The method of claim 23, wherein said Tn5 transposase is a hyperactive Tn5 transposase.

25. The method of any prior claim, further comprising performing fluorescent in situ hybridization (FISH) on DNA from said chromatin.

26. A composition comprising a transposase complex comprising a transposase bound to at least one nucleic acid adapter, wherein either said transposase or said at least one nucleic acid adaptor comprises a detectable label.

27. The composition of ciaim 26, wherein said at least one nucleic acid adapter comprises i) a first oligonucleotide comprising the nucleotide sequence of SEQ ID NO:1 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO:1, and ii) a second oligonucleotide comprising a sequence sufficiently complementary to and capable of hybridizing with a portion of said first oligonucleotide such that said at least one nucleic acid adapter comprises at least a portion that is double-stranded, wherein said double stranded portion comprises a recognition sequence for said transposase, wherein said at least one nucleic acid adapter is capable of transposase catalyzed insertion into accessible chromatin.

28. The composition of claim 26, wherein said at least one nucleic acid adapter comprises (i) a first nucleic acid adapter comprising a first oligonucleotide comprising the nucleotide sequence of SEQ ID NO: l or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: l and a second oligonucleotide comprising the nucleotide sequence of SEQ ID NO:2 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO:2, and (ii) a second nucleic acid adapter

comprising a third oligonucleotide comprising the nucleotide sequence of SEQ ID NO: l or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: l and a fourth oligonucleotide comprising the nucleotide sequence of SEQ ID NO:3 or a nucleotide sequence having at least 95% identity to the sequence of SEQ ID NO: 3.

29. The composition of any of claims 26-28, wherein said detectable label is a fluorophore, a metal particle, a magnetic particle, an isotopic label, a chemiluminescent label, a ligand, a mass tag, a quantum dot or a hapten.

30. The composition of claim 29, wherein said fluorophore is an ATTO fluorescent dye.