CLAIMS

1. A method of preparing a population of target nucleic acids for sequencing comprising:

(a) providing a substrate having a surface comprising capture probes;

(b) contacting the surface with a reaction volume comprising a plurality of template nucleic acids and transposomes, wherein each transposome comprises a transposon sequence and a transposase, wherein the template nucleic acids are prepared by contacting a target nucleic acid with a plurality of transposomes; and

(c) associating the template nucleic acids with the capture probes; wherein step (c) comprises contacting the capture probes and the template nucleic acids with a recombinase.

2. The method of claim 1, wherein the template nucleic acids and the capture probes each comprise an affinity moiety selected from the group consisting of biotin, avidin, and streptavidin.

3. The method of claims 1 or 2, wherein step (c) comprises binding the affinity moiety of the template nucleic acids with the affinity moiety of the capture probes.

4. The method of any one of claims 1-3, wherein the transposon sequence comprises a sequence selected from the group consisting of a barcode, unique molecular identifier, a sequencing primer, and a fragmentation site; and wherein the method further comprises cleaving the fragmentation site.

5. The method of claim 4, wherein the fragmentation site is cleaved after step (c).

6. The method of any one of claims 1-5, wherein the transposase is removed by contacting the transposase with a protease or SDS after step (b) or after step (c).

7. The method of any one of claims 1-6, wherein at least one transposome is different from at least one other transposome.

8. The method of any one of claims 1-7, wherein the surface comprises at least about 10,000 associated template nucleic acids per mm^2.

9. The method of any one of claims 1-7, wherein the surface comprises at least about 100,000 associated template nucleic acids per mm^2.

10. The method of any one of claims 1-7, wherein the surface comprises at least about 1,000,000 associated template nucleic acids per mm^2.

11. A reaction vessel for preparing and sequencing a library of template nucleic acids from a target nucleic acid according to the method of any one of claims 1-10, comprising: a substrate comprising a surface having a capture probes; and a reaction volume in fluid communication with the surface, wherein the reaction volume comprises:
a transposase,
a plurality of template nucleic acids prepared by contacting a target nucleic acid with a plurality of transposomes, each transposome comprising a transposon sequence and the transposase,
a polymerase or ligase; and a recombinase.

12. The reaction vessel of claim 11, wherein the capture probes are attached at sites that form a repeating pattern on the surface, and the capture probes are restricted to the sites on the surface and absent at interstitial regions between the sites.

13. The reaction vessel of claims 11 or 12, wherein the reaction volume comprises a protease or SDS, and reagents for removing the transposase in the presence of the protease or SDS.

14. The reaction vessel of any one of claims 11-13, wherein the reaction volume

comprises reagents for associating the template nucleic acids with the capture probes in the presence of the recombinase.

15. The reaction vessel of any one of claims 11-14, wherein at least one of the template nucleic acids and at least one of the capture probes each comprise an affinity moiety.

16. The reaction vessel of claim 15, wherein the affinity moiety is selected from the group consisting of biotin, avidin, and streptavidin.

17. The reaction vessel of any one of claims 15-16, wherein the affinity moiety of at least one of the template nucleic acids is attached to the affinity moiety of at least one of the capture probe.

18. The reaction vessel of any one of claims 11-17, wherein the transposon sequence comprises a sequence selected from the group consisting of a barcode, an unique molecular identifier, a sequencing primer, and a fragmentation site.

19. The reaction vessel of any one of claims 11-18, wherein the transposome comprises two transposons; and optionally, wherein the transposon sequences are different from each other.

20. The reaction vessel of any one of claims 11-19, wherein the surface comprises at least about 10,000 template nucleic acids per mm^2.

21. The reaction vessel of claim 11-19, wherein the surface comprises at least about 100,000 template nucleic acids per mm^2.

22. The reaction vessel of claim 11-19, wherein the surface comprises at least about 1,000,000 template nucleic acids per mm^2.

23. A flow cell comprising the reaction vessel of any one of claims 11-22.

24. A system for sequencing a target nucleic acid comprising:
the reaction vessel of any one of claims 11-22;
a thermocycler for modulating the temperature of the reaction vessel;
and a detector for collecting signals from the reaction vessel.

25. The system of claim 24, comprising a processor comprising instructions to modulate the temperature of the reaction vessel to perform steps comprising: transposing the transposon sequences into the target nucleic acid, extending the template nucleic acids with the polymerase or ligase, and associating the template nucleic acids with the capture moieties.

26. The system of claim 25, wherein the instructions to modulate the temperature of the reaction vessel to perform steps comprises amplifying the template nucleic acids associated with the capture probes.

27. The system of claim 26, wherein the amplification is bridge amplification.