

CLAIMS

1. A method of preparing a population of target nucleic acids for sequencing comprising:
 - (a) providing a substrate having a surface comprising a capture moiety;
 - 5 (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
 - 10 (c) 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 moiety each comprise an affinity moiety selected from the group consisting of biotin, avidin, and streptavidin.
- 15 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
- 20 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.
- 25 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 mm².
- 30 9. The method of any one of claims 1-7, wherein the surface comprises at least about 100,000 associated template nucleic acids per mm².
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 mm².

11. A reaction vessel for sequencing a target nucleic acid of any one of claims 1-10, comprising: a substrate comprising a surface having a capture moiety; and a reaction volume in fluid communication with the surface comprising:
a transposase,
5 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, and
a polymerase or ligase; wherein the capture moiety are a plurality of capture probes, wherein the capture probes are attached at sites that form a repeating
10 pattern on the surface.
12. The reaction vessel of claim 11, wherein 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 reagents for removing the transposase in the presence of a protease
15 or SDS.
14. The reaction vessel of any one of claims 11-13, wherein the capture moiety are plurality of capture probes, and wherein the reaction volume comprises reagents for associating the template nucleic acids with the capture probes in the presence of a recombinase.
- 20 15. The reaction vessel of any one of claims 11-14, wherein the capture moiety are a plurality of capture probes, and 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.
- 25 17. The reaction vessel of any one of claims 11-16, wherein the capture moiety are plurality of capture probes, and wherein the capture probes comprise a recombinase.
18. 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
30 least one of the capture probe.
19. The reaction vessel of any one of claims 11-18, 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.

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

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

22. The reaction vessel of claim 11-20, wherein the surface comprises at least about 100,000 template nucleic acids per mm^2 .

10 23. The reaction vessel of claim 11-20, wherein the surface comprises at least about 1,000,000 template nucleic acids per mm^2 .

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

25. A system for sequencing a target nucleic acid comprising:

the reaction vessel of any one of claims 11-23;

a thermocycler for modulating the temperature of the reaction vessel;

15 and a detector for collecting signals from the reaction vessel.

26. The system of claim 25, 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
20 template nucleic acids with the capture moieties.

27. The system of claim 26, wherein the capture moiety are plurality of capture probes, and 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.

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