

Claims

1. A method, comprising:
loading degradable hydrogel beads onto a sequencing flow cell under conditions sufficient for capture of the degradable hydrogel beads on a surface of the sequencing flow cell, wherein:
the degradable hydrogel beads contain sequencing libraries prepared from encapsulated genetic material; or
the degradable hydrogel beads contain encapsulated genetic material, and the method further comprises preparing sequencing libraries in the captured degradable hydrogel beads from the genetic material; and
loading a liquid diffusion barrier onto the sequencing flow cell that surrounds the hydrogel beads;
and
degrading the captured hydrogel beads in the presence of the liquid diffusion barrier to inhibit diffusion of the sequencing libraries beyond a diameter of the corresponding hydrogel bead, and to allow transport and seeding of the sequencing libraries to the surface of the sequencing flow cell.
2. The method of claim 1, wherein the genetic material is selected from at least one of target nucleic acid molecules, or cells, and cell lysate comprising target nucleic acid molecules.
3. The method of claim 1 or claim 2, wherein the sequencing libraries comprise DNA or RNA of at least 150 nucleotides in length.
4. The method of claim 2, wherein the target nucleic acid molecule is genomic DNA.
5. The method of any one of the prior claims, wherein the liquid diffusion barrier is an oil, a viscous aqueous solution, or a combination thereof.
6. The method of claim 5, wherein the oil is mineral oil, silicone oil, perfluorinated oil, or a combination of two or more thereof.
7. The method of claim 5, wherein the viscous aqueous solution is a solution containing polyethylene glycol (PEG), poly-vinyl-pyrrolidone, pluronic dextran, sucrose, poly(*N*-isopropylacrylamide) or polyethylene oxide-polypropylene oxide-polyethylene oxide (PEO-PPO-PEO)/laponite, or a combination of two or more thereof.
8. The method of any one of the prior claims, wherein the hydrogel beads are degraded by:
(a) contacting the hydrogel beads with a reagent that cleaves a reversible crosslinker that crosslinks polymers of the hydrogel;
(b) heating the hydrogel beads to about 90°C;

(c) exposing the hydrogel beads to a wavelength of light that cleaves a photo-cleavable crosslinker that crosslinks polymer of the hydrogel; or

(d) a combination of (a) and (b); (a) and (c); (b) and (c); or (a), (b), and (c).

9. The method of claim 8, wherein the reagent comprises dithiothreitol (DTT), tris(2-carboxyethyl)phosphine (TCEP), tris(3-hydroxypropyl)phosphine (THP), or a combination of two or more thereof.

10. The method of any one of the prior claims, wherein the hydrogel beads have a diameter of from about 5 μm to about 120 μm .

11. The method of any of the prior claims, wherein the hydrogel beads are hollow hydrogel beads comprising hollow cores comprising the genetic material.

12. The method of any one of the prior claims, wherein the hydrogel beads comprise pores having a diameter of sufficient size to allow diffusion of reagents through the hydrogel beads while retaining the encapsulated sequencing libraries.

13. The method of claim 12, wherein the pores have a diameter of from about 10 nm to about 100 nm.

14. The method of any one of the prior claims, wherein preparing the sequencing libraries comprises performing a tagmentation reaction on target nucleic acid molecules within the hydrogel beads.

15. The method of claim 14, wherein the tagmentation reaction comprises contacting the target nucleic acid molecules with a transposase mixture comprising adapter sequences and transposomes.

16. The method of any one of the prior claims, wherein the capture of the hydrogel beads on the surface of the sequencing flow cell comprises one or more of:

physical constraint of the hydrogel beads on the surface of the sequencing flow cell; and

specific binding of a first member of a specific binding pair on the hydrogel beads to a second member of the specific binding pair on the surface of the sequencing flow cell.

17. The method of claim 16, comprising the physical constraint of the hydrogel beads on the surface of the sequencing flow cell, wherein the diameter of the hydrogel beads is from about 5% to about 30% greater than the height of the flow cell to constrain the beads in the flow cell.

18. The method of any one of the prior claims, wherein the diameter of the hydrogel beads is about 110 μm , and the height of the sequencing flow cell is about 100 μm .

19. The method of claim 16, wherein the sequencing flow cell is a patterned flow cell, and the second member of the specific binding pair is located at wells of the patterned flow cell.

20. The method of any one of the prior claims, wherein the sequencing libraries are not barcoded to identify individual hydrogel beads.

21. The method of any one of the prior claims, further comprising amplifying target nucleic acid molecules encapsulated with the degradable hydrogel beads.

22. The method of claim 21, wherein the amplification involves multiple displacement amplification.

23. The method of claim 21, wherein the encapsulated target nucleic acid molecules are genomic DNA and the amplification involves whole-genome amplification.

24. The method of any one of the prior claims, further comprising sequencing the sequencing libraries.

25. The method of claim 24, wherein the location on the surface of the flow cell of sequencing libraries seeded from respective degradable hydrogel beads is used as a spatial index for reads generated from the sequencing of the sequence libraries.