

Claims:

1. A method of preparing immobilized templates for a nucleic acid sequencing reaction comprising:

5 (a) providing a solid support having a plurality of forward and reverse amplification primers immobilized thereon, wherein a subset of said plurality of amplification primers comprises a cleavage site;

(b) amplifying a target nucleic acid template using the subset of amplification primers on the support to produce a plurality of double-stranded nucleic acid molecules, wherein both strands of each double-stranded nucleic acid molecule are attached to the solid support at their 5' ends;

10 (c) cleaving the subset of amplification primers at the cleavage site to produce a linearized amplification product comprising a cleaved non-immobilized strand and a complementary immobilized strand; and

(d) subjecting the amplification product to partially-denaturing conditions to facilitate hybridization of a 3' terminal portion of the cleaved non-immobilized strand with a complementary immobilized amplification primer, followed by extension of the immobilized amplification primer to generate an immobilized copy of the non-immobilized strand of the amplification product.

15 2. The method of claim 1, wherein the subset of surface bound primers are the forward primers.

3. The method of claim 1, wherein the subset of surface bound primers are the reverse primers.

4. The method of claim 1, wherein the partially-denaturing conditions comprise adding one or more components of a recombinase/polymerase amplification reaction to facilitate strand invasion.

5. The method of claim 1, wherein the partially-denaturing conditions comprise subjecting the template to conditions suitable for template walking.

6. The method of claim 1, wherein step (d) comprises applying primers in solution to facilitate hybridization of the primers to the non-immobilized end of the immobilized amplification product.

7. The method of claim 6, wherein the subset of primers comprises forward amplification primers and the primers in solution comprise forward amplification primers.
8. The method of claim 6, wherein the subset of primers comprises reverse amplification primers and the primers in solution comprise reverse amplification primers.
9. The method of any of claims 1-8, further comprising sequencing the target nucleic acid.
10. The method of claim 9, wherein sequencing the target nucleic acid comprises:
- hybridizing one or more sequencing primers to an immobilized nucleic acid strand;
 - extending the one or more sequencing primers by incorporating one or more labeled nucleotides into a nascent strand; and
 - detecting the labeled nucleotides, thereby obtaining sequence information about the target nucleic acid.
11. The method of any of claims 1-10, wherein said solid support is planar.
12. The method of any of claims 1-11, wherein said solid support comprises microwells.
13. The method of any of claims 1-12, wherein said target nucleic acid has a length of at least 10, 20, 50, 100, 200 or at least 500 nucleotides.