

What is claimed is:

1. A method of sequencing a target sequence comprising:
 - a) hybridizing a sample nucleic acid with a capture nucleic acid molecule and a blocking nucleic acid molecule, wherein the sample nucleic acid comprises the target sequence and non-target sequence;
 - b) isolating the capture nucleic acid molecule hybridized to the target sequence; and
 - c) sequencing the isolated target sequence.
2. The method of claim 1, wherein the non-target sequence comprises a repetitive and/or related region of nucleic acid.
3. The method of claim 1, wherein the blocking nucleic acid molecule and the capture nucleic acid molecule comprise at least about 60 to at least 120 nucleic acids.
4. The method of claim 1, wherein the capture nucleic acid is labeled.
5. The method of claim 4, wherein the capture nucleic acid is labeled with a label selected from the group consisting of radioactive phosphates, biotin, fluorophores, enzymes or combinations thereof.
6. The method of claim 1, wherein the blocking nucleic acid molecule is present in 10x fold excess of the capture nucleic acid molecule.
7. The method of claim 1, wherein the blocking nucleic acid molecule has at least about 70% sequence identity to the capture nucleic acid molecule.
8. The method of claim 1, wherein the blocking nucleic acid molecule has at least about four nucleic acid molecules different from the capture nucleic acid molecule.
9. The method of claim 1, wherein the target sequence comprises at least about 60 to about at least 120 nucleic acids.
10. The method of claim 1, wherein the sequencing comprises next generation sequencing.
11. A method of improving sequencing specificity and/or accuracy of a target sequence comprising:
 - a) hybridizing a sample nucleic acid with a capture nucleic acid molecule and a blocking nucleic acid molecule wherein the sample nucleic acid comprises the target sequence and non-target sequence;
 - b) isolating the capture nucleic acid molecule hybridized to the target sequence; and

c) sequencing the target sequence.

12. The method of claim 11, wherein the non-target sequence comprises a repetitive and/or related region of nucleic acid.
13. The method of claim 11, wherein the blocking nucleic acid molecule and the capture nucleic acid molecule comprise at least about 60 to at least 120 nucleic acids.
14. The method of claim 11, wherein the capture nucleic acid is labeled.
15. The method of claim 14, wherein the capture nucleic acid is labeled with a label selected from the group consisting of radioactive phosphates, biotin, fluorophores, enzymes or combinations thereof.
16. The method of claim 11, wherein the blocking nucleic acid molecule is present in 10x fold excess of the capture nucleic acid molecule.
17. The method of claim 11, wherein the blocking nucleic acid molecule has at least about 70% sequence identity to the capture nucleic acid molecule.
18. The method of claim 11, wherein the blocking nucleic acid molecule has at least about four nucleic acid molecules different from the capture nucleic acid molecule.
19. The method of claim 11, wherein the target sequence comprises at least about 60 to at least 120 nucleic acids.
20. The method of claim 11, wherein the sequencing comprises next generation sequencing.