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, wherein the blocking nucleic acid molecule comprises 60-120 nucleotides, has at least 89% sequence identity to the capture nucleic acid molecule, has at least four bases different from the capture nucleic acid molecule, and is configured to hybridize to the 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 capture nucleic acid molecule comprises at least 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 10 fold excess of the capture nucleic acid molecule.

7. The method of claim 1, wherein the target sequence comprises at least 60 to at least 120 nucleic acids.

8. The method of claim 1, wherein the sequencing comprises next generation sequencing.

9. 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, wherein the blocking nucleic acid molecule comprises 60-120 nucleotides, has at least 89% sequence identity to the capture

nucleic acid molecule, has at least four bases different from the capture nucleic acid molecule, and is configured to hybridize to the non-target sequence;

b) isolating the capture nucleic acid molecule hybridized to the target sequence; and

c) sequencing the target sequence.

10. The method of claim 9, wherein the non-target sequence comprises a repetitive and/or related region of nucleic acid.

11. The method of claim 9, wherein the capture nucleic acid molecule comprises at least 60 to at least 120 nucleic acids.

12. The method of claim 9, wherein the capture nucleic acid is labeled.

13. The method of claim 12, wherein the capture nucleic acid is labeled with a label selected from the group consisting of radioactive phosphates, biotin, fluorophores, enzymes or combinations thereof.

14. The method of claim 9, wherein the blocking nucleic acid molecule is present in 10 fold excess of the capture nucleic acid molecule.

15. The method of claim 9, wherein the target sequence comprises at least 60 to at least 120 nucleic acids.

16. The method of claim 9, wherein the sequencing comprises next generation sequencing.