What is claimed is:

1. A method of capturing a nucleic acid from a sample comprising a target nucleic acid and non-target nucleic acids, the method comprising:
    a. contacting a double-stranded target nucleic acid with a nucleic acid targeting nucleic acid (NATNA) and a CRISPR Cas9 or Cas12a endonuclease to cleave the target nucleic acid adjacent to a protospacer adjacent motif (PAM) to thereby generate a 3'-end in the double stranded target nucleic acid;
    b. contacting a double-stranded target nucleic acid, having a 3'-end generated by cleavage of the nucleic acid with a CRISPR Cas9 or Cas12a endonuclease, with fewer than four of the dATP, dCTP, dGTP and dTTP, and a DNA polymerase possessing 3'-5'-exonuclease activity wherein the 3'-5' exonuclease activity is exhibited in the presence of fewer than four of the dATP, dCTP, dGTP and dTTP, and the 3'-5' exonuclease activity stops at the nucleotide identical to one of the fewer than four dATP, dCTP, dGTP and dTTP thereby generating a first 5'-overhang at a first 5'-end and a first recessed 3'-end in the target nucleic acid;
    c. contacting the nucleic acid with an adaptor having a second 5'-overhang at a second 5'-end, the second 5'-overhang capable of hybridizing to the first 5'-overhang thereby forming a hybrid between the first and second 5'-overhangs; wherein the second 5'overhang comprises a sequence adjacent to the PAM and the PAM, and
    d. linking the first recessed 3'-end with the second 5'-end thereby capturing the target nucleic acid by forming an adapted nucleic acid.

2. The method of claim 1, wherein the adaptor further comprises a second recessed 3'-end, and the linking in step d. further comprises linking the first 5'-end with the second 3'-end.

3. The method of claim 1, wherein the 3'-end of the double-stranded target nucleic acid is a part of a 3'-overhang.

4. The method of claim 1, wherein the DNA polymerase is selected from the group consisting of: a Family A polymerase, a Family B polymerase or a Family C polymerase having the Exo I, Exo II and Exo III domains of the Klenow fragment of the *E. coli* Pol I, a DNA polymerase having aspartame residues corresponding to the residues D355, D424 and D501 of the Klenow fragment of *E. coli* Pol I, T4 DNA polymerase, RB69 DNA polymerase, Klenow fragment, T7 DNA polymerase, *E. coli* Pol III delta fragment, eukaryotic pol epsilon, eukaryotic pol delta, and mitochondrial pol gamma.

5. The method of claim 1, wherein each 5'-overhang is 2-15 nucleotides long.

6. The method of claim 1, wherein the adaptor comprises at least one of a nucleic acid barcode selected from a unique molecular ID (UMI) and a sample ID (SID), a sequencing primer binding site and an amplification primer binding site.

7. The method of claim 1, wherein the adaptor comprises a sequence selected from SEQ ID NOs: 7-11.

8. The method of claim 1, further comprising amplifying the captured nucleic acid.

9. The method of claim 8, wherein an amplification primer anneals to a primer binding site in the adaptor and the amplification primer comprises a sequence selected from SEQ ID NOs: 12-16.

10. The method of claim 1, wherein the adaptor is linked to a capture moiety, and the method further comprises capturing the capture moiety in the adapted nucleic acid thereby capturing the nucleic acid.

11. The method of claim 10, wherein the capture moiety is selected from biotin, an antigen capable of binding to a capture antibody, and a capture sequence capable of hybridizing to a capture nucleic acid.

12. The method of claim 1, further comprising sequencing the captured nucleic acid.

13. The method of claim 12, wherein a sequencing primer anneals to a primer binding site present in an amplification primer.

14. The method of claim 1, wherein the captured nucleic acid is 1, 10 or 100 kb long.

15. The method of claim 1, wherein no purification steps are performed between steps b. and c. or b. and d.

16. The method of claim 1, wherein the NATNA is an engineered guide RNA optionally comprising one or more DNA residues.