Claims:

1. A method of trimming nucleic acid fragments for sequencing comprising the steps of:

    a. Amplifying a nucleic acid fragment with a primer comprising a sequence substantially complementary to a target sequence and a first recognition site for a restriction enzyme;

    b. Digesting the amplified nucleic acid fragment with a first restriction enzyme to remove the primer of the nucleic acid fragment thereby exposing the target sequence;

    c. Ligating the target sequence with an adaptor comprising a second recognition site for a restriction enzyme; and

    d. Digesting the ligated sequence with a second restriction enzyme at the ligated sequence for further trimming the nucleic acid fragment for sequencing.

2. The method of claim 1 wherein the first restriction enzyme cleaves the sequence outside of the first recognition site and the second restriction enzyme cleaves the sequence outside of the second recognition sites.

3. The method of claim 1 wherein the first or second restriction enzyme is selected from BpmI or MmeI.

4. The method of claim 1 wherein the first or second recognition sites comprise SEQ ID NO.: 1 and the first or second restriction enzyme comprises SEQ ID NO.:2.

5. The method of claim 1 further comprising the step of forming a nucleic acid library using whole genome amplification prior to step (a).

6. The method of claims 5 further comprising the step of computationally removing any bias in the nucleic acid library.

7. A method of trimming a nucleic acid comprising the steps of:

a. Amplifying a nucleic acid with a pair of primers, wherein each primer comprises a restriction enzyme recognition site, thereby producing an amplified nucleic acid fragment;

b. Digesting the amplified nucleic acid fragment with a restriction enzyme that recognizes the restriction enzyme recognition site of step (a) thereby producing a digested nucleic acid fragment;

c. Ligating the digested nucleic acid fragment with a pair of adaptors, wherein each adaptor comprises a restriction enzyme recognition site thereby producing a ligated nucleic acid fragment; and

d. Digesting the ligated nucleic acid fragment with a restriction enzyme that recognizes the restriction enzyme recognition site, thereby at producing a trimmed target nucleic acid fragment.

8. A method of trimming a nucleic acid comprising the steps of:

a. Amplifying a nucleic acid with a pair of primers, wherein each primer comprises a restriction enzyme recognition site, thereby producing an amplified nucleic acid fragment;

b. Digesting the amplified nucleic acid fragment with a restriction enzyme that recognizes the restriction enzyme recognition site of step (a) and cleaves nucleic acid outside of the restriction enzyme recognition site of step (a), thereby producing a digested nucleic acid fragment;

c. Ligating the digested nucleic acid fragment with a pair of adaptors, wherein each adaptor comprises a restriction enzyme recognition site thereby producing a ligated nucleic acid fragment; and

d. Digesting the ligated nucleic acid fragment with a restriction enzyme that recognizes the restriction enzyme recognition site of step (c) and cleaves nucleic acid outside of the restriction enzyme recognition site of step (c), thereby at producing a trimmed target nucleic acid fragment.