WE CLAIM:

1. A method for assembling two or more nucleic acids, comprising:

(a) contacting a first nucleic acid with a first nuclease agent, wherein the first nuclease agent comprises a Cas protein and a guide RNA (gRNA) (gRNA-Cas complex), a zinc finger nuclease, or a Transcription Activator-Like Effector Nuclease (TALEN), wherein the first nuclease agent cleaves the first nucleic acid at a first target site to produce a first digested nucleic acid with an overlapping end sequence shared by a second nucleic acid;

(b) contacting the first digested nucleic acid and the second nucleic acid with an exonuclease to expose complementary sequences between the first digested nucleic acid and the second nucleic acid; and

(c) assembling the two nucleic acid fragments generated from step (b).

2. The method of claim 1, wherein step (c) comprises:

(i) annealing the exposed complementary sequences;

(ii) extending the 3’ ends of the annealed complementary sequences; and

(iii) ligating the first and the second nucleic acids.

3. The method of claim 1 or 2, wherein the two or more nucleic acids are double stranded.

4. The method of any one of claims 1-3, wherein step (a) further comprises contacting the second nucleic acid with a second nuclease agent, wherein the second nuclease agent cleaves the second nucleic acid at a second target site to produce a second digested nucleic acid with the overlapping end sequence, and

wherein the second nucleic acid of step (b) is the second digested nucleic acid.

5. The method of any one of claims 1-4, wherein the first nuclease agent comprises the Cas protein and the gRNA, wherein the Cas protein is a Cas9 protein, the gRNA comprises a nucleic acid sequence encoding a Clustered Regularly Interspaced Short

Palindromic Repeats (CRISPR) RNA (crRNA) and a trans-activating CRISPR RNA (tracrRNA), and the first target site is immediately flanked by a Protospacer Adjacent Motif (PAM) sequence.

6. The method of claim 5, wherein the Cas9 protein comprises a RuvC domain and a HNH domain, at least one of which lacks endonuclease activity.

7. The method of any one of claims 1-6, wherein the overlapping end sequence ranges from 20 bp to 200 bp long.

8. The method of any one of claims 1-7, wherein the first nucleic acid, the second nucleic acid, or both nucleic acids are derived from a bacterial artificial chromosome.

9. The method of claim 8, wherein the bacterial artificial chromosome comprises a human DNA, a rodent DNA, a synthetic DNA, a human polynucleotide sequence, or a combination thereof.

10. A method for assembling two or more nucleic acids, comprising:

(a) contacting a first nucleic acid with at least one nuclease agent, wherein the at least one nuclease agent comprises a Cas protein and a guide RNA (gRNA) (gRNA-Cas complex), a zinc finger nuclease, or a Transcription Activator-Like Effector Nuclease (TALEN), wherein the at least one nuclease agent cleaves the first nucleic acid at a first target site to generate a first digested nucleic acid;

(b) contacting the first digested nucleic acid with a second nucleic acid, a joiner oligo, and an exonuclease,

wherein the joiner oligo comprises:

(i) a first complementary sequence that is complementary to the first digested nucleic acid;

(ii) a spacer; and

(iii) a second complementary sequence that is complementary to the second nucleic acid;

wherein the exonuclease exposes the first and second complementary sequences; and

(c) assembling the joiner oligo with the first digested nucleic acid and the second nucleic acid.

11. The method of claim 10, wherein assembling in step (c) comprises:

(i) annealing the first complementary sequence of the joiner oligo to the first digested nucleic acid and the second complementary sequence of the joiner oligo to the second nucleic acid; and

(ii) ligating the joiner oligo to the first digested nucleic acid and the second nucleic acid.

12. The method of claim 11, wherein step (i) further comprises extending the 3' end of the first digested nucleic acid and/or the second nucleic acid.

13. The method of any one of claims 10-12, wherein the first complementary sequence of the joiner oligo is between 15 and 120 complementary bases, and the second complementary sequence of the joiner oligo is between 15 and 120 complementary bases.

14. The method of any one of claims 10-13, wherein the two or more nucleic acids are double-stranded.

15. The method of any one of claims 10-14, wherein the spacer of the joiner oligo comprises non-complementary nucleic acids.

16. The method of any one of claims 10-14, wherein the first digested nucleic acid is seamlessly assembled to the second nucleic acid.

17. The method of claim 16, wherein the at least one nuclease agent is designed to cleave an at least 20 bp fragment from the end of the first nucleic acid at which the seamless assembly will occur,

wherein the spacer of the joiner oligo comprises a sequence identical to the at least 20 bp fragment, wherein no nucleic acid bases are present between the first complementary sequence and the at least 20 bp fragment, and no nucleic acid bases are present between the second complementary sequence and the at least 20 bp fragment,

such that assembly of the first digested nucleic acid with the joiner oligo and the second nucleic acid reconstitutes the at least 20 bp fragment and seamlessly assembles the first nucleic acid and the second nucleic acid.

18. The method of claim 17, wherein the at least 20 bp fragment is double-stranded.

19. The method of any one of claims 10-18, wherein the spacer is between about 20 bp to about 120 bp.

20. The method of any one of claims 10-19, wherein step (a) further comprises:

(i) contacting the second nucleic acid with a second nuclease agent, wherein the second nuclease agent cleaves the second nucleic acid to produce a second digested nucleic acid comprising a nucleotide sequence that is complementary to the second complementary sequence of the joiner oligo, wherein the first digested nucleic acid is assembled to the second digested nucleic acid; or

(ii) contacting the second nucleic acid with a restriction enzyme or meganuclease, wherein the restriction enzyme or meganuclease cleaves the second nucleic acid to produce a second digested nucleic acid comprising a nucleotide sequence that is complementary to the second complementary sequence in the joiner oligo, wherein the first digested nucleic acid is assembled to the second digested nucleic acid.

21. The method of any one of claims 10-20, wherein the joiner oligo is assembled to the first nucleic acid and the second nucleic acid in the same reaction.

22. The method of any one of claims 10-20, wherein the joiner oligo is assembled to the first nucleic acid and the second nucleic acid sequentially.

23. The method of any one of claims 10-22, wherein the at least one nuclease agent comprises the Cas protein and the gRNA, wherein the Cas protein is a Cas9 protein, wherein the gRNA comprises a nucleic acid sequence encoding a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) RNA (crRNA) and a trans-activating CRISPR

RNA (tracrRNA), and wherein the first target site is immediately flanked by a Protospacer Adjacent Motif (PAM) sequence.

24. The method of claim 23, wherein the Cas9 protein comprises a RuvC domain and a HNH domain, at least one of which lacks endonuclease activity.

25. The method of any one of claims 10-24, wherein the first nucleic acid, the second nucleic acid, or both nucleic acids are derived from a bacterial artificial chromosome.

26. The method of any one of claims 10-25, wherein the first nucleic acid, the second nucleic acid, or both nucleic acids comprise a human DNA, a rodent DNA, a synthetic DNA, or a combination thereof.

27. The method of any one of claims 16-26, wherein the joiner oligo comprises a linear double stranded DNA fragment.

28. The method of claim 27, wherein the linear double stranded DNA fragment does not comprise a selection cassette.

29. The method of claim 27 or 28, wherein the joiner oligo is from about 50 bp to about 400 bp.

30. The method of claim 29, wherein the joiner oligo is from about 100 bp to about 300 bp.

31. The method of any one of claims 10-30, wherein the first complementary sequence of the joiner oligo is between 20 and 80 complementary bases and the second complementary sequence of the joiner oligo is between 20 and 80 complementary bases.

32. The method of any one of claims 10-31, wherein the method is for seamlessly assembling the two or more nucleic acids,

wherein the two or more nucleic acids are double-stranded nucleic acids,

wherein the cleaving in step (a) removes a double-stranded fragment from the end of the first nucleic acid at which the seamless assembly will occur,

wherein the joiner oligo in step (b) is a linear double-stranded DNA that is from about 50 bp to about 400 bp,

wherein the spacer in the joiner oligo comprises a sequence identical to the fragment, wherein no nucleic acid bases are present between the first complementary sequence and the sequence identical to the fragment, and no nucleic acid bases are present between the second complementary sequence and the sequence identical to the fragment, and

wherein the assembly in step (c) reconstitutes the fragment.

33. The method of any preceding claim, wherein the first nucleic acid, the second nucleic acid, or both nucleic acids are at least 10 kb.

34. The method of any preceding claim, wherein at least three nucleic acids are assembled.