What is claimed is:

1. A method of treating a mixture of first double-stranded polynucleotides from a first species and second double-stranded polynucleotides from a second species, the method comprising:

protecting ends of the first double-stranded polynucleotides and any ends of the second double-stranded polynucleotides;

after protecting the ends of the first and second double-stranded polynucleotides, selectively generating free ends within the first double-stranded polynucleotides; and

degrading the first double-stranded polynucleotides from the free ends toward the protected ends.

2. The method of claim 1, wherein selectively generating the free ends within the first double-stranded polynucleotides comprises hybridizing CRISPR-associated protein guide RNA ribonucleoproteins (Cas-gRNA RNPs) to sequences that are present within the first double-stranded polynucleotides and that are not present within the second double-stranded polynucleotides, and cutting the sequences with the Cas-gRNA RNPs.

3. The method of claim 2, wherein the sequences comprise mammalian specific repetitive elements.

4. The method of claim 3, wherein the mammalian specific repetitive elements comprise human specific repetitive elements.

5. The method of claim 1, wherein the first double-stranded nucleotides comprise a plurality of chromosomes from the first species.

6. The method of any one of claims 1 to 5, wherein the second species is bacterial, fungal, or viral.

7. The method of any one of claims 1 to 6, wherein protecting ends of the first and second double-stranded polynucleotides comprises ligating hairpin adapters to the ends.

8. The method of any one of claims 1 to 6, wherein protecting ends of the first and second double-stranded polynucleotides comprises 5’-dephosphorylating the ends.

9. The method of any one of claims 1 to 6, wherein protecting ends of the first and second double-stranded polynucleotides comprises adding modified bases to the ends.

10. The method of claim 9, wherein the modified bases comprise phosphorothioate bonds.

11. The method of claim 9 or claim 10, wherein the modified bases are added using a terminal transferase.

12. The method of any one of claims 1 to 11, wherein degrading the first double-stranded polynucleotides is performed using an exonuclease.

13. The method of any one of claims 1 to 12, wherein the free ends include 3' ends.

14. The method of claim 13, wherein degrading the first double-stranded polynucleotides is performed using exonuclease III.

15. The method of any one of claims 1 to 12, wherein the free ends include 5' ends.

16. The method of claim 15, wherein degrading the first double-stranded polynucleotides is performed using Lambda exonuclease.

17. The method of any one of claims 1 to 16, further comprising subsequently ligating amplification adapters to the ends of any remaining double-stranded polynucleotides in the mixture.

18. The method of claim 17, wherein the amplification adapters include unique molecular identifiers (UMIs).

19. The method of claim 17 or claim 18, further comprising subsequently amplifying and sequencing the double-stranded polynucleotides.

20. The method of any one of claims 1 to 19, wherein the first double-stranded polynucleotides comprise double-stranded DNA.

21. The method of any one of claims 1 to 20, wherein the second double-stranded polynucleotides comprise double-stranded DNA.

22. The method of any one of claims 1 to 21, wherein the second double-stranded polynucleotides comprise circular DNA.

23. The method of any one of claims 1 to 22, wherein the Cas comprises Cas9.

24. A composition, comprising:

first double-stranded polynucleotides from a first species, wherein ends of the first double-stranded polynucleotides are protected;

second double-stranded polynucleotides from a second species, wherein any ends of the second double-stranded polynucleotides are protected; and

CRISPR-associated protein guide RNA ribonucleoproteins (Cas-gRNA RNPs) hybridized to sequences that are present within the first double-stranded polynucleotides and that are not present within the second double-stranded polynucleotides, the Cas-gRNA RNPs being for cutting the sequences so as to selectively generate free ends within the first double-stranded polynucleotides.

25. The composition of claim 24, wherein the sequences comprise mammalian specific repetitive elements.

26. The composition of claim 25, wherein the mammalian specific repetitive elements comprise human repetitive elements.

27. The composition of any one of claims 24 to 26, wherein the second species is bacterial, fungal, or viral.

28. The composition of any one of claims 24 to 27, wherein the ends of the first and second double-stranded polynucleotides are protected using hairpin adapters.

29. The composition of any one of claims 24 to 28, wherein the ends of first and second double-stranded polynucleotides are protected using 5’-dephosphorylation.

30. The composition of any one of claims 24 to 29, wherein the ends of the first and second double-stranded polynucleotides are protected using modified bases.

31. The composition of claim 30, wherein the modified bases comprise phosphorothioate bonds.

32. The composition of any one of claims 24 to 31, wherein the free ends include 3' ends.

33. The composition of any one of claims 24 to 31, wherein the free ends include 5' ends.

34. The composition of any one of claims 24 to 33, wherein the first double-stranded polynucleotides comprise double-stranded DNA.

35. The composition of any one of claims 24 to 34, wherein the second double-stranded polynucleotides comprise double-stranded DNA.

36. The composition of any one of claims 24 to 35, wherein the second double-stranded polynucleotides comprise circular DNA.

37. The composition of any one of claims 24 to 36, wherein the Cas comprises Cas9.