THAT WHICH IS CLAIMED:

1. A nucleic acid molecule comprising a polynucleotide encoding an RNA-guided nuclease (RGN) polypeptide, wherein said polynucleotide comprises a nucleotide sequence encoding an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to ~~any one of~~ SEQ ID NO~~s~~: 1~~, 50, 24, 43, 16, and 35~~;

wherein said RGN polypeptide is capable of binding a target DNA sequence, and wherein said target DNA sequence is located 5' and adjacent to a protospacer adjacent motif (PAM) site having the sequence set forth as SEQ ID NO: 7 ~~in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence~~.

2. The nucleic acid molecule of claim 1, wherein said polynucleotide encoding an RGN polypeptide is operably linked to a promoter heterologous to said polynucleotide.

3. The nucleic acid molecule of claim 1 or 2, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1.

4. The nucleic acid molecule of claim 1 or 2, wherein said RGN polypeptide comprises the amino acid sequence set forth as SEQ ID NO: 1.

~~3~~5. The nucleic acid molecule of claim 1 or 2, wherein said RGN polypeptide is nuclease dead or functions as a nickase.

~~4~~6. The nucleic acid molecule of claim ~~3~~5, wherein the RGN polypeptide is operably fused to a base-editing polypeptide.

~~5~~7. A vector comprising the nucleic acid molecule of any one of claims ~~1-4~~1-6.

~~6~~8. The vector of claim ~~5~~7, wherein said vector further comprises at least one nucleotide sequence encoding said guide RNA, and wherein the guide RNA comprises a CRISPR RNA comprising a CRISPR repeat, ~~sequence selected from the group consisting of:~~

~~a) a CRISPR repeat~~ wherein said CRISPR repeat comprises a nucleotide sequence having at least ~~90%~~95% sequence identity to SEQ ID NO: 2~~, wherein said RGN~~

~~polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;~~

~~b) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 51, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 50;~~

~~c) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 24;~~

~~d) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 44, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 43;~~

~~e) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 16; and~~

~~f) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 35~~.

~~7~~9. The vector of claim ~~6~~8, wherein the guide RNA further comprises a tracrRNA ~~selected from the group consisting of:~~

~~a) a tracrRNA~~ comprising a nucleotide sequence having at least 90% sequence identity to SEQ ID NO: 3~~, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ ID NO: 2 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;~~

~~b) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 52, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ ID NO: 51 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 50;~~

~~c) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ ID NO: 25 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 24;~~

~~d) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 45, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ~~

~~ID NO: 44 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 43;~~

~~e) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 18, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ ID NO: 17 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 16; and~~

~~f) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 37, wherein the CRISPR repeat sequence of said guide RNA has at least 90% sequence identity to SEQ ID NO: 36 and said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 35~~.

10. The vector of claim 8 or 9, wherein said CRISPR repeat comprises the nucleotide sequence set forth as SEQ ID NO: 2.

11. The vector of claim 9 or 10, wherein said tracrRNA comprises a nucleotide sequence having at least 95% sequence identity to SEQ ID NO: 3.

12. The vector of any one of claims 9-11, wherein said tracrRNA comprises the nucleotide sequence set forth as SEQ ID NO: 3.

~~8~~13. A cell comprising the nucleic acid molecule of any one of claims ~~1-4~~1-6 or the vector of any one of claims ~~5-7~~7-12.

~~9~~14. A nucleic acid molecule comprising a polynucleotide encoding a CRISPR RNA (crRNA), wherein said crRNA comprises a spacer sequence and a CRISPR repeat ~~sequence~~, wherein said CRISPR repeat ~~sequence~~ comprises a nucleotide sequence having at least ~~90~~95% sequence identity to ~~any one of~~ SEQ ID NO~~s~~: 2~~, 17, 25, 36, 44, 51, and 63~~;

wherein a guide RNA comprising:

a) said crRNA; and

b) a trans-activating CRISPR RNA (tracrRNA) capable of hybridizing to said CRISPR repeat ~~sequence~~ of said crRNA;

is capable of hybridizing to a target DNA sequence ~~in a sequence specific manner through the spacer sequence of said crRNA~~ when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90%

sequence identity to SEQ ID NO: 1, and wherein said target DNA sequence is located 5' and adjacent to a protospacer adjacent motif (PAM) site having the sequence set forth as SEQ ID NO: 7.

15. The nucleic acid molecule of claim 14, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1.

16. The nucleic acid molecule of claim 14 or 15, wherein said RGN polypeptide comprises the amino acid sequence set forth as SEQ ID NO: 1.

17. The nucleic acid molecule of any one of claims 14-16, wherein said CRISPR repeat comprises the nucleotide sequence set forth as SEQ ID NO: 2.

~~10~~18. The nucleic acid molecule of any one of claims ~~9~~14-17, wherein said polynucleotide encoding a crRNA is operably linked to a promoter heterologous to said polynucleotide.

~~11~~19. A vector comprising the nucleic acid molecule of any one of claims 14-18 ~~9 or 10~~.

~~12~~20. The vector of claim ~~11~~19, wherein said vector further comprises a polynucleotide encoding said tracrRNA.

~~13~~21. A nucleic acid molecule comprising a polynucleotide encoding a trans-activating CRISPR RNA (tracrRNA) comprising a nucleotide sequence having at least 90% sequence identity to ~~any one of~~ SEQ ID NO~~s~~: 3~~, 18, 26, 37, 45, 52, and 62~~;

wherein a guide RNA comprising:

a) said tracrRNA; and

b) a crRNA comprising a spacer sequence and a CRISPR repeat ~~sequence, wherein said tracrRNA is~~ capable of hybridizing ~~with~~ to said tracrRNA~~CRISPR repeat sequence of said crRNA~~;

is capable of hybridizing to a target DNA sequence ~~in a sequence specific manner through the spacer sequence of said crRNA~~ when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90%

sequence identity to SEQ ID NO: 1, and wherein said target DNA sequence is located 5' and adjacent to a protospacer adjacent motif (PAM) site having the sequence set forth as SEQ ID NO: 7, and

wherein said polynucleotide encoding a tracrRNA is operably linked to a promoter heterologous to said polynucleotide.

22. The nucleic acid molecule of claim 21, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1.

23. The nucleic acid molecule of claim 21 or 22, wherein said RGN polypeptide comprises the amino acid sequence set forth as SEQ ID NO: 1.

24. The nucleic acid molecule of any one of claims 21-23, wherein said tracrRNA comprises a nucleotide sequence having at least 95% sequence identity to SEQ ID NO: 3.

25. The nucleic acid molecule of any one of claims 21-24, wherein said tracrRNA comprises the nucleotide sequence set forth as SEQ ID NO: 3.

~~14~~26. A vector comprising the nucleic acid molecule of any one of claims 21-25 ~~13~~.

~~15~~27. The vector of claim ~~13 or 14~~26, wherein said vector further comprises a polynucleotide encoding said crRNA.

~~16~~28. A system for binding a target DNA sequence, said system comprising:

a) one or more guide RNAs (gRNAs) capable of hybridizing to said target DNA sequence or one or more nucleotide sequences encoding the one or more ~~guide RNAs (~~gRNAs~~)~~; and

b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to ~~any one of~~ SEQ ID NO~~s~~: 1, ~~50, 24, 43, 16, and 35~~ or a nucleotide sequence encoding the RGN polypeptide;

wherein said target DNA sequence is located 5' and adjacent to a protospacer adjacent motif (PAM) site having the sequence set forth as SEQ ID NO: 7~~the one or more guide RNAs are capable of hybridizing to the target DNA sequence~~, and

wherein the one or more ~~guide RNAs~~gRNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence.

~~17~~29. The system of claim ~~16~~28, wherein at least one of said nucleotide sequences encoding the one or more ~~guide RNAs~~gRNAs and said nucleotide sequence encoding the RGN polypeptide is operably linked to a promoter heterologous to said nucleotide sequence.

~~18~~30. The system of claim ~~16 -~~28 or ~~17~~29, wherein the target DNA sequence is within a eukaryotic cell.

31. The system of any one of claims 28-30, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1.

32. The system of any one of claims 28-31, wherein said RGN polypeptide comprises the amino acid sequence set forth as SEQ ID NO: 1.

~~19~~33. The system of any one of claims ~~16 -18~~28-30, wherein said RGN polypeptide is nuclease dead or functions as a nickase, and wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

~~20~~34. The system of any one of claims ~~16 -18~~28-32, wherein said system further comprises one or more donor polynucleotides or one or more nucleotide sequences encoding the one or more donor polynucleotides.

~~21~~35. A method for binding a target DNA sequence comprising delivering a system according to any one of claims ~~16 -20~~28-34 to said target DNA sequence or a cell comprising the target DNA sequence.

~~22~~36. A method for cleaving and/or modifying a target DNA sequence, comprising contacting the target DNA sequence with:

a) an RNA-guided nuclease (RGN) polypeptide, wherein said RGN comprises an amino acid sequence having at least 90% sequence identity to ~~any one of~~ SEQ ID NO~~s~~: 1~~,~~ ~~50, 24, 43, 16, and 35~~; and

b) one or more guide RNAs capable of targeting the RGN of (a) to the target DNA sequence;

wherein said target DNA sequence is located 5' and adjacent to a protospacer adjacent motif (PAM) site having the sequence set forth as SEQ ID NO: 7,

and wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence and cleavage and/or modification of said target DNA sequence occurs.

37. The method of claim 36, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1.

38. The method of claim 36 or 37, wherein said RGN polypeptide comprises the amino acid sequence set forth as SEQ ID NO: 1.

39. The method of claim 36, wherein said RGN polypeptide is nuclease dead or functions as a nickase, and wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

~~23~~40. The method of any one of claims ~~22~~36-39, wherein said modified target DNA sequence comprises deletion or mutation of at least one nucleotide from the target DNA sequence.

~~24. The method of claim 22 or 23, wherein said RGN polypeptide is nuclease dead or functions as a nickase, and wherein the RGN polypeptide is operably linked to a base-editing polypeptide.~~

~~25~~41. The method of any one of claims ~~22~~36-38, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

~~26~~42. The method of any one of claims ~~22-25~~36-41, wherein the target DNA sequence is within a cell.

~~27~~43. The method of claim ~~26~~42, wherein the cell is a eukaryotic cell.

~~28~~44. The method of any one of claims ~~26 or 27~~36-38, further comprising culturing the cell under conditions in which the RGN polypeptide is expressed and cleaves the target DNA sequence to produce a modified DNA sequence; and selecting a cell comprising said modified DNA sequence.

~~29. A cell comprising a modified target DNA sequence according to the method of claim 28.~~

~~30. A nucleic acid molecule comprising a polynucleotide encoding a deaminase polypeptide, wherein said polynucleotide comprises a nucleotide sequence encoding a deaminase polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 399, 420, 374, 383, 397, 407, 408, 411, 414, and 416;~~

~~wherein said deaminase polypeptide is capable of deaminating at least one nucleotide in a target polynucleotide.~~

~~31. The nucleic acid molecule of claim 30, wherein said polynucleotide encoding a deaminase polypeptide is operably linked to a promoter heterologous to said polynucleotide.~~

~~32. The nucleic acid molecule of claim 30 or 31, wherein said deaminase polypeptide is operably fused to an RNA-guided nuclease polypeptide that is capable of localizing said deaminase polypeptide to said target polynucleotide.~~

~~33. The nucleic acid molecule of claim 32, wherein said RNA-guided nuclease polypeptide is a nickase.~~

~~34. A vector comprising the nucleic acid molecule of any one of claims 30-33.~~

~~35. A cell comprising the nucleic acid molecule of any one of claims 30-33 or the vector of claim 34.~~

~~36. A nucleic acid molecule comprising a polynucleotide encoding an adenosine deaminase polypeptide, wherein said polynucleotide comprises a nucleotide sequence~~

~~encoding an adenosine deaminase polypeptide comprising an amino acid sequence selected from the group consisting of:~~

~~a) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 514;~~

~~b) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 572, and comprising a lysine at a position corresponding to position 102 of SEQ ID NO: 572, a tyrosine at a position corresponding to position 104 of SEQ ID NO: 572, and a threonine at a position corresponding to position 106 of SEQ ID NO: 572;~~

~~c) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 573;~~

~~d) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 574, and comprising a glutamic acid at a position corresponding to position 101 of SEQ ID NO: 574, a serine at a position corresponding to position 103 of SEQ ID NO: 574, and a lysine at a position corresponding to position 105 of SEQ ID NO: 574;~~

~~e) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 575, and comprising a lysine at a position corresponding to position 101 of SEQ ID NO: 575, a leucine at a position corresponding to position 103 of SEQ ID NO: 575, and a glutamic acid at a position corresponding to position 105 of SEQ ID NO: 575;~~

~~f) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 576, and comprising an alanine at a position corresponding to position 105 of SEQ ID NO: 576 and an argnine at a position corresponding to position 107 of SEQ ID NO: 576;~~

~~g) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 577, and comprising a glycine at a position corresponding to position 102 of SEQ ID NO: 577, a serine at a position corresponding to position 104 of SEQ ID NO: 577, and an arginine at a position corresponding to position 106 of SEQ ID NO: 577;~~

~~h) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 578, and comprising a serine at a position corresponding to position 105 of SEQ ID NO: 578 and a threonine at a position corresponding to position 107 of SEQ ID NO: 578;~~

~~i) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 579, and comprising a serine at a position corresponding to position 102 of SEQ ID NO: 579, a glutamine at a position corresponding to position 104 of SEQ ID NO: 579, and a glycine at a position corresponding to position 106 of SEQ ID NO: 579;~~

~~j) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 580, and comprising a glycine at a position corresponding to position 111 of SEQ ID NO: 580;~~

~~k) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 581, and comprising a glutamine at a position corresponding to position 104 of SEQ ID NO: 581,~~

~~a glycine at a position corresponding to position 106 of SEQ ID NO: 581, and a glutamic acid at a position corresponding to position 108 of SEQ ID NO: 581;~~

~~l) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 582, and comprising an arginine at a position corresponding to position 102 of SEQ ID NO: 582, a tryptophan at a position corresponding to position 104 of SEQ ID NO: 582, and a glutamic acid at a position corresponding to position 106 of SEQ ID NO: 582;~~

~~m) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 583, and comprising an arginine at a position corresponding to position 104 of SEQ ID NO: 583 and a serine at a position corresponding to position 106 of SEQ ID NO: 583; and~~

~~n) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 584, and comprising a phenylalanine at a position corresponding to position 110 of SEQ ID NO: 584, a serine at a position corresponding to position 112 of SEQ ID NO: 584, and a threonine at a position corresponding to position 114 of SEQ ID NO: 584;~~

~~wherein said adenosine deaminase polypeptide is capable of deaminating at least one adeonisine in a target polynucleotide.~~

~~37. The nucleic acid molecule of claim 36, wherein said polynucleotide encoding an adenosine deaminase polypeptide is operably linked to a promoter heterologous to said polynucleotide.~~

~~38. The nucleic acid molecule of claim 36 or 37, wherein said adenosine deaminase polypeptide is operably fused to an RNA-guided nuclease polypeptide that is capable of localizing said adenosine deaminase polypeptide to said target polynucleotide.~~

~~39. The nucleic acid molecule of claim 38, wherein said RNA-guided nuclease polypeptide is a nickase.~~

~~40. A vector comprising the nucleic acid molecule of any one of claims 36-39.~~

~~41. A cell comprising the nucleic acid molecule of any one of claims 36-39 or the vector of claim 40.~~

~~42. A fusion protein comprising:~~

~~a) a DNA-binding polypeptide capable of binding to a target polynucleotide; and~~

b) a deaminase polypeptide, wherein said deaminase polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 399, 420, 374, 383, 397, 407, 408, 411, 414, and 416, and wherein said deaminase polypeptide is capable of deaminating at least one nucleotide in said target polynucleotide.

43. The fusion protein of claim 42, wherein the DNA-binding polypeptide is an RNA-guided nuclease with nickase activity.

44. A fusion protein comprising:

a) a DNA-binding polypeptide capable of binding to a target polynucleotide; and

b) an adenosine deaminase polypeptide comprising an amino acid sequence selected from the group consisting of:

i) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 514;

ii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 572, and comprising a lysine at a position corresponding to position 102 of SEQ ID NO: 572, a tyrosine at a position corresponding to position 104 of SEQ ID NO: 572, and a threonine at a position corresponding to position 106 of SEQ ID NO: 572;

iii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 573;

iv) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 574, and comprising a glutamic acid at a position corresponding to position 101 of SEQ ID NO: 574, a serine at a position corresponding to position 103 of SEQ ID NO: 574, and a lysine at a position corresponding to position 105 of SEQ ID NO: 574;

v) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 575, and comprising a lysine at a position corresponding to position 101 of SEQ ID NO: 575, a leucine at a position corresponding to position 103 of SEQ ID NO: 575, and a glutamic acid at a position corresponding to position 105 of SEQ ID NO: 575;

vi) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 576, and comprising an alanine at a position corresponding to position 105 of SEQ ID NO: 576 and an argnine at a position corresponding to position 107 of SEQ ID NO: 576;

vii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 577, and comprising a glycine at a position corresponding to position 102 of SEQ ID

~~NO: 577, a serine at a position corresponding to position 104 of SEQ ID NO: 577, and an arginine at a position corresponding to position 106 of SEQ ID NO: 577;~~

~~viii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 578, and comprising a serine at a position corresponding to position 105 of SEQ ID NO: 578 and a threonine at a position corresponding to position 107 of SEQ ID NO: 578;~~

~~ix) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 579, and comprising a serine at a position corresponding to position 102 of SEQ ID NO: 579, a glutamine at a position corresponding to position 104 of SEQ ID NO: 579, and a glycine at a position corresponding to position 106 of SEQ ID NO: 579;~~

~~x) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 580, and comprising a glycine at a position corresponding to position 111 of SEQ ID NO: 580;~~

~~xi) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 581, and comprising a glutamine at a position corresponding to position 104 of SEQ ID NO: 581, a glycine at a position corresponding to position 106 of SEQ ID NO: 581, and a glutamic acid at a position corresponding to position 108 of SEQ ID NO: 581;~~

~~xii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 582, and comprising an arginine at a position corresponding to position 102 of SEQ ID NO: 582, a tryptophan at a position corresponding to position 104 of SEQ ID NO: 582, and a glutamic acid at a position corresponding to position 106 of SEQ ID NO: 582;~~

~~xiii) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 583, and comprising an arginine at a position corresponding to position 104 of SEQ ID NO: 583 and a serine at a position corresponding to position 106 of SEQ ID NO: 583; and~~

~~xiv) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 584, and comprising a phenylalanine at a position corresponding to position 110 of SEQ ID NO: 584, a serine at a position corresponding to position 112 of SEQ ID NO: 584, and a threonine at a position corresponding to position 114 of SEQ ID NO: 584;~~

~~wherein said adenosine deaminase polypeptide is capable of deaminating at least one adeonisine in a target polynucleotide.~~

~~45. The fusion protein of claim 44, wherein the DNA-binding polypeptide is an RNA-guided nuclease with nickase activity.~~

~~46. A system for modifying a target polynucleotide sequence, said system comprising:~~

~~a) one or more guide RNAs capable of hybridizing to said target polynucleotide sequence or one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and~~

~~b) a fusion protein of any one of claims 42-45 or a nucleotide sequence encoding said fusion protein;~~

~~wherein the one or more guide RNAs are capable of hybridizing to the target polynucleotide sequence, and~~

~~wherein the one or more guide RNAs are capable of forming a complex with the RNA-guided DNA-binding polypeptide of the fusion protein in order to direct said fusion protein to bind to and modify said target polynucleotide sequence.~~

~~47. The system of claim 46, wherein at least one of said nucleotide sequence encoding the one or more guide RNAs and said nucleotide sequence encoding the fusion protein is operably linked to a promoter heterologous to said nucleotide sequence.~~

~~48. A method for deaminating a target polynucleotide, said method comprising contacting said target polynucleotide with a deaminase comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 399, 420, 374, 383, 397, 407, 408, 411, 414, and 416, wherein said deaminase polypeptide deaminates at least one nucleotide in said target polynucleotide.~~

~~49. A method for deaminating at least one adenosine in a target polynucleotide, said method comprising contacting said target polynucleotide with an adenosine deaminase polypeptide comprising an amino acid sequence selected from the group consisting of:~~

~~a) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 514;~~

~~b) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 572, and comprising a lysine at a position corresponding to position 102 of SEQ ID NO: 572, a tyrosine at a position corresponding to position 104 of SEQ ID NO: 572, and a threonine at a position corresponding to position 106 of SEQ ID NO: 572;~~

~~c) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 573;~~

~~d) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 574, and comprising a glutamic acid at a position corresponding to position 101 of SEQ ID NO:~~

574, a serine at a position corresponding to position 103 of SEQ ID NO: 574, and a lysine at a position corresponding to position 105 of SEQ ID NO: 574;

e) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 575, and comprising a lysine at a position corresponding to position 101 of SEQ ID NO: 575, a leucine at a position corresponding to position 103 of SEQ ID NO: 575, and a glutamic acid at a position corresponding to position 105 of SEQ ID NO: 575;

f) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 576, and comprising an alanine at a position corresponding to position 105 of SEQ ID NO: 576 and an argnine at a position corresponding to position 107 of SEQ ID NO: 576;

g) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 577, and comprising a glycine at a position corresponding to position 102 of SEQ ID NO: 577, a serine at a position corresponding to position 104 of SEQ ID NO: 577, and an arginine at a position corresponding to position 106 of SEQ ID NO: 577;

h) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 578, and comprising a serine at a position corresponding to position 105 of SEQ ID NO: 578 and a threonine at a position corresponding to position 107 of SEQ ID NO: 578;

i) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 579, and comprising a serine at a position corresponding to position 102 of SEQ ID NO: 579, a glutamine at a position corresponding to position 104 of SEQ ID NO: 579, and a glycine at a position corresponding to position 106 of SEQ ID NO: 579;

j) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 580, and comprising a glycine at a position corresponding to position 111 of SEQ ID NO: 580;

k) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 581, and comprising a glutamine at a position corresponding to position 104 of SEQ ID NO: 581, a glycine at a position corresponding to position 106 of SEQ ID NO: 581, and a glutamic acid at a position corresponding to position 108 of SEQ ID NO: 581;

l) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 582, and comprising an arginine at a position corresponding to position 102 of SEQ ID NO: 582, a tryptophan at a position corresponding to position 104 of SEQ ID NO: 582, and a glutamic acid at a position corresponding to position 106 of SEQ ID NO: 582;

m) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 583, and comprising an arginine at a position corresponding to position 104 of SEQ ID NO: 583 and a serine at a position corresponding to position 106 of SEQ ID NO: 583; and

n) an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 584, and comprising a phenylalanine at a position corresponding to position 110 of SEQ ID NO: 584, a serine at a position corresponding to position 112 of SEQ ID NO: 584, and a threonine at a position corresponding to position 114 of SEQ ID NO: 584;

wherein said adenosine deaminase polypeptide deaminates at least one adeonisine in a target polynucleotide.

50. A method for modifying a target polynucleotide, said method comprising contacting said target polynucleotide with a fusion protein of claim 42 or 44, wherein said DNA-binding polypeptide binds to said target polynucleotide and said deaminase deaminates at least one nucleotide in said target polynucleotide.

51. A method for modifying a target polynucleotide, said method comprising contacting said target polynucleotide with a fusion protein of claim 43 or 45, and introducing one or more guide RNAs (gRNAs) or one or more nucleotide sequences encoding the one or more gRNAs;

wherein the one or more gRNAs hybridize to said target polynucleotide and form a complex with the RNA-guided DNA-binding polypeptide of the fusion protein, thereby directing said fusion protein to bind to said target polynucleotide sequence and said deaminase polypeptide of the fusion protein deaminates at least one nucleotide in said target polynucleotide, thereby modifying said target polynucleotide.