THAT WHICH IS CLAIMED IS:

1. A first complex comprising:

(a) a first sequence-specific DNA binding protein that is capable of binding to a first site on a target nucleic acid; and

(b) a first DNA-dependent DNA polymerase.

2. The first complex of claim 1, further comprising a first DNA encoded repair template.

3. The first complex of claim 1 or claim 2, further comprising a first DNA endonuclease, wherein the DNA endonuclease is capable of introducing a single stranded nick or a double strand break or the first sequence-specific DNA binding protein that is capable of binding to a first site on a target nucleic acid further comprises endonuclease activity that is capable of introducing a single stranded nick or a double strand break.

4. A ~~first complex~~method of modifying a target nucleic acid, the method comprising contacting the target nucleic acid with:

(a) a first sequence-specific DNA binding protein that is capable of binding to a first site on a target nucleic acid ~~and comprises endonuclease activity that is capable of introducing a single stranded nick or a double strand break~~;

~~(b) a first DNA-dependent DNA polymerase; and~~

~~(c) a first DNA encoded repair template.~~

~~5. A first complex comprising:~~

~~(a) a first sequence-specific DNA binding protein that is capable of binding to a first site on a target nucleic acid;~~

(b) a first DNA-dependent DNA polymerase;

(c) a first DNA endonuclease; and

(d) a first DNA encoded repair template, thereby modifying the target nucleic acid.

~~6~~5. The ~~first~~ method of claim 4, wherein the first sequence-specific DNA binding protein, the

first DNA-dependent DNA polymerase, the first DNA endonuclease, and the first DNA encoded repair template form a complex ~~of any one of claims 1 to~~(that interacts with the target nucleic acid).

6. The method of claim 4 or 5, wherein the first sequence-specific DNA binding protein is ~~from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN) and/or an Argonaute protein.~~

~~7. The first complex of any one of claims 3 to 6, wherein, wherein the first DNA endonuclease is an endonuclease (e.g., Fok1), a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), and/or a transcription activator-like effector nuclease (TALEN).~~

~~8. The first complex of any one of claims 3 to 7, wherein the first DNA endonuclease is a nuclease or a nickase.~~

~~9. The first complex of any one of claims 1 to 8, further comprising a guide nucleic acid (e.g., a crRNA, crDNA).~~

~~10. The first complex of any one of claims 1, 2, or 6 to 9, wherein the first sequence-specific DNA binding protein comprises endonuclease or nickase activity.~~

~~11. The first complex of claim 10, wherein the endonuclease or nickase activity of the first sequence-specific DNA binding protein is from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), and/or a transcription activator-like effector nuclease (TALEN).~~

~~12. The first complex of any one of claims 1 to 11, wherein the first sequence-specific DNA binding protein is fused (at its N-terminus or C-terminus)~~fused to the first DNA-dependent DNA polymerase, optionally via a linker.

~~13. The first complex of any one of claims 1 to 12, wherein the first DNA-dependent DNA polymerase exhibits high fidelity and/or high processivity.~~

~~14. The first complex of any one of claims 1 to 12, wherein the first DNA-dependent DNA polymerase exhibits a high distributive profile.~~

~~15. The first complex of any one of claims 1 to 14, wherein the first DNA-dependent DNA polymerase comprises 3’ 5’ exonuclease activity, 5’ 3’ exonuclease activity and/or 5’ 3’ RNA-dependent DNA polymerase activity.~~

~~16. The first complex of claim 15, wherein the first DNA-dependent DNA polymerase is modified to remove one or more of 3’ 5’ exonuclease activity, 5’ 3’ exonuclease activity and 5’ 3’ RNA-dependent DNA polymerase activity.~~

~~17. The first complex of any one of claims 1 to 16, wherein the first DNA-dependent DNA polymerase comprises a Klenow fragment or sub-fragment thereof.~~

~~18. The first complex of any one of claims 1 to 17, wherein the first DNA-dependent DNA polymerase is fused to a sequence non-specific DNA binding protein.~~

~~19. The first complex of claim 18, wherein the sequence-nonspecific dsDNA binding protein is from Sso7d from Sulfolobus solfataricus.~~

~~20. The first complex of any one of claims 1 to 19, wherein the first DNA-dependent DNA polymerase is a DNA-dependent DNA polymerase from a human, a yeast, a bacterium, or a plant.~~

~~21. The first complex of any one of claims 1 to 19, wherein the first DNA-dependent DNA polymerase is DNA polymerase ε (e.g., human and yeast), DNA polymerase δ, E. coli polymerase I, Phusion® DNA polymerase, Vent® DNA polymerase, Vent (exo-)® DNA polymerase, Deep Vent® DNA polymerase, Deep Vent (exo-)® DNA polymerase, 9°Nm™~~

~~DNA polymerase, Q5® DNA polymerase, Q5U® DNA polymerase, Pfu DNA polymerase, and/or Phire™ DNA polymerase.~~

~~22. The first complex of any one of claims 1 to 20, wherein the first DNA polymerase is a human DNA-dependent DNA polymerase ε, plant DNA-dependent DNA polymerase ε and/or yeast DNA-dependent DNA polymerase ε.~~

~~23. The first complex of any one of claims 1 to 22, wherein the first DNA-dependent DNA polymerase is a distributive polymerase.~~

~~24. The first complex of any one of claims 1 to 23~~7. The method of claim 4 or 5, wherein the first sequence-specific DNA binding protein is fused to a peptide tag and the first DNA-dependent DNA polymerase is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting the first DNA-dependent DNA polymerase to the first sequence-specific DNA binding protein that is fused to the peptide tag.

~~25~~8. The ~~first complex~~method of ~~any one of claims 1 to 23~~claim 4 or 5, wherein the first DNA-dependent DNA polymerase is fused to a peptide tag and the first sequence-specific DNA binding protein is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting the first DNA-dependent DNA polymerase to the first sequence-specific DNA binding protein that is fused to the affinity polypeptide.

~~26~~9. The ~~first complex~~method of claim ~~24~~7 or ~~claim 25~~8, wherein the peptide tag comprises a GCN4 peptide tag (e.g., Sun-Tag), a c-Myc affinity tag, an HA affinity tag, a His affinity tag, an S affinity tag, a methionine-His affinity tag, an RGD-His affinity tag, a FLAG octapeptide, a strep tag or strep tag II, a V5 tag, and/or a VSV-G epitope.

~~27~~10. The ~~first complex~~method of any one of claims ~~24~~7 to ~~26~~9, wherein the affinity polypeptide is an antibody, optionally a scFv antibody, an affibody, an anticalin, a monobody, and/or a DARPin.

~~28~~11. The ~~first complex~~method of any one of claims ~~9~~4 to ~~23, wherein the~~10, wherein the first DNA binding domain and/or first DNA endonuclease is a CRISPR-Cas effector protein.

12. The method of claim 11, further comprising contacting the target nucleic acid with a first guide nucleic acid (e.g., a crRNA, crDNA).

13. The method of claim 12, wherein the first DNA encoded repair template is linked to the first guide nucleic acid, thereby guiding the first DNA encoded repair template to the target nucleic acid.

14. The method of claim 12 or 13, wherein the first guide nucleic acid is linked to a RNA-recruiting motif and the first DNA-dependent DNA polymerase is fused to an affinity polypeptide that is capable of binding the RNA recruiting motif, thereby guiding the first DNA-dependent DNA polymerase to the target nucleic acid.

~~29~~15. The ~~first complex~~method of claim ~~28~~14, wherein the RNA recruiting motif is linked to the 5' end or to the 3' end of the CRISPR nucleic acid (e.g., a recruiting crRNA, a recruiting crDNA).

~~30~~16. The ~~first complex~~method of claim ~~28~~14 or ~~claim 29~~15, wherein the RNA recruiting motif and a corresponding affinity polypeptide are a telomerase Ku binding motif (e.g., Ku binding hairpin) and the affinity polypeptide of Ku (e.g., Ku heterodimer); a telomerase Sm7 binding motif and the affinity polypeptide of Sm7; an MS2 phage operator stem-loop and the affinity polypeptide MS2 Coat Protein (MCP), a PP7 phage operator stem-loop and the affinity polypeptide PP7 Coat Protein (PCP); an SfMu phage Com stem-loop and the affinity polypeptide Com RNA binding protein; a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF); and/or a synthetic RNA-aptamer and the corresponding aptamer ligand.

~~31~~17. The ~~first complex~~method of claim ~~28~~14 or ~~claim 29~~15, wherein the RNA recruiting motif and corresponding affinity polypeptide are an MS2 phage operator stem-loop and the affinity

polypeptide MS2 Coat Protein (MCP), and/or a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF).

~~32~~18. The ~~first complex~~method of any one of claims ~~9~~11 to ~~31, wherein the first DNA-encoded repair template is linked to the guide nucleic acid.~~

~~33. The first complex of any one of claims 1 to 32, wherein the first DNA binding domain and/or first DNA endonuclease is a CRISPR-Cas effector protein.~~

~~34. The first complex of claim 33~~17, wherein the CRISPR-Cas effector protein is from a Type ~~I CRISPR-Cas system, a Type~~ II CRISPR-Cas system~~, a Type III CRISPR-Cas system, a Type IV CRISPR-Cas system~~ or a Type V CRISPR-Cas system.

~~35~~19. The ~~first complex of claim 33, wherein the CRISPR-Cas effector protein is from a Type II CRISPR-Cas system or a Type V CRISPR-Cas system.~~

~~36. The first complex of claim 34 or claim 35, wherein the Type V CRISPR-Cas effector protein is a Cas12a, Cas12b, Cas12c (C2c3), Cas12d (CasY), Cas12e (CasX), Cas12g, Cas12h, Cas12i, C2c1, C2c4, C2c5, C2c8, C2c9, C2c10, Cas14a, Cas14b, and/or a Cas14c.~~

~~37. The first complex~~method of any one of claims ~~33~~11 to ~~34~~18, wherein the CRISPR-Cas effector protein is a Cas9 effector protein or a Cas12 effector protein.

~~38.~~ 20. The method of any one of claims 4 to 19, further comprising contacting the target nucleic acid with a second complex comprising:

(a) a second sequence-specific DNA binding protein that is capable of binding to a second site on ~~a~~the target nucleic acid; and

(b) a DNA-encoded repair template.

~~39. The second complex of claim 38, wherein the second sequence-specific DNA binding protein is from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-~~

guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN) and/or an Argonaute protein.

40. The second complex of claim 39, further comprising a second DNA endonuclease, wherein the second DNA endonuclease is capable of introducing a single stranded nick or a double strand break.

41. The second complex of claim 40, wherein the second DNA endonuclease is from polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN).

42. The second complex of claim 38 or claim 39, wherein the second sequence-specific DNA binding protein that is capable of binding to a second site on a target nucleic acid further comprises endonuclease activity that is capable of introducing a single stranded nick or a double strand break.

43. The second complex of claim 42, wherein the second sequence-specific DNA binding protein that further comprises endonuclease activity is a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), or a transcription activator-like effector nuclease (TALEN)).

44. The second complex of any one of claims 38 to 43, further comprising a second DNA-dependent DNA polymerase.

45. The second complex of any one of claims 38 to 43, wherein the second DNA-encoded repair template is linked to an DNA recruiting motif and the second sequence-specific DNA binding protein is fused to an affinity polypeptide that is capable of interacting with the DNA recruiting motif, optionally wherein the DNA recruiting motif/affinity polypeptide comprises a HUH-tag, DNA aptamer, msDNA of bacterial retron or T-DNA recruitment.

~~46. The second complex of any one of claims 38 to 45, wherein the second sequence-specific DNA binding protein is fused (at its N-terminus or C-terminus) to a Porcine Circovirus 2 (PCV) Rep protein and the DNA template comprises a PCV recognition site.~~

~~47. The second complex of any one of claims 38 to 46, wherein the second DNA-encoded repair template is linked to a guide nucleic acid.~~

~~48. An engineered (modified) DNA-dependent DNA polymerase fused to an affinity polypeptide that is capable of interacting with a peptide tag or an RNA recruiting motif.~~

~~49. The engineered DNA-dependent DNA polymerase of claim 48, wherein the DNA-dependent DNA polymerase is fused to a sequence non-specific DNA binding domain.~~

~~50. The engineered DNA-dependent DNA polymerase of claim 49, wherein the sequence-nonspecific dsDNA binding protein is from Sso7d from Sulfolobus solfataricus.~~

~~51. The engineered DNA-dependent DNA polymerase of any one of claims 48 to 50, wherein the DNA-dependent DNA polymerase exhibits increased processivity, increased fidelity, increased affinity, increased sequence specificity, decreased sequence specificity and/or increased cooperativity [as compared to the same DNA-dependent DNA polymerase that is not engineered as described herein].~~

~~52. The engineered DNA-dependent DNA polymerase of claim 48 to 51, wherein the DNA-dependent DNA polymerase does not comprise at least one of 5′→3′ polymerase activity, 3'→5' exonuclease activity, 5'→3' exonuclease activity, and/or 5′→3′ RNA-dependent DNA polymerase activity.~~

~~53. A third complex comprising a third sequence-specific DNA binding protein that is cable of binding to a third site on a target nucleic acid that is on a different strand from the first site and second site and a third DNA endonuclease, thereby improving mismatch repair and boosting the efficiency of repair.~~

~~54. A polynucleotide encoding the first complex of any one of claims 1 to 37.~~

~~55. A polynucleotide encoding the second complex of any one of claims 38 to 47.~~

~~56. A polynucleotide encoding the third complex of claim 53.~~

~~57. A polynucleotide encoding the engineered DNA-dependent DNA polymerase of any one of claims 48 to 52.~~

~~58. An expression cassette or vector comprising one or more of the polynucleotides of any one of claims 54 to 57.~~

~~59. An RNA molecule comprising (a) a nucleic acid sequence that mediates interaction with a CRISPR-Cas effector protein; (b) a nucleic acid sequence that directs the CRISPR-Cas effector protein to a specific nucleic acid target site through a DNA-RNA interaction, and (c) a nucleic acid sequence that forms a stem loop structure that can interact with the engineered DNA-dependent DNA polymerase of claims 48 to 52.~~

~~60. A method of modifying a target nucleic acid, the method comprising contacting the target nucleic acid with the first complex of any one of claims 4 to 37, thereby modifying the target nucleic acid.~~

~~61. The method of claim 60, further comprising contacting the target nucleic acid with the second complex of any one of claims 38 to 47, thereby modifying the target nucleic acid.~~

~~62. The method of claim 61, further comprising contacting the target nucleic acid with the third complex of claim 53, thereby improving the repair efficiency of the modifying of the target nucleic acid.~~

~~63. A method of modifying a target nucleic acid, the method comprising~~

~~contacting the target nucleic acid with:~~

~~(a) a first sequence-specific DNA-binding protein that is capable of binding to a first site on a target nucleic acid;~~

~~(b) a first DNA-dependent DNA polymerase;~~

~~(c) a first DNA endonuclease; and~~

~~(d) a first DNA-encoded repair template, thereby modifying the target nucleic acid.~~

~~64. The method of claim 63, wherein the first sequence-specific DNA-binding protein, the first DNA-dependent DNA polymerase, the first DNA endonuclease, and the first DNA-encoded repair template form a complex (that interacts with the target nucleic acid).~~

~~65. The method of claim 63 or claim 64, wherein the first sequence-specific DNA-binding protein is from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN) and/or an Argonaute protein.~~

~~66. The method of any one of claims 63 to 65, wherein the first DNA endonuclease is an endonuclease (e.g., Fok1), a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), and/or a transcription activator-like effector nuclease (TALEN).~~

~~67. The method of any one of claims 63 to 66, wherein the first DNA endonuclease is a nuclease or a nickase.~~

~~68. A method of modifying a target nucleic acid, the method comprising~~

~~contacting the target nucleic acid with:~~

~~(a) a first sequence-specific DNA-binding protein that is capable of binding to a first site on a target nucleic acid and comprises nickase activity and/or endonuclease activity that is capable of introducing a single stranded nick or a double strand break;~~

~~(b) a first DNA-dependent DNA polymerase; and~~

~~(c) a first DNA-encoded repair template, thereby modifying the target nucleic acid.~~

~~69. The method of claim 68, wherein the first sequence-specific DNA binding protein comprising endonuclease activity, the first DNA-dependent DNA polymerase, and the first DNA encoded repair template form a complex (that interacts with the target nucleic acid).~~

~~70. The method of claim 68 or claim 69, wherein the endonuclease activity and/or nickase activity of the first sequence-specific DNA binding protein is from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), and/or a transcription activator-like effector nuclease (TALEN).~~

~~71. The method of any one of claims 63 to 70, wherein the first sequence-specific DNA binding protein is fused to the first DNA-dependent DNA polymerase, optionally via a linker.~~

~~72. The method of any one of claims 63 to 70, wherein the first sequence-specific DNA binding protein is fused to a peptide tag and the first DNA-dependent DNA polymerase is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting the first DNA-dependent DNA polymerase to the first sequence-specific DNA binding protein that is fused to the peptide tag.~~

~~73. The method of any one of claims 63 to 70, wherein the first DNA-dependent DNA polymerase is fused to a peptide tag and the first sequence-specific DNA binding protein is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting the first DNA-dependent DNA polymerase to the first sequence-specific DNA binding protein that is fused to the affinity polypeptide.~~

~~74. The method of claim 72 or claim 73, wherein the peptide tag comprises a GCN4 peptide tag (e.g., Sun-Tag), a c-Myc affinity tag, an HA affinity tag, a His affinity tag, an S affinity tag, a methionine-His affinity tag, an RGD-His affinity tag, a FLAG octapeptide, a strep tag or strep tag II, a V5 tag, and/or a VSV-G epitope.~~

~~75. The method of any one of claims 72 to 74, wherein the affinity polypeptide is an antibody, optionally a scFv antibody, an affibody, an anticalin, a monobody, and/or a DARPin.~~

76. The method of any one of claims 63 to 75, wherein the first DNA binding domain and/or first DNA endonuclease is a CRISPR-Cas effector protein.

77. The method of claim 76, further comprising contacting the target nucleic acid with a first guide nucleic acid (e.g., a crRNA, crDNA).

78. The method of claim 77, wherein the first DNA encoded repair template is linked to the first guide nucleic acid, thereby guiding the first DNA encoded repair template to the target nucleic acid.

79. The method of claim 77 or claim 78, wherein the first guide nucleic acid is linked to a RNA-recruiting motif and the first DNA-dependent DNA polymerase is fused to an affinity polypeptide that is capable of binding the RNA recruiting motif, thereby guiding the first DNA-dependent DNA polymerase to the target nucleic acid.

80. The method of claim 79, wherein the RNA recruiting motif is linked to the 5' end or to the 3' end of the CRISPR nucleic acid (e.g., a recruiting crRNA, a recruiting crDNA).

81. The method of claim 79 or claim 80, wherein the RNA recruiting motif and a corresponding affinity polypeptide are a telomerase Ku binding motif (e.g., Ku binding hairpin) and the affinity polypeptide of Ku (e.g., Ku heterodimer); a telomerase Sm7 binding motif and the affinity polypeptide of Sm7; an MS2 phage operator stem-loop and the affinity polypeptide MS2 Coat Protein (MCP), a PP7 phage operator stem-loop and the affinity polypeptide PP7 Coat Protein (PCP); an SfMu phage Com stem-loop and the affinity polypeptide Com RNA binding protein; a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF); and/or a synthetic RNA-aptamer and the corresponding aptamer ligand.

82. The method of claim 79 or claim 80, wherein the RNA recruiting motif and corresponding affinity polypeptide are an MS2 phage operator stem-loop and the affinity polypeptide MS2 Coat Protein (MCP), and/or a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF).

~~83. The method of any one of claims 76 to 82, wherein the CRISPR-Cas effector protein is from a Type I CRISPR-Cas system, a Type II CRISPR-Cas system, a Type III CRISPR-Cas system, a Type IV CRISPR-Cas system or a Type V CRISPR-Cas system.~~

~~84. The method of any one of claims 76 to 82, wherein the CRISPR-Cas effector protein is from a Type II CRISPR-Cas system or a Type V CRISPR-Cas system.~~

~~85. The method of claim 84, wherein the Type V CRISPR-Cas effector protein is a Cas12a, Cas12b, Cas12c (C2c3), Cas12d (CasY), Cas12e (CasX), Cas12g, Cas12h, Cas12i, C2c1, C2c4, C2c5, C2c8, C2c9, C2c10, Cas14a, Cas14b, and/or a Cas14c~~

~~86. The method of any one of claims 76 to 84, wherein the CRISPR-Cas effector protein is a Cas9 effector protein or a Cas12 effector protein.~~

~~87. The method of any one of claims 63 to 86, further comprising contacting the target nucleic acid with a second complex comprising:~~

~~(a) a second sequence-specific DNA binding protein that is capable of binding to a second site on the target nucleic acid; and~~

~~(b) a DNA-encoded repair template.~~

~~88. The method of claim 87~~21. The method of claim 20, wherein the target nucleic acid is further contacted with a second DNA endonuclease, wherein the second DNA endonuclease is capable of introducing a single stranded nick or a double strand break or wherein the second sequence-specific DNA binding protein comprises endonuclease activity that is capable of introducing a single stranded nick or a double strand break.

~~89~~22. The method of claim ~~88, wherein the second DNA endonuclease is from polynucleotide-guided endonuclease, a CRISPR-Cas endonuclease (e.g., CRISPR-Cas effector protein), a protein-guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN),~~20 or ~~the second sequence-specific DNA binding protein that comprises endonuclease activity is a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a~~

~~protein-guided endonuclease (e.g., a zinc-finger nuclease), a transcription activator-like effector nuclease (TALEN).~~

~~90. The method of any one of claims 87 to 89, wherein the second sequence-specific DNA binding protein that is capable of binding to a second site on the target nucleic acid, the second DNA-encoded repair template, and optionally the DNA endonuclease form a complex that interacts with the second site on the target nucleic acid.~~

~~91. The method of any one of claims 87 to 90, wherein the second sequence-specific DNA binding protein is fused to a peptide tag and the second DNA endonuclease is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting the second DNA endonuclease to the second sequence-specific DNA binding protein that is fused to the peptide tag.~~

~~92. The method of any one of claims 87 to 91, wherein the second DNA endonuclease is fused to a peptide tag and the second sequence-specific DNA binding protein is fused to an affinity polypeptide that is capable of binding the peptide tag, thereby recruiting second DNA endonuclease to the second sequence-specific DNA binding protein that is fused to the affinity polypeptide.~~

~~93. The method of claim 87 or claim 92, wherein the peptide tag comprises a GCN4 peptide tag (e.g., Sun-Tag), a c-Myc affinity tag, an HA affinity tag, a His affinity tag, an S affinity tag, a methionine-His affinity tag, an RGD-His affinity tag, a FLAG octapeptide, a strep tag or strep tag II, a V5 tag, and/or a VSV-G epitope.~~

~~94. The method of any one of claims 89 to 93, wherein the affinity polypeptide is an antibody, optionally a scFv antibody, an affibody, an anticalin, a monobody, and/or a DARPin.~~

~~95. The method of any one of claims 87 to 94, wherein the second DNA-encoded repair template is linked to a DNA recruiting motif and the second sequence-specific DNA binding protein is fused to an affinity polypeptide that is capable of interacting with the DNA recruiting~~

motif, optionally wherein the DNA recruiting motif/affinity polypeptide comprises a HUH-tag, DNA-aptamer, msDNA of bacterial retron or T-DNA recruitment.

96. The method of any one of claims 87 to 95, wherein the second sequence-specific DNA binding protein is fused to a Porcine Circovirus 2 (PCV) Rep protein and the DNA-encoded repair template comprises a PCV recognition site.

97. The method of any one of claims 89 to 96, wherein the second sequence-specific DNA binding protein is from a polynucleotide-guided endonuclease, a CRISPR-Cas effector protein, a protein-guided endonuclease (e.g., a zinc finger nuclease), a transcription activator-like effector nuclease (TALEN) and/or an Argonaute protein.

98. The method of any one of claims 89 to 97, wherein the second DNA binding domain and/or second DNA endonuclease is a CRISPR-Cas effector protein.

99. The method of claim 98, further comprising contacting the target nucleic acid with a second guide nucleic acid (e.g., a crRNA, crDNA).

100. The method of claim 99, wherein the second DNA-encoded repair template is linked to the second guide nucleic acid, thereby guiding the second DNA-encoded repair template to the target nucleic acid.

101. The method of claim 99 or claim 100, wherein the second guide nucleic acid is linked to a RNA-recruiting motif and the second DNA endonuclease is fused to an affinity polypeptide that is capable of binding the RNA recruiting motif, thereby guiding the second DNA endonuclease to the target nucleic acid.

102. The method of claim 101, wherein the RNA recruiting motif is linked to the 5' end or to the 3' end of the guide nucleic acid (e.g., a recruiting crRNA, a recruiting crDNA).

~~103. The method of claim 101 or claim 102, wherein the RNA recruiting motif and a corresponding affinity polypeptide are a telomerase Ku binding motif (e.g., Ku binding hairpin) and the affinity polypeptide of Ku (e.g., Ku heterodimer); a telomerase Sm7 binding motif and the affinity polypeptide of Sm7; an MS2 phage operator stem-loop and the affinity polypeptide MS2 Coat Protein (MCP), a PP7 phage operator stem-loop and the affinity polypeptide PP7 Coat Protein (PCP); an SfMu phage Com stem-loop and the affinity polypeptide Com RNA binding protein; a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF); and/or a synthetic RNA-aptamer and the corresponding aptamer ligand~~

~~104. The method of claim 101 or claim 102, wherein the RNA recruiting motif and corresponding affinity polypeptide are an MS2 phage operator stem-loop and the affinity polypeptide MS2 Coat Protein (MCP), and/or a PUF binding site (PBS) and the affinity polypeptide Pumilio/fem-3 mRNA binding factor (PUF).~~

~~105. The method of any one of claims 87 to 104~~21, further comprising contacting the target nucleic acid with a second DNA-dependent DNA polymerase.

~~106~~23. The method of any one of claims ~~87-105~~20 to 22, comprising contacting the target nucleic acid with a third complex, the third complex comprising a third sequence-specific DNA binding protein that is cable of binding to a third site on the target nucleic acid that is on a different strand from the first site and the second site, wherein the third sequence-specific DNA binding protein comprises nuclease or nickase activity, thereby improving the repair efficiency of the modifying of the target nucleic acid.

~~107. The method of any one of claims 63 to 106, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is modified to remove one or more of 3’-5’ exonuclease activity, 5’-3’ exonuclease activity and 5’-3’ RNA-dependent DNA polymerase activity.~~

~~108. The method of any one of claims 63 to 107, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase comprises a Klenow fragment or sub-fragment thereof.~~

~~109. The method of any one of claims 63 to 108, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is fused to a sequence non-specific DNA binding protein.~~

~~110. The method of claim 109, wherein the sequence-nonspecific dsDNA binding protein is from Sso7d from Sulfolobus solfataricus.~~

~~111. The method of any one of claims 63 to 110, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is a DNA-dependent DNA polymerase from a human, a yeast, a bacterium, or a plant.~~

~~112. The method of any one of claims 63 to 111, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is DNA polymerase ε (e.g., human and yeast), DNA polymerase δ, E.coli polymerase I, Phusion® DNA polymerase, Vent® DNA polymerase, Vent (exo-)® DNA polymerase, Deep Vent® DNA polymerase, Deep Vent (exo-)® DNA polymerase, 9°Nm™ DNA polymerase, Q5® DNA polymerase, Q5U® DNA polymerase, Pfu DNA polymerase, and/or Phire™ DNA polymerase.~~

~~113. The method of any one of claims 63 to 111, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is a human DNA-dependent DNA polymerase ε, plant DNA-dependent DNA polymerase ε and/or yeast DNA-dependent DNA polymerase ε.~~

~~114. The method of any one of claims 63 to 113, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase exhibits high fidelity and/or high processivity.~~

115. The method of any one of claims 63 to 113, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase exhibits a high distributive profile.

116. The method of any one of claims 63 to 115, wherein the first DNA-dependent DNA polymerase and/or the second DNA-dependent DNA polymerase is the engineered DNA-dependent DNA polymerase of any one of claims 48 to 52.

117. A system for modifying a target nucleic acid comprising the first complex of any one of claims 4, 6 to 9 or 12 to 37, a polynucleotide encoding the same, and/or the expression cassette or vector comprising the polynucleotide, wherein

(a) the first sequence-specific DNA binding protein comprising DNA endonuclease activity binds to a first site on the target nucleic acid;

(b) the first DNA-dependent DNA polymerase is capable of interacting with the first sequence-specific DNA binding protein and is recruited to the first sequence specific DNA binding protein and to the first site on the target nucleic acid, and

(c) (i) the first DNA encoded repair template is linked to a first guide nucleic acid that comprises a spacer sequence having substantial complementarity to the first site on the target nucleic acid, thereby guiding the first DNA encoded repair template to the first site on the target nucleic acid, or

(c)(ii) the first DNA encoded repair template is capable of interacting with the first sequence-specific DNA binding protein or the first DNA-dependent DNA polymerase and is recruited to the first sequence-specific DNA binding protein or the first DNA-dependent DNA polymerase and to the first site on the target nucleic acid, thereby modifying the target nucleic acid.

118. A system for modifying a target nucleic acid comprising the first complex of any one of claims 5 to 9 or 12 to 37, a polynucleotide encoding the same, and/or the expression cassette or vector comprising the polynucleotide, wherein

(a) the first sequence-specific DNA binding protein binds to a first site on the target nucleic acid,

(b) the first DNA-endonuclease is capable of interacting with the first sequence-specific DNA-binding protein and/or a guide nucleic acid and is recruited to the first sequence-specific DNA-binding protein and to the first site on the target nucleic acid;

(c) the first DNA-dependent DNA polymerase is capable of interacting with the first sequence-specific DNA-binding protein and/or a guide nucleic acid and is recruited to the first sequence-specific DNA-binding protein and to the first site on the target nucleic acid; and

(d) (i) the first DNA-encoded repair template is linked to a guide nucleic acid that comprises a spacer sequence having substantial complementarity to the first site on the target nucleic acid, thereby guiding the first DNA-encoded repair template to the first site on the target nucleic acid, or

(d)(ii) the first DNA-encoded repair template is capable of interacting with the first sequence-specific DNA-binding protein or the first DNA-dependent DNA-polymerase and is recruited to the sequence-specific DNA-binding protein or the first DNA-dependent DNA-polymerase and to the first site on the target nucleic acid, thereby modifying the target nucleic acid.

119. The system for modifying a target nucleic acid of claim 117 or 118, further comprising the second complex of any one of claims 38 to 47, a polynucleotide encoding the same, and/or an expression cassette and/or vector comprising the polynucleotide, wherein the second sequence-specific DNA-binding domain binds to a second site proximal to the first site on the target nucleic acid and the second DNA-encoded repair template is recruited to the second sequence-specific DNA-binding protein (via covalent or non-covalent interactions), thereby modifying the target nucleic acid.

120. A method of modifying a target nucleic acid, the method comprising

contacting the target nucleic acid with:

the complex of anyone of claims 117 to 119, thereby modifying the target nucleic acid.