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;

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

(c) an RNA:DNA hybrid guide comprising a first DNA encoded repair template that is linked to an RNA guide nucleic acid to guide the first DNA encoded repair template to the target nucleic acid.

2. The first complex of claim 1, 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.

3. 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) an RNA:DNA hybrid guide comprising a first DNA encoded repair template that is linked to an RNA guide nucleic acid to guide the first DNA encoded repair template to the target nucleic acid, thereby modifying the target nucleic acid.

4. The method of claim 3, 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.

5. The method of claim 3 or 4, wherein the first sequence-specific DNA binding protein is fused to the first DNA-dependent DNA polymerase, optionally via a linker.

6. The method of claim 3 or 4, 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.

7. The method of claim 3 or 4, 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.

8. The method of claim 6 or 7, wherein the peptide tag comprises a GCN4 peptide 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.

9. The method of any one of claims 6 to 8, wherein the affinity polypeptide is an antibody, optionally a scFv antibody, an affibody, an anticalin, a monobody, and/or a DARPin.

10. The method of any one of claims 3 to 9, wherein the first DNA binding domain and/or first DNA endonuclease is a CRISPR-Cas effector protein.

11. The method any one of claims 1-10, wherein the RNA guide nucleic acid is linked to an 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.

12. The method of claim 11, wherein the RNA recruiting motif is linked to the 5' end or to the 3' end of the CRISPR nucleic acid.

13. The method of claim 11 or 12, wherein the RNA recruiting motif and a corresponding affinity polypeptide are a telomerase Ku binding motif and the affinity polypeptide of Ku; 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.

14. The method of claim 12 or 13, 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).

15. The method of any one of claims 10 to 14, wherein the CRISPR-Cas effector protein is from a Type II CRISPR-Cas system or a Type V CRISPR-Cas system.

16. The method of any one of claims 10 to 15, wherein the CRISPR-Cas effector protein is a Cas9 effector protein or a Cas12 effector protein.

17. The method of any one of claims 3 to 16, 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.

18. The method of claim 17, 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.

19. The method of claim 17 or 18, further comprising contacting the target nucleic acid with a second DNA-dependent DNA polymerase.

20. The method of any one of claims 17 to 19, 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.