WHAT IS CLAIMED IS:

1. A protein-nucleic acid complex comprising an engineered RNA-guided nucleobase modifying system in association with a chromosome of a bacterial cell, wherein the engineered RNA-guided nucleobase modifying system is targeted to a specific locus in the chromosome of the bacterial cell, and the chromosome of the bacterial cell encodes an HU family DNA-binding protein comprising an amino acid sequence with at least 50% sequence identity to SEQ ID NO: 1.

2. The protein-nucleic acid complex of claim 1, wherein the engineered RNA guided nucleobase modifying system comprises (i) a CRISPR system comprising a CRISPR protein and guide RNA (gRNA) and (ii) a nucleobase modifying enzyme or catalytic domain thereof, wherein the CRISPR protein is a nuclease deficient variant or a nickase.

3. The protein-nucleic acid complex of claim 2, wherein the CRISPR system is a Type I CRISPR system, a type II CRISPR system, a type III CRISPR system, a Type IV CRISPR system, a type V CRISPR system, or a type VI CRISPR system.

4. The protein-nucleic acid complex of claims 2 or 3, wherein the CRISPR protein is Cas9, Cas12, Cas13, Cas14, or CasX.

5. The protein-nucleic acid complex of any one of claims 2 to 4, wherein the gRNA is a dual molecule gRNA comprising a CRISPR RNA (crRNA) and a transacting crRNA (tracrRNA).

6. The protein-nucleic acid complex of any one of claims 2 to 4, wherein the gRNA is a single molecule gRNA comprising a fused hybrid of a CRISPR RNA (crRNA) and a transacting crRNA (tracrRNA).

7. The protein-nucleic acid complex of any one of claims 2 to 6, wherein the nucleobase modifying enzyme or catalytic domain thereof is chosen from cytidine deaminase 1 (CDA1), cytidine deaminase 2 (CDA2), activation-induced cytidine deaminase (AICDA),

apolipoprotein B mRNA-editing complex (APOBEC) family cytidine deaminase, APOBEC1 complementation factor/APOBEC1 stimulating factor (ACF1/ASF) cytidine deaminase, cytosine deaminase acting on RNA (CDAR), cytosine deaminase acting on tRNA (CDAT), tRNA adenine deaminase, adenosine deaminase, adenosine deaminase acting on RNA (ADAR), or adenosine deaminase acting on tRNA (ADAT).

8. The protein-nucleic acid complex of any one of claims 2 to 7, wherein the nucleobase modifying enzyme or catalytic domain thereof is a cytidine deaminase or catalytic domain thereof, and the engineered RNA guided nucleobase modifying system further comprises at least one uracil glycosylase inhibitor domain.

9. The protein-nucleic acid complex of any one of claims 2 to 8, wherein the CRISPR protein is linked directly or via a linker to the nucleobase modifying enzyme or the catalytic domain thereof.

10. The protein-nucleic acid complex of any one of claims 2 to 8, wherein the nucleobase modifying enzyme or catalytic domain thereof is linked directly or via a linker to an adaptor protein, and the CRISPR protein or the gRNA comprises an aptamer sequence capable of binding to the adaptor protein.

11. The protein-nucleic acid complex of claim 10, wherein the aptamer sequence is chosen from MS2/MSP, PP7/PCP, Com, N22, AP205, BZ13, F1, F2, fd, fr, GA, ID2, JP34, JP500, JP501, KU1, M11, M12, MX1, NL95, PRR1, ϕCb5, ϕCb8r, ϕCb12r, ϕCb23r, Qβ, R17, SP, TW18, TW19, VK, or 7s.

12. The protein-nucleic acid complex of any one of claims 2 to 11, wherein the engineered RNA guided nucleobase modifying system comprises a nuclease deficient Cas9 or Cas12a variant linked to a cytidine deaminase or catalytic domain thereof.

13. The protein-nucleic acid complex of any one of claims 1 to 12, wherein the engineered RNA-guided nucleobase modifying system is expressed from a nucleic acid that encodes the engineered RNA-guided nucleobase modifying system and is integrated into the bacterial chromosome.

14. The protein-nucleic acid complex of any one of claims 1 to 12, wherein the engineered RNA-guided nucleobase modifying system is expressed from a nucleic acid that encodes the engineered RNA-guided nucleobase modifying system and is carried on an extrachromosomal vector.

15. The protein-nucleic acid complex of any one of claims 1 to 14, wherein the amino acid sequence of the HU family DNA-binding protein encoded on the chromosome of the bacterial cell has at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity to SEQ ID NO: 1.

16. The protein-nucleic acid complex of any one of claims 1 to 15, wherein the bacteria is a *Bacteroides* species or a strain level variant thereof.

17. The protein-nucleic acid complex of claim 16, wherein the *Bacteroides* species or strain level variant thereof is chosen from *B. thetaiotaomicron*, *B. vulgatus*, *B. cellulosilyticus*, *B. fragilis*, *B. helcogenes*, *B. ovatus*, *B. salanitronis*, *B. uniformis*, or *B. xylanisolvens.*

18. A method for modifying at least one nucleobase in a chromosome of a target bacterial cell, the method comprising expressing the engineered RNA-guided nucleobase modifying system of any one of claims 1 to 17 in the target bacterial cell, wherein the engineered RNA-guided nucleobase modifying system is targeted to a specific locus in the chromosome of the target bacterial cell and the engineered RNA-guided nucleobase modifying system modifies at least one nucleobase within the specific locus, such that expression of a gene comprising the

specific locus is altered, modified, and/or inactivated, and wherein the chromosome of the target bacterial cell encodes an HU family DNA-binding protein comprising an amino acid sequence with at least 50% sequence identity to SEQ ID NO: 1.

19. The method of claim 18, wherein modification of the at least one nucleobase results in introduction of at least one single nucleotide polymorphism and/or at least one stop codon within the specific locus in the chromosome of the target bacterial cell.