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(71) Applicants: **THE BROAD INSTITUTE, INC.** [US/US];
415 Main Street, Cambridge, MA 02142 (US). **PRESI-
DENT AND FELLOWS OF HARVARD COLLEGE**
[US/US]; 17 Quincy Street, Cambridge, MA 02138 (US).

(72) Inventors: **LIU, David, R.**; C/o THE BROAD INSTI-
TUTE, INC., 415 Main Street, Cambridge, MA 02142 (US).

NELSON, James, William; C/o THE BROAD INSTI-
TUTE, INC., 415 Main Street, Cambridge, MA 02142 (US).

(74) Agent: **MCCOOL, Gabriel, J.** et al.; Wolf, Greenfield &
Sacks, P.C., 600 Atlantic Avenue, Boston, MA 02210-2206
(US).

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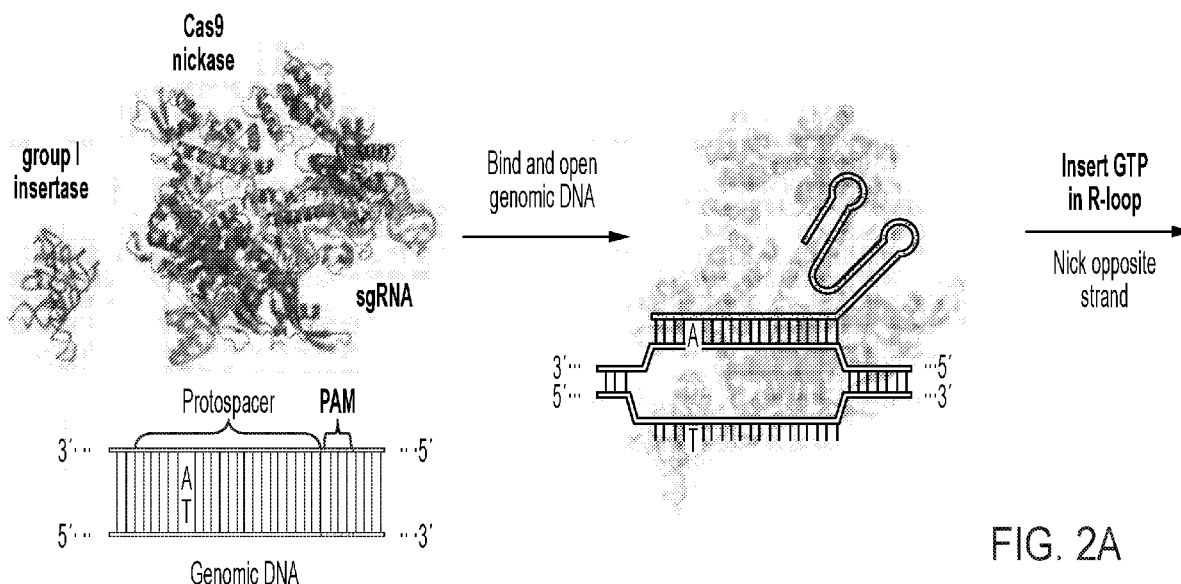


FIG. 2A

(57) **Abstract:** The present specification provides compositions and methods that are capable of directly installing an insertion or deletion of a given nucleotide at a specified genetic locus. The compositions and methods involve the novel combination of the use of an engineered RNA enzyme (i.e., "ribozyme") that is capable of site-specifically inserting or deleting a single nucleotide at a genetic locus and the use of a nucleic acid programmable DNA binding protein (napDNAbp) (e.g., Cas9) to target the engineered ribozyme to a specified genetic locus, thereby allowing for the direct installation of an insertion or deletion at the specified genetic locus by the engineered ribozyme.

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SYSTEM FOR GENOME EDITING

GOVERNMENT SUPPORT

[0001] This invention was made with government support. The government has certain rights in the invention.

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0002] This PCT application claims priority to U.S. Provisional Application No. 62/833,494, filed April 12, 2019, the contents of which are incorporated herein by reference.

BACKGROUND OF THE DISCLOSURE

[0003] Small genomic insertions or deletions are known to cause a wide variety of genetic diseases. In addition, pathogenic single nucleotide mutations contribute to approximately 67% of human diseases for which there is a genetic component⁷. Unfortunately, treatment options for patients with these genetic disorders remain extremely limited, despite decades of gene therapy exploration⁸. Perhaps the most parsimonious solution to this therapeutic challenge is direct correction of single nucleotide mutations in patient genomes, which would address the root cause of disease and would likely provide lasting benefit. Although such a strategy was previously unthinkable, recent improvements in genome editing capabilities brought about by the advent of the CRISPR/Cas system⁹ have now brought this therapeutic approach within reach. By straightforward design of a guide RNA (gRNA) sequence that contains ~20 nucleotides complementary to the target DNA sequence, nearly any conceivable genomic site can be specifically accessed by CRISPR associated (Cas) nucleases^{1,2}. To date, several monomeric bacterial Cas nuclease systems have been identified and adapted for genome editing applications¹⁰. This natural diversity of Cas nucleases, along with a growing collection of engineered variants¹¹⁻¹⁴, offers fertile ground for developing new genome editing technologies.

[0004] While gene disruption with CRISPR is now a mature technique, precision editing of single base pairs in the human genome remains a major challenge³. Homology directed repair (HDR) has long been used in human cells and other organisms to insert, correct, or exchange DNA sequences at sites of double strand breaks (DSBs) using donor DNA repair templates that encode the desired edits¹⁵. However, traditional HDR has very low efficiency in most human cell types, particularly in non-dividing cells, and competing non-homologous end joining (NHEJ) leads predominantly to insertion-deletion (indel) byproducts¹⁶. Other issues relate to the generation of DSBs, which can give rise to large chromosomal

rearrangements and deletions at target loci¹⁷, or activate the p53 axis leading to growth arrest and apoptosis^{18,19}.

[0005] Several approaches have been explored to address these drawbacks of HDR. For example, repair of single-stranded DNA breaks (nicks) with oligonucleotide donors has been shown to reduce indel formation, but yields of desired repair products remain low²⁰. Other strategies attempt to bias repair toward HDR over NHEJ using small molecule and biologic reagents²¹⁻²³. However, the effectiveness of these methods is likely cell-type dependent, and perturbation of the normal cell state could lead to undesirable and unforeseeable effects.

[0006] Recently, the inventors, led by Prof. David Liu et al. developed base editing as a technology that edits target nucleotides without creating DSBs or relying on HDR^{4-6, 24-27}. Direct modification of DNA bases by Cas-fused deaminase enzymes allows for C•G to T•A, or A•T to G•C, base pair conversions in a short target window (~5-7 bases) with very high efficiency. As a result, base editors have been rapidly adopted by the scientific community. However, the following factors limit their generality for precision genome editing: (1) “bystander editing” of non-target C or A bases within the target window are observed; (2) target nucleotide product mixtures are observed; (3) target bases must be located 15±2 nucleotides upstream of a PAM sequence; and (5) repair of small insertion and deletion mutations is not possible.

[0007] Moreover, current methods to repair small genomic insertions or deletions are inefficient, generally restricted to mitotic cells, and prone to result in the stochastic insertion or deletion of random nucleotides (indels). No published method directly enables the insertion or deletion of a given nucleotide at a specified genetic locus. The development of such a technology would advance genome editing therapeutics by enabling the direct correction of frameshift mutations.

[0008] Therefore, the development of programmable editors that are flexibly capable of directly introducing any desired small genomic insertion or deletion, for example, frameshift mutations, at a specified site with high specificity and efficiency would substantially expand the scope and therapeutic potential of genome editing technologies based on CRISPR.

SUMMARY OF THE DISCLOSURE

[0009] In one aspect, the present disclosure provides a genome editing strategy for the site-specific insertion of single nucleotides (e.g., G, A, T, or C) into defined genomic loci that combine the use of a napDNA_{bp}, guide RNA, and an engineered ribozyme. In another aspect, the disclosure provides a genome editing system for the site-specific insertion or

deletion of one or more nucleotides into defined genomic loci. As such, the present disclosure provides for compositions, methods of gene editing, fusion proteins, nucleoprotein complexes, nucleotide sequences encoding said fusion proteins and nucleoprotein complexes, vectors comprising nucleotide sequences encoding the fusion proteins and nucleoprotein complexes, isolated cells and cell lines comprising the vectors, pharmaceutical compositions comprising any of the compositions described herein, pharmaceutical kits for carrying out genome editing using the compositions described herein, and methods of delivery the genome editing system to cells under *in vitro* or *in vivo* conditions.

[0010] In certain aspects, the present specification relates to genome editing system comprising a napDNAbp, a guide RNA, and an engineered RNA that is capable of inserting or deleting one or more nucleotides at a target site. The genome editing system comprises compositions (e.g., fusion proteins and nucleoprotein complexes) and methods that are capable of directly installing an insertion or deletion of a given nucleotide at a specified genetic locus. The compositions and methods involve the novel combination of the use an engineered ribozyme that is capable of site-specifically inserting or deleting a single nucleotide at a genetic locus when combined with the use of a nucleic acid programmable DNA binding protein (napDNAbp) (e.g., Cas9) and a guide RNA to target the engineered ribozyme to a specified genetic locus, thereby allowing for the direct installation of an insertion or deletion at the specified genetic locus by the engineered ribozyme.

[0011] The genome editing system described herein embraces multiple possible configurations. For instance, in one embodiment, the genome editing system comprises a napDNAbp (e.g., Cas9) complexed with a guide RNA, and an engineered ribozyme provided in trans. In other embodiments, the engineered ribozyme may be provided in trans but may be recruited or co-localized to the napDNAbp/guide RNA complex at a target site through a recruitment means, such as an RNA-protein recruitment system. As an example of such a system, the napDNAbp may be modified by fusing it to an MS2 bacteriophage coat protein (MCP), and the ribozyme may be modified to contain an MS2 hairpin, which recognizes and binds to the MCP. Due to these modifications, the napDNAbp may recruit the ribozyme provided in trans through the interaction between the MCP on the napDNAbp and the MS2 hairpin element on the ribozyme. Any other known recruitment means may be used and the disclosure is not intended to be limited to the MCP/MS2 recruitment system. In other embodiments, the genome editing system comprises a napDNAbp (e.g., Cas9) complexed with a guide RNA, and an engineered ribozyme provided in cis, e.g., whereby the ribozyme is coupled to either the napDNAbp or the guide RNA. For example, the ribozyme could be

coupled to the napDNAbp via a chemical linker (e.g., covalent bond, alkylene linker, polymeric linker, peptide linker). Or, the ribozyme could be coupled to the guide RNA as a transcriptional fusion, i.e., whereby the ribozyme sequence and the guide RNA sequence are transcribed as a single RNA molecule. It should be appreciated that the foregoing concepts, and additional concepts discussed below, may be arranged in any suitable combination, as the present disclosure is not limited in this respect. Further, other advantages and novel features of the present disclosure will become apparent from the following detailed description of various non-limiting embodiments when considered in conjunction with the accompanying figures.

[0012] In one embodiment, a previously evolved version of the group I self-splicing intron was modified to site-specifically insert and subsequently ligate into place a single guanosine nucleotide into single-stranded DNA (e.g., SEQ ID NOs: 88, 89, 156, or 157). Subsequently, the ability of this ribozyme to act on double-stranded DNA that was bound by a Cas9:guide RNA complex *in vitro* was demonstrated before its ability to function in human cells and bacteria was examined. It was found that localizing the ribozyme to the same genetic locus as Cas9 enabled it to modify its genomic target.

[0013] It should be appreciated that the foregoing concepts, and additional concepts discussed below, may be arranged in any suitable combination, as the present disclosure is not limited in this respect. Further, other advantages and novel features of the present disclosure will become apparent from the following detailed description of various non-limiting embodiments when considered in conjunction with the accompanying figures.

[0014] The present disclosure further relates to the following numbered paragraphs.

1. An engineered ribozyme represented by the structure of FIG. 1A.
2. An engineered ribozyme represented by the structure of FIG. 3B.
3. An engineered ribozyme comprising a deletion in the 3' terminal end sufficient to remove the self-insertion activity of the ribozyme.
4. The engineered ribozyme of paragraph 3, wherein the deletion in the 3' terminal end comprises a deletion of the terminal 1-5 nucleotides of the ribozyme.
5. The engineered ribozyme of paragraph 3, further comprising an active site that catalyzes the insertion of a nucleotide into target site of a substrate single strand DNA molecule.

6. The engineered ribozyme of paragraph 5, wherein the active site comprises a region that hybridizes to the substrate single strand DNA molecule.
7. The engineered ribozyme of paragraph 6, wherein the region is 5 nucleotides, or 6 nucleotides, or 7 nucleotides, or 8 nucleotides and whose sequence is complementary to the substrate single strand DNA molecule.
8. The engineered ribozyme of paragraph 5, wherein the active site comprises a nucleotide that forms a wobble base pair with the substrate single strand DNA molecule.
9. The engineered ribozyme of paragraph 5, wherein the active site comprises an unpaired nucleotide.
10. The engineered ribozyme of paragraph 5, wherein the active site comprises in a 5'-3' direction a region that hybridizes to the substrate single strand DNA molecule, a nucleotide that forms a wobble base pair with the substrate single strand DNA molecule, and an unpaired nucleotide.
11. The engineered ribozyme of paragraph 10, wherein the ribozyme inserts a nucleotide immediate adjacent to the wobble base pair.
12. A ribozyme-mediated programmable nucleic acid editing construct comprising a ribozyme and a nucleic acid programmable DNA binding protein (napDNAbp) which is capable of installing an insertion of one or more nucleotides at a target site in a DNA molecule.
13. The editing construct of paragraph 12, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.
14. The editing construct of paragraph 13, wherein the one or more nucleotides is a G or A.
15. The editing construct of paragraph 13, wherein the one or more nucleotides is a C or T.
16. The editing construct of paragraph 12, wherein the ribozyme is represented by the structure of FIG. 1A or FIG. 3B.

17. The editing construct of paragraph 12, wherein the ribozyme is a modified group I intron from *Tetrahymena thermophila*.
18. The editing construct of paragraph 12, wherein the ribozyme further comprises a targeting moiety.
19. The editing construct of paragraph 18, wherein the targeting moiety is an MS2 hairpin structure.
20. The editing construct of paragraph 12, wherein the ribozyme and the napDNAbp are not fusion proteins.
21. The editing construct of paragraph 12, wherein the napDNAbp further comprises a targeting moiety receptor capable of binding to a ribozyme comprising a cognate targeting moiety.
22. The editing construct of paragraph 12, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
23. The editing construct of paragraph 12, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).
24. The editing construct of paragraph 12, wherein the napDNAbp is selected from the group consisting of: Cas9, CasX, CasY, Cpf1, C2c1, C2c2, C2C3, and Argonaute and optionally has a nickase activity
25. The editing construct of paragraph 12, wherein the napDNAbp when complexed with a guide RNA functions to bind to the target site in the DNA molecule and form an R-loop.
26. The editing construct of paragraph 24, wherein the R-loop comprise a single strand DNA region comprising the target site for binding the ribozyme.
27. A complex comprising the editing construct of any of paragraphs 12-26 and a guide RNA.
28. The complex of paragraph 27, wherein the guide RNA is fused to the ribozyme.
29. The complex of paragraph 27, wherein the guide RNA is bound to the napDNAbp.

30. A polynucleotide encoding the ribozyme of any of paragraphs 1-11.
31. A polynucleotide encoding the editing construct of any of paragraphs 12-26.
32. A vector comprising the polynucleotide of paragraph 30.
33. A vector comprising the polynucleotide of paragraph 31.
34. A cell comprising an editing construct of any of paragraphs 12-26.
35. A cell comprising a ribozyme of any of paragraphs 1-11.
36. A pharmaceutical composition comprising a ribozyme of any of paragraphs 1-11, an editing construct of any of paragraphs 12-26, or a vector of any of paragraphs 32-33.
37. A method for introducing a new nucleobase pair into a target site of a DNA molecule, comprising contacting a single-stranded R-loop formed in the DNA molecule by a bound napDNAbp with an engineered ribozyme, wherein the engineered ribozyme is configured to insert a nucleobase into an insertion site located in the R-loop.
38. The method of paragraph 37, wherein DNA repair and/or replication of a cell process the nucleobase insertion to form the new nucleobase pair in the DNA molecule.
39. The method of paragraph 37, wherein the engineered ribozyme is represented by the structure of FIG. 1A.
40. The method of paragraph 37, wherein the engineered ribozyme is represented by the structure of FIG. 3B.
41. The method of paragraph 37, wherein the engineered ribozyme comprises a deletion in the 3' terminal end sufficient to remove the self-insertion activity of the ribozyme.
42. The method of paragraph 37, wherein the engineered ribozyme comprises an active site that catalyzes the insertion of the nucleobase.
43. The method of paragraph 37, wherein the engineered ribozyme comprises an active site having a region that hybridizes to the single-stranded R-loop.

44. The method of paragraph 37, wherein the engineered ribozyme comprises a nucleotide that forms a wobble base pair with the single-stranded R-loop.
45. The method of paragraph 37, wherein the engineered ribozyme comprises an unpaired nucleotide.
46. The method of paragraph 37, wherein the engineered ribozyme comprises an active site comprising in a 5'-3' direction a region that hybridizes to the single-stranded R-loop, a nucleotide that forms a wobble base pair with the the single-stranded R-loop, and an unpaired nucleotide.
47. The method of paragraph 37, wherein the ribozyme inserts the nucleobase immediate adjacent a wobble base pair formed between the ribozyme and the single-stranded R-loop.
48. The method of paragraph 37, wherein the ribozyme further comprises a targeting moiety.
49. The method of paragraph 48, wherein the targeting moiety is an MS2 hairpin structure.
50. The method of paragraph 37, wherein the ribozyme and the napDNAbp are not fusion proteins.
51. The method of paragraph 37, wherein the napDNAbp further comprises a targeting moiety receptor capable of binding to a ribozyme comprising a cognate targeting moiety.
52. The method of paragraph 37, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
53. The method of paragraph 37, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).
54. The method of paragraph 37, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.
55. An engineered ribozyme comprising SEQ ID NO: 88, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least

93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 88.

56. An engineered ribozyme comprising SEQ ID NO: 89, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 89.

57. An engineered ribozyme comprising SEQ ID NO: 156, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 156.

58. An engineered ribozyme comprising SEQ ID NO: 157, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 157.

59. A genome editing system comprising a nucleic acid programmable DNA binding protein (napDNAbp), a guide RNA, and a ribozyme.

60. The genome editing system of paragraph 59, wherein the ribozyme comprises any of SEQ ID NOs: 88, 89, 156, or 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 88, 89, 156, or 157.

61. The genome editing system of paragraph 59, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.

62. The genome editing system of paragraph 61, wherein the one or more nucleotides is a G or A.

63. The genome editing system of paragraph 61, wherein the one or more nucleotides is a C or T.

64. The genome editing system of paragraph 59, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
65. The genome editing system of paragraph 59, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).
66. The genome editing system of paragraph 59, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.
67. The genome editing system of paragraph 59, wherein the napDNAbp comprises a recruitment domain.
68. The genome editing system of paragraph 67, wherein the recruitment domain is a MS2 bacteriophage coat protein.
69. The genome editing system of paragraph 67, wherein the MS2 bacteriophage coat protein comprises SEQ ID NO: 94, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO: 94.
70. The genome editing system of paragraph 67, wherein the ribozyme comprises the SEQ ID NO: 89, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 89.
71. The genome editing system of paragraph 67, wherein the ribozyme comprises the SEQ ID NO: 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 157.
72. The genome editing system of paragraph 59, wherein the napDNAbp comprise an additional one or more functional domains.
73. The genome editing system of paragraph 72, wherein the one or more functional domains is an NLS.

74. The genome editing system of paragraph 72, wherein the one or more functional domains is an intein or a split-intein.
75. The genome editing system of paragraph 72, wherein the one or more functional domains are coupled via one or more linkers.
76. The genome editing system of paragraph 73, wherein the NLS comprises SEQ ID NOs: 9, 118, 10, 119, or 121-126, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 9, 118, 10, 119, or 121-126.
77. The genome editing system of paragraph 74, wherein the intein or split-intein comprises SEQ ID NOs: 1-8, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 1-8.
78. The genome editing system of paragraph 75, wherein the linker comprises SEQ ID NOs: 102-113, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 102-113.
79. The genome editing system of paragraph 59, wherein the napDNAbp when complexed with the guide RNA functions to bind to a target site in a DNA molecule, forming an R-loop.
80. The genome editing system of paragraph 79, wherein the R-loop comprises a single strand DNA region comprising a complementary region that binds to the ribozyme.
81. The genome editing system of paragraph 80, wherein the complementary region binds to the P0 site of the ribozyme.
82. One or more polynucleotides encoding the genome editing system of any of paragraphs 59-81.
83. A vector comprising the polynucleotide of paragraph 82.
84. The vector of paragraph 83, wherein the vector is an rAAV.

85. The vector of paragraph 84, wherein the rAAV is an rAAV2, rAAV6, rAAV8, rPHP.B, rPHP.eB, or rAAV9.
86. A cell comprising the vector of any of paragraphs 83-85.
87. A pharmaceutical composition comprising a genome editing system of any of paragraphs 59-81, a polynucleotide of paragraph 82, or a vector of paragraphs 83-85, and a pharmaceutically acceptable excipient.
88. A method for installing one or more nucleobases at a target site in a DNA sequence, comprising contacting the DNA sequence with a genome editing system of any of paragraphs 59-80.
89. The method of paragraph 88, wherein the genome editing system comprises a nucleic acid programmable DNA binding protein (napDNAbp), a guide RNA, and a ribozyme.
90. The method of paragraph 89, wherein the ribozyme comprises any of SEQ ID NOs: 88, 89, 156, or 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 88, 89, 156, or 157.
91. The method of paragraph 89, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.
92. The method of paragraph 88, wherein the method installs a G, A, T, or C, or a combination thereof.
93. The method of paragraph 88, wherein the method installs a frameshift mutation.
94. The method of paragraph 89, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
95. The method of paragraph 89, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).

96. The method of paragraph 89, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.
97. The method of paragraph 89, wherein the napDNAbp comprises a recruitment domain.
98. The method of paragraph 89, wherein the recruitment domain is a MS2 bacteriophage coat protein.
99. The method of paragraph 98, wherein the MS2 bacteriophage coat protein comprises SEQ ID NO: 94, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO: 94.
100. The method of paragraph 98, wherein the ribozyme comprises the SEQ ID NO: 89, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 89.
101. The method of paragraph 98, wherein the ribozyme comprises the SEQ ID NO: 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 157.
102. An engineered ribozyme that catalyzes the insertion of a nucleotide into a single-stranded DNA molecule.
103. The engineered ribozyme of paragraph 102, wherein the nucleotide is G.
104. The engineered ribozyme of paragraph 102, wherein the nucleotide is A.
105. The engineered ribozyme of paragraph 102, wherein the nucleotide is T.
106. The engineered ribozyme of paragraph 102, wherein the nucleotide is C.

BRIEF DESCRIPTION OF THE DRAWINGS

[0015] The following drawings form part of the present specification and are included to further demonstrate certain embodiments of the present disclosure, which can be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

[0016] FIG. 1A shows the sequence and secondary structure of (a) an exemplary engineered ribozyme based on the ribozyme of *Tetrahymena* group I intron with mutations identified in directed evolution that enable the ribozyme to bind and cleave ssDNA (blue and/or indicated with a “star”) and insertions and deletions that enable nucleotide (e.g., GTP) insertion (red boxes). For example, element (b) refers to the deletion of the terminal nucleotides (e.g., the terminal 4 nucleotides) of the ribozyme, which inactivates the self-insertion activity of the ribozyme for self-insertion into the DNA target or substrate with which the ribozyme is interacting. This is also shown in more details in FIG. 3B. Element (c) shows engineered changes in the active site which interacts with the substrate DNA, catalyzing the insertion of the nucleotide at the target site of the target DNA substrate. Element (d) refers to the location or site of insertion of an MS2 hairpin (AUCUU sequence is removed and replaced with the MS2 hairpin), which functions as a targeting moiety to localize the engineered ribozyme to a bound napDNAbp/guide RNA complex to a target DNA site, wherein the napDNAbp is modified to incorporate a cognate targeting moiety receptor.

[0017] FIG. 1B shows the mechanism of group I intron-catalyzed splicing.

[0018] FIG. 2A is a schematic showing the targeted repair of frameshifts via single-nucleotide insertion into genomic DNA enabled by a ribozyme and Cas9-based molecular machine. In reference to FIG. 2A and also the detailed illustration of FIG. 2D, binding of the sgRNA:Cas9 complex to genomic DNA forms a ssDNA R-loop opposite the strand occupied by the guide RNA. The engineered e ribozyme (“group I insertase” as provided in this illustration in trans) then binds to its single strand DNA substrate, whereby a portion of the ribozyme (e.g., the P0 region) anneals to the single strand DNA of the R loop over a short complementary (or partly complementary) sequence (e.g., at least a 3, at least a 4, at least a 5, at least a 6, at least a 7, at least a 8, at least a 9, at least a 10, at least an 11, at least a 12, at least a 13, at least a 14, or at least a 15 nucleotide stretch in the R loop region). Once hybridized to the R loop at the complementary region, the ribozyme installs a nick in the R loop strand, and then catalyzes the insertion of a G into the nick site, and finally, the ligation between the newly inserted G and the adjacent nucleotide (here, T).

[0019] FIG. 2B shows the structure of the active site of the *Azoarcus* group I intron (top) and T7 DNA polymerase.

[0020] FIG. 2C shows the design of shifting strategy to enable the ribozyme to ligate the nick that results from GTP insertion, based on the structures in FIG. 1C.

[0021] FIG. 2D shows the design of extended P0 to enable ligation of GTP in ssDNA.

[0022] FIG. 3A depicts ribozyme-catalyzed insertion and ligation of GTP into ssDNA, as shown via polyacrylamide gel electro-phoresis (PAGE) analysis of 5'-radiolabeled DNA substrate (left) and high-throughput sequencing (HTS, right). NR indicates no reaction, P product alone, and +E the addition of the ribozyme in FIG. 1A.

[0023] FIG. 3B shows the design features of an (a) exemplary engineered ribozyme contemplated herein. The element identified as (b) represents the backbone portion of an exemplary engineered ribozyme, which can include the nucleotides in FIG. 1A identified with a "star" symbol, which enable the ribozyme to bind and act on DNA, as opposed to a natural RNA substrate. Examples of such modifications can be found described in Joyce et al., "Selection *in vitro* of an RNA enzyme that specifically cleaves single-stranded DNA," Nature, 1990, p. 467, which is incorporated herein by reference. Element (c) refers to the deletion of the terminal nucleotides (e.g., the terminal 4 nucleotides) of the ribozyme, which inactivates or removes the self-insertion activity of the ribozyme for self-insertion into the DNA target or substrate with which the ribozyme is interacting. Element (d) refers to a GTP (nucleotide) substrate, which is inserted by the ribozyme into the DNA at the insertion site between elements (h) and (i) to change the sequence from GATCTGGG-5' to GAGTCTGGG-5'. Without being bound by theory, and in reference to the stepwise mechanism of FIG. 2D, insertion would result in the breakage of the phosphodiester bond between the A and T nucleotides in the DNA substrate, inserting of a G from the GTP at the insertion site through formation of a phosphiester bond between the inserted G and the existing A on the DNA strand. The downstream A-G- would then shift such that the G would hybridize to the unpaired C in the ribozyme (the C located at element (g)), causing at the same time the pairing of the inserted G with the U on the ribozyme in element (h). Lastly, the ribozyme would catalyze the ligation of the introduced G to the upstream T in element (i), thereby introducing a G into the target DNA sequence. Through subsequent DNA repair and/or replication processes, a complete nucleobase pair will have been inserted/incorporated into the double strand DNA target.

[0024] Element (d) can preferably be a GTP or an ATP. In some embodiments, element (d) can be a TTP or a CTP. Element (e) refers to G nucleotides which facilitate effective transcription of the ribozyme. Element (f) refers to an extension of the P0 region of the ribozyme, which improves the binding of the substrate DNA to the ribozyme (e.g., as

described further in Tsang and Joyce, “Specialization of the DNA-cleaving activity of a group I ribozyme through in vitro evolution,” *J. Mol. Biol.*, 1996, 262(1):31-42, which is incorporated herein by reference). The length of this region can vary, e.g., can be from about 1-10 nucleobase pairs, or 2-12 nucleobase pairs, or 3-13 nucleobase pairs, or 4-14 nucleobase pairs, or from 5-20 nucleobase pairs. Element (g) is an unpaired nucleotide, which results in fewer required purines of element (h) needed to shift the substrate sequences upon insertion of the new nucleotide (e.g., GTP). In the example shown is an unpaired C, however this can be G, A, or T, in some embodiments.

[0025] Element (h) is a series of pyrimidine-purine nucleobase pairs (e.g., can be 1, 2, 3, 4, or 5 or more U-G, U-A, or C-G nucleobase pairs) that sit adjacent to the “wobble” nucleobase pair of element (i). The nucleobases of element (h) function to enable shifting in the active site of the ribozyme upon insertion of the nucleotide of element (d) (e.g., the GTP). The nucleobases of element (h) also enable the ligation step at the nick site formed subsequent or simultaneous to the GTP insertion (i.e., or another nucleotide of element (d)). Element (i) is a “wobble” nucleobase pair. In the example, the wobble nucleobase is a G-T pair, but other wobble pairs are acceptable. Element (j) represents the region of the active site which recognizes the DNA substrate (i.e., the target sequence). The region shown has the sequence 5'-GGACCC-3', which is exemplary. This sequence can be represented more broadly at 5'-SSSWST-3', wherein S is G or C and W is A or T.

[0026] The “active” site of the ribozyme for purposes of this disclosure can comprise elements (i) and (h). More broadly, the “active” site may refer to regions (g), (h), (i), and (j) since all four regions are involved in different aspects of the mechanism of insertion by the ribozyme. In general, element (j) binds and interacts with the target DNA substrate, element (i) is a “wobble” pair that helps define the location of the insertion point as between element (i) and (h), element (h) facilitates the upward (i.e., in the 5' to 3' direction, i.e., downstream shifting) shifting of the DNA substrate following the breakage or nicking of the phosphodiester bond between elements (h) and (i) on the DNA substrate. Element (g) also facilitates the downstream shift of the nicked portion of the DNA substrate (due to the interaction of the C on the ribozyme and the G on the DNA), making room for insertion of the G into the nicked site, and the subsequent ligation of that nucleotide to reform the DNA now-modified +1 nucleotide DNA substrate.

[0027] FIG. 3C depicts graphs showing that extended, bulged P0 results in improved ratio of desired product to cleaved intermediates, as determined by PAGE without a large loss in activity.

[0028] FIG. 4 shows a model for ribozyme-mediated programmable editing which is implemented with two Cas9:guide RNA complexes that bind on either side of a ribozyme binding site. In particular, the model shows Cas9- and ribozyme-mediated nucleotide insertion in dsDNA in vitro. Two Cas9:sgRNA complexes are targeted to either side of the ribozyme binding site, and the targeted strand bound to the sgRNA is nicked, resulting in dissociation of the intervening sequence to form a single strand DNA (ssDNA) region. The resulting ssDNA is able to be recognized by the ribozyme, and nucleotide insertion occurs, as shown in FIG. 2D or FIG. 3B.

[0029] FIG. 5A shows HTS analysis of nucleotide insertion reactions following incubation with catalytically inert Cas9 (dCas9) and ribozyme. Distances D1 and D2 indicate number of nucleotides between the ribozyme target site and either the 3' or 5' PAM recognized by Cas9, as shown in FIG. 4A.

[0030] FIG. 5B shows HTS analysis of nucleotide insertion reactions with substrates with a single nick in the target dsDNA.

[0031] FIG. 5C shows HTS analysis of nucleotide insertion reactions with substrates with two nicks in the target dsDNA.

[0032] FIG. 6A shows a scheme for indel formation following ribozyme- and Cas9-catalyzed strand cleavage. Cleavage of opposing strands in close proximity creates a staggered double-strand break, leading to error prone non-homologous or microhomology-mediated end-joining (NHEJ/MMEJ), resulting in stochastic insertions or deletions.

[0033] FIG. 6B shows HTS analysis of HEK293T cells transfected with plasmids encoding ribozyme, sgRNA, and Cas9 bearing a D10A mutation that inactivates the RuvC domain (nCas9), resulting in nicking of the target strand as opposed to double-strand break.

Transfection of neither nCas9 alone nor in conjunction with ribozyme results in double-strand breaks.

[0034] FIG. 7A is an illustration showing enhanced targeting of ribozyme to genomic locus bound by Cas9 via fusion of the MS2 bacteriophage coat protein to Cas9 and incorporation of the MS2 RNA hairpin into the ribozyme.

[0035] FIG. 7B is an illustration showing MS2 hairpins installed in the L6 loop (grey) of the modified group I intron. Three different versions of the MS2 handle were constructed, varying the number of MS2 hairpins and the length and sequence of the linker between both them and the ribozyme core.

[0036] FIG. 7C shows HTS analysis of HEK293T cells transfected with plasmids encoding various MS2-ribozymes, MS2-fused nCas9, and sgRNA targeted to the HEK4 genomic locus.

[0037] FIG. 7D shows HTS analysis of HEK293T cells transfected as in E, targeted to another genomic locus. In both cases, significant ac-cumulation of indels are observed, indicative of ribozyme cutting activity.

[0038] FIG. 8 provides an illustration of a selection scheme for ribozymes that perform DNA cleavage. See Beaudry & Joyce, Science 1992.

[0039] FIG. 9 is a schematic showing that ribozymes can insert a single nucleotide into DNA in bacteria. (Top) illustration of relevant plasmids expressing the ribozyme and Cas9 upon being induced with L-arabinose. (Middle) Scheme showing DNA target site and portions of the DNA which would basepair to either the guide or ribozyme. The PAM is also shown. (Bottom) Sanger sequencing results of bacteria that survived on kanamycin following ribozyme/Cas9 expression. All colonies contained the inserted G that would be expected if the ribozyme were functioning as designed.

DEFINITIONS

[0040] Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by one of ordinary skill in the art to which this invention belongs. The following references provide one of skill in the art to which this invention pertains with a general definition of many of the terms used in this invention: Singleton et al., Dictionary of Microbiology and Molecular Biology (2d ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); Hale & Marham, The Harper Collins Dictionary of Biology (1991); and Lackie et al., The Dictionary of Cell & Molecular Biology (3d ed. 1999); and Cellular and Molecular Immunology, Eds. Abbas, Lichtman and Pober, 2nd Edition, W.B. Saunders Company. For the purposes of the present invention, the following terms are further defined.

Antisense strand

[0041] In genetics, the “antisense” strand of a segment within double-stranded DNA is the template strand, and which is considered to run in the 3' to 5' orientation. By contrast, the “sense” strand is the segment within double-stranded DNA that runs from 5' to 3', and which is complementary to the antisense strand of DNA, or template strand, which runs from 3' to 5'. In the case of a DNA segment that encodes a protein, the sense strand is the strand of DNA that has the same sequence as the mRNA, which takes the antisense strand as its template during transcription, and eventually undergoes (typically, not always) translation into a protein. The antisense strand is thus responsible for the RNA that is later translated to protein, while the sense strand possesses a nearly identical makeup to that of the mRNA.

Note that for each segment of dsDNA, there will possibly be two sets of sense and antisense, depending on which direction one reads (since sense and antisense is relative to perspective). It is ultimately the gene product, or mRNA, that dictates which strand of one segment of dsDNA is referred to as sense or antisense.

Bi-specific ligand

[0042] The term "bi-specific ligand" or "bi-specific moiety," as used herein, refers to a ligand that binds to two different ligand-binding domains. In certain embodiments, the ligand is a small molecule compound, or a peptide, or a polypeptide. In other embodiments, ligand-binding domain is a "dimerization domain," which can be install as a peptide tag onto a protein. In various embodiments, two proteins each comprising the same or different dimerization domains can be induced to dimerize through the binding of each dimerization domain to the bi-specific ligand. As used herein, "bi-specific ligands" may be equivalently refer to "chemical inducers of dimerization" or "CIDs". In one embodiment, a napDNAbp or guide RNA modified to comprise a first dimerization domain can be used to recruit a ribozyme comprising a second dimerization domain via their coupling through a bi-specific ligand.

cDNA

[0043] The term "cDNA" refers to a strand of DNA copied from an RNA template. cDNA is complementary to the RNA template.

Circular permutant

[0044] As used herein, the term "circular permutant" refers to a protein or polypeptide (e.g., a Cas9) comprising a circular permutation, which is change in the protein's structural configuration involving a change in order of amino acids appearing in the protein's amino acid sequence. In other words, circular permutants are proteins that have altered N- and C-termini as compared to a wild-type counterpart, e.g., the wild-type C-terminal half of a protein becomes the new N-terminal half. Circular permutation (or CP) is essentially the topological rearrangement of a protein's primary sequence, connecting its N- and C-terminus, often with a peptide linker, while concurrently splitting its sequence at a different position to create new, adjacent N- and C-termini. The result is a protein structure with different connectivity, but which often can have the same overall similar three-dimensional (3D) shape, and possibly include improved or altered characteristics, including, reduced proteolytic susceptibility, improved catalytic activity, altered substrate or ligand binding, and/or improved thermostability. Circular permutant proteins can occur in nature (e.g.,

concanavalin A and lectin). In addition, circular permutation can occur as a result of posttranslational modifications or may be engineered using recombinant techniques.

Circularly permuted Cas9

[0045] The term “circularly permuted Cas9” refers to any Cas9 protein, or variant thereof, that has been occurs as a circular permutant, whereby its N- and C-termini have been topically rearranged. Such circularly permuted Cas9 proteins (“CP-Cas9”), or variants thereof, retain the ability to bind DNA when complexed with a guide RNA (gRNA). See, Oakes et al., “Protein Engineering of Cas9 for enhanced function,” *Methods Enzymol*, 2014, 546: 491–511 and Oakes et al., “CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification,” *Cell*, January 10, 2019, 176: 254-267, each of are incorporated herein by reference. The instant disclosure contemplates any previously known CP-Cas9 or use a new CP-Cas9 so long as the resulting circularly permuted protein retains the ability to bind DNA when complexed with a guide RNA (gRNA). Exemplary CP-Cas9 proteins are SEQ ID NOs: 67-76.

CRISPR

[0046] CRISPR is a family of DNA sequences (i.e., CRISPR clusters) in bacteria and archaea that represent snippets of prior infections by a virus that have invaded the prokaryote. The snippets of DNA are used by the prokaryotic cell to detect and destroy DNA from subsequent attacks by similar viruses and effectively compose, along with an array of CRISPR-associated proteins (including Cas9 and homologs thereof) and CRISPR-associated RNA, a prokaryotic immune defense system. In nature, CRISPR clusters are transcribed and processed into CRISPR RNA (crRNA). In certain types of CRISPR systems (e.g., type II CRISPR systems), correct processing of pre-crRNA requires a trans-encoded small RNA (tracrRNA), endogenous ribonuclease 3 (rnc) and a Cas9 protein. The tracrRNA serves as a guide for ribonuclease 3-aided processing of pre-crRNA. Subsequently, Cas9/crRNA/tracrRNA endonucleolytically cleaves linear or circular dsDNA target complementary to the RNA. Specifically, the target strand not complementary to crRNA is first cut endonucleolytically, then trimmed 3′-5′ exonucleolytically. In nature, DNA-binding and cleavage typically requires protein and both RNAs. However, single guide RNAs (“sgRNA”, or simply “gRNA”) can be engineered so as to incorporate aspects of both the crRNA and tracrRNA into a single RNA species – the guide RNA. See, e.g., Jinek M., Chylinski K., Fonfara I., Hauer M., Doudna J.A., Charpentier E. *Science* 337:816-821(2012), the entire contents of which is hereby incorporated by reference. Cas9 recognizes a short motif in the CRISPR repeat sequences (the PAM or protospacer adjacent motif) to help

distinguish self versus non-self. CRISPR biology, as well as Cas9 nuclease sequences and structures are well known to those of skill in the art (see, *e.g.*, “Complete genome sequence of an M1 strain of *Streptococcus pyogenes*.” Ferretti *et al.*, J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E., *Proc. Natl. Acad. Sci. U.S.A.* 98:4658-4663(2001); “CRISPR RNA maturation by trans-encoded small RNA and host factor RNase III.” Deltcheva E., Chylinski K., Sharma C.M., Gonzales K., Chao Y., Pirzada Z.A., Eckert M.R., Vogel J., Charpentier E., *Nature* 471:602-607(2011); and “A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity.” Jinek M., Chylinski K., Fonfara I., Hauer M., Doudna J.A., Charpentier E. *Science* 337:816-821(2012), the entire contents of each of which are incorporated herein by reference). Cas9 orthologs have been described in various species, including, but not limited to, *S. pyogenes* and *S. thermophilus*. Additional suitable Cas9 nucleases and sequences will be apparent to those of skill in the art based on this disclosure, and such Cas9 nucleases and sequences include Cas9 sequences from the organisms and loci disclosed in Chylinski, Rhun, and Charpentier, “The tracrRNA and Cas9 families of type II CRISPR-Cas immunity systems” (2013) *RNA Biology* 10:5, 726-737; the entire contents of which are incorporated herein by reference.

Dimerization domain

[0047] The term “dimerization domain” refers to a ligand-binding domain that binds to a binding moiety of a bi-specific ligand. A “first” dimerization domain binds to a first binding moiety of a bi-specific ligand and a “second” dimerization domain binds to a second binding moiety of the same bi-specific ligand. When the first dimerization domain is fused to a first protein (*e.g.*, via PE, as discussed herein) and the second dimerization domain (*e.g.*, via PE, as discussed herein) is fused to a second protein, the first and second protein dimerize in the presence of a bi-specific ligand, wherein the bi-specific ligand has at least one moiety that binds to the first dimerization domain and at least another moiety that binds to the second dimerization domain. In one embodiment, a napDNAbp or guide RNA modified to comprise a first dimerization domain can be used to recruit a ribozyme comprising a second dimerization domain via their coupling through a bi-specific ligand.

Downstream

[0048] As used herein, the terms “upstream” and “downstream” are terms of relativity that define the linear position of at least two elements located in a nucleic acid molecule (whether single or double-stranded) that is orientated in a 5′-to-3′ direction. In particular, a first

element is upstream of a second element in a nucleic acid molecule where the first element is positioned somewhere that is 5' to the second element. For example, a SNP is upstream of a Cas9-induced nick site if the SNP is on the 5' side of the nick site. Conversely, a first element is downstream of a second element in a nucleic acid molecule where the first element is positioned somewhere that is 3' to the second element. For example, a SNP is downstream of a Cas9-induced nick site if the SNP is on the 3' side of the nick site. The nucleic acid molecule can be a DNA (double or single stranded), RNA (double or single stranded), or a hybrid of DNA and RNA. The analysis is the same for single strand nucleic acid molecule and a double strand molecule since the terms upstream and downstream are in reference to only a single strand of a nucleic acid molecule, except that one needs to select which strand of the double stranded molecule is being considered. Often, the strand of a double stranded DNA which can be used to determine the positional relativity of at least two elements is the "sense" or "coding" strand. In genetics, a "sense" strand is the segment within double-stranded DNA that runs from 5' to 3', and which is complementary to the antisense strand of DNA, or template strand, which runs from 3' to 5'. Thus, as an example, a SNP nucleobase is "downstream" of a promoter sequence in a genomic DNA (which is double-stranded) if the SNP nucleobase is on the 3' side of the promoter on the sense or coding strand.

Effective amount

[0049] The term "effective amount," as used herein, refers to an amount of a biologically active agent that is sufficient to elicit a desired biological response. For example, in some embodiments, an effective amount of the various components of the herein described compositions (e.g., the engineered ribozymes and/or napDNAbp complexes) may refer to the amount of the composition or its individual components that are sufficient to edit a target site nucleotide sequence, e.g., a genome (e.g., by installing a single base insertion or deletion, or to correct a frameshift mutation). As will be appreciated by the skilled artisan, the effective amount of an agent, e.g., a fusion protein, a nuclease, a hybrid protein, a protein dimer, a complex of a protein (or protein dimer) and a polynucleotide, or a polynucleotide, may vary depending on various factors as, for example, on the desired biological response, e.g., on the specific allele, genome, or target site to be edited, on the cell or tissue being targeted, and on the agent being used.

Frameshift mutation

[0050] As used herein, a "frameshift mutation" is a deletion or addition of 1, 2, or 4 nucleotides that change the ribosome reading frame and cause premature termination of translation at a new nonsense or chain termination codon (TAA, TAG, and TGA). Likewise,

insertions, deletions, and point mutations can all generate a nonsense codon mutation, directly stopping translation. Functional equivalent

[0051] The term “functional equivalent” refers to a second biomolecule that is equivalent in function, but not necessarily equivalent in structure to a first biomolecule. For example, a “Cas9 equivalent” refers to a protein that has the same or substantially the same functions as Cas9, but not necessarily the same amino acid sequence. In the context of the disclosure, the specification refers throughout to “a protein X, or a functional equivalent thereof.” In this context, a “functional equivalent” of protein X embraces any homolog, paralog, fragment, naturally occurring, engineered, mutated, or synthetic version of protein X which bears an equivalent function.

Fusion protein

[0052] The term “fusion protein” as used herein refers to a hybrid polypeptide which comprises protein domains from at least two different proteins. One protein may be located at the amino-terminal (N-terminal) portion of the fusion protein or at the carboxy-terminal (C-terminal) protein thus forming an “amino-terminal fusion protein” or a “carboxy-terminal fusion protein,” respectively. A protein may comprise different domains, for example, a nucleic acid binding domain (*e.g.*, the gRNA binding domain of Cas9 that directs the binding of the protein to a target site) and a nucleic acid cleavage domain or a catalytic domain of a nucleic-acid editing protein. Another example includes a Cas9 or equivalent thereof to a reverse transcriptase. Any of the proteins provided herein may be produced by any method known in the art. For example, the proteins provided herein may be produced via recombinant protein expression and purification, which is especially suited for fusion proteins comprising a peptide linker. Methods for recombinant protein expression and purification are well known, and include those described by Green and Sambrook, *Molecular Cloning: A Laboratory Manual* (4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2012)), the entire contents of which are incorporated herein by reference. For example, the genome editing system described herein may comprise a fusion protein between a napDNAbp and one or more other functional domains, such as, but not limited to a NLS.

Guide RNA

[0053] As used herein, the term “guide RNA” is a particular type of guide nucleic acid which is mostly commonly associated with a Cas protein of a CRISPR-Cas9 and which associates with Cas9, directing the Cas9 protein to a specific sequence in a DNA molecule that includes complementarity to protospacer sequence of the guide RNA. However, this term also embraces the equivalent guide nucleic acid molecules that associate with Cas9

equivalents, homologs, orthologs, or paralogs, whether naturally occurring or non-naturally occurring (e.g., engineered or recombinant), and which otherwise program the Cas9 equivalent to localize to a specific target nucleotide sequence. The Cas9 equivalents may include other nDNAbs from any type of CRISPR system (e.g., type II, V, VI), including Cpf1 (a type-V CRISPR-Cas systems), C2c1 (a type V CRISPR-Cas system), C2c2 (a type VI CRISPR-Cas system) and C2c3 (a type V CRISPR-Cas system). Further Cas-equivalents are described in Makarova et al., “C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector,” *Science* 2016; 353(6299), the contents of which are incorporated herein by reference. Exemplary sequences and structures of guide RNAs are provided herein. In addition, methods for designing appropriate guide RNA sequences are provided herein. As used herein, the “guide RNA” may also be referred to as a “traditional guide RNA” to contrast it with the modified forms of guide RNA termed “extended guide RNAs” which have been invented for the TPRT editing methods and composition disclosed herein.

Host cell

[0054] The term “host cell,” as used herein, refers to a cell that can host, replicate, and express a vector described herein, e.g., a vector comprising a nucleic acid molecule encoding a fusion protein comprising a Cas9 or Cas9 equivalent and a reverse transcriptase.

Inteins

[0001] As used herein, the term “intein” refers to auto-processing polypeptide domains found in organisms from all domains of life and can be used in the context of delivery a genome editing system of the disclosure by splitting the polypeptide elements into two or more small fragments, joinable in the cell by inteins and split-intein sequences.

[0002] An intein (*intervening protein*) carries out a unique auto-processing event known as protein splicing in which it excises itself out from a larger precursor polypeptide through the cleavage of two peptide bonds and, in the process, ligates the flanking extein (external protein) sequences through the formation of a new peptide bond. This rearrangement occurs post-translationally (or possibly co-translationally), as intein genes are found embedded in frame within other protein-coding genes. Furthermore, intein-mediated protein splicing is spontaneous; it requires no external factor or energy source, only the folding of the intein domain. This process is also known as *cis*-protein splicing, as opposed to the natural process of *trans*-protein splicing with “split inteins.” Inteins are the protein equivalent of the self-splicing RNA introns (see Perler et al., *Nucleic Acids Res.* 22:1125-1127 (1994)), which catalyze their own excision from a precursor protein with the concomitant fusion of the

flanking protein sequences, known as exteins (reviewed in Perler et al., Curr. Opin. Chem. Biol. 1:292-299 (1997); Perler, F. B. Cell 92(1):1-4 (1998); Xu et al., EMBO J. 15(19):5146-5153 (1996)).

[0055] As used herein, the term “protein splicing” refers to a process in which an interior region of a precursor protein (an intein) is excised and the flanking regions of the protein (exteins) are ligated to form the mature protein. This natural process has been observed in numerous proteins from both prokaryotes and eukaryotes (Perler, F. B., Xu, M. Q., Paulus, H. Current Opinion in Chemical Biology 1997, 1, 292-299; Perler, F. B. Nucleic Acids Research 1999, 27, 346-347). The intein unit contains the necessary components needed to catalyze protein splicing and often contains an endonuclease domain that participates in intein mobility (Perler, F. B., Davis, E. O., Dean, G. E., Gimble, F. S., Jack, W. E., Neff, N., Noren, C. J., Thomer, J., Belfort, M. Nucleic Acids Research 1994, 22, 1127-1127). The resulting proteins are linked, however, not expressed as separate proteins. Protein splicing may also be conducted in trans with split inteins expressed on separate polypeptides spontaneously combine to form a single intein which then undergoes the protein splicing process to join to separate proteins.

[0056] The elucidation of the mechanism of protein splicing has led to a number of intein-based applications (Comb, et al., U.S. Pat. No. 5,496,714; Comb, et al., U.S. Pat. No. 5,834,247; Camarero and Muir, J. Amer. Chem. Soc., 121:5597-5598 (1999); Chong, et al., Gene, 192:271-281 (1997), Chong, et al., Nucleic Acids Res., 26:5109-5115 (1998); Chong, et al., J. Biol. Chem., 273:10567-10577 (1998); Cotton, et al. J. Am. Chem. Soc., 121:1100-1101 (1999); Evans, et al., J. Biol. Chem., 274:18359-18363 (1999); Evans, et al., J. Biol. Chem., 274:3923-3926 (1999); Evans, et al., Protein Sci., 7:2256-2264 (1998); Evans, et al., J. Biol. Chem., 275:9091-9094 (2000); Iwai and Pluckthun, FEBS Lett. 459:166-172 (1999); Mathys, et al., Gene, 231:1-13 (1999); Mills, et al., Proc. Natl. Acad. Sci. USA 95:3543-3548 (1998); Muir, et al., Proc. Natl. Acad. Sci. USA 95:6705-6710 (1998); Otomo, et al., Biochemistry 38:16040-16044 (1999); Otomo, et al., J. Biomol. NMR 14:105-114 (1999); Scott, et al., Proc. Natl. Acad. Sci. USA 96:13638-13643 (1999); Severinov and Muir, J. Biol. Chem., 273:16205-16209 (1998); Shingledecker, et al., Gene, 207:187-195 (1998); Southworth, et al., EMBO J. 17:918-926 (1998); Southworth, et al., Biotechniques, 27:110-120 (1999); Wood, et al., Nat. Biotechnol., 17:889-892 (1999); Wu, et al., Proc. Natl. Acad. Sci. USA 95:9226-9231 (1998a); Wu, et al., Biochim Biophys Acta 1387:422-432 (1998b); Xu, et al., Proc. Natl. Acad. Sci. USA 96:388-393 (1999); Yamazaki, et al., J. Am. Chem. Soc., 120:5591-5592 (1998)). Each reference is incorporated herein by reference.

Ligand-dependent intein

[0057] The term “ligand-dependent intein,” as used herein refers to an intein that comprises a ligand-binding domain. Typically, the ligand-binding domain is inserted into the amino acid sequence of the intein, resulting in a structure intein (N) – ligand-binding domain – intein (C). Typically, ligand-dependent inteins exhibit no or only minimal protein splicing activity in the absence of an appropriate ligand, and a marked increase of protein splicing activity in the presence of the ligand. In some embodiments, the ligand-dependent intein does not exhibit observable splicing activity in the absence of ligand but does exhibit splicing activity in the presence of the ligand. In some embodiments, the ligand-dependent intein exhibits an observable protein splicing activity in the absence of the ligand, and a protein splicing activity in the presence of an appropriate ligand that is at least 5 times, at least 10 times, at least 50 times, at least 100 times, at least 150 times, at least 200 times, at least 250 times, at least 500 times, at least 1000 times, at least 1500 times, at least 2000 times, at least 2500 times, at least 5000 times, at least 10000 times, at least 20000 times, at least 25000 times, at least 50000 times, at least 100000 times, at least 500000 times, or at least 1000000 times greater than the activity observed in the absence of the ligand. In some embodiments, the increase in activity is dose dependent over at least 1 order of magnitude, at least 2 orders of magnitude, at least 3 orders of magnitude, at least 4 orders of magnitude, or at least 5 orders of magnitude, allowing for fine-tuning of intein activity by adjusting the concentration of the ligand. Suitable ligand-dependent inteins are known in the art, and include those provided below and those described in published U.S. Patent Application U.S. 2014/0065711 A1; Mootz *et al.*, “Protein splicing triggered by a small molecule.” *J. Am. Chem. Soc.* 2002; **124**, 9044–9045; Mootz *et al.*, “Conditional protein splicing: a new tool to control protein structure and function *in vitro* and *in vivo*.” *J. Am. Chem. Soc.* 2003; **125**, 10561–10569; Buskirk *et al.*, *Proc. Natl. Acad. Sci. USA*. 2004; **101**, 10505-10510; Skretas & Wood, “Regulation of protein activity with small-molecule-controlled inteins.” *Protein Sci.* 2005; **14**, 523-532; Schwartz, *et al.*, “Post-translational enzyme activation in an animal via optimized conditional protein splicing.” *Nat. Chem. Biol.* 2007; **3**, 50-54; Peck *et al.*, *Chem. Biol.* 2011; **18** (5), 619-630; the entire contents of each are hereby incorporated by reference. Exemplary sequences are as follows:

NAME	SEQUENCE OF LIGAND-DEPENDENT INTEIN
2-4 INTEIN:	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVV SWFDQGT RDVIGLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGD RVAGPGGSGNSLALS LTADQMVSALLDAEPPILYSEYDPTSPFSEAS MMGLLTNLADRELVHMINWAKRVP GFVDLTLHDQAHLLECAWLEI

	LMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLLAT SSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRA LDKITDTLIHLMAKAGTLTQQHQRLAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADALDD KFLHDMMLAEELRYSVIREVLPTRRARTFDLEVEELHTLVAEGVVH NC (SEQ ID NO: 1)
3-2 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAVAKDGTLLARPVVS WFDQGTRDVIGLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGDR VAGPGGSGNSLALSALTADQMVSALLDAEPPILYSEYDPTSPFSEASM MGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLCAWLEIL MIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLLATS SRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRA LDKITDTLIHLMAKAGTLTQQHQRLAQLLLILSHIRHMSNKGMEHL YSMKYTNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADALDDK FLHDMMLAEELRYSVIREVLPTRRARTFDLEVEELHTLVAEGVVHN C (SEQ ID NO: 2)
30R3-1 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVV SWFDQGTRDVIGLRIAGGATVWATPDHKVLTEYGWRAAGELRKG DRVAGPGGSGNSLALSALTADQMVSALLDAEPPILYSEYDPTSPFSEA SMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLCAWL EILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLL ATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH RALDKITDTLIHLMAKAGTLTQQHQRLAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADAL DDKFLHDMMLAEELRYSVIREVLPTRRARTFDLEVEELHTLVAEGVV VHNC (SEQ ID NO: 3)
30R3-2 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVV SWFDQGTRDVIGLRIAGGATVWATPDHKVLTEYGWRAAGELRKG DRVAGPGGSGNSLALSALTADQMVSALLDAEPPILYSEYDPTSPFSEA SMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLCAWL EILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLL ATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH RALDKITDTLIHLMAKAGTLTQQHQRLAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADAL DDKFLHDMMLAEELRYSVIREVLPTRRARTFDLEVEELHTLVAEGVV VHNC (SEQ ID NO: 4)
30R3-3 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVV SWFDQGTRDVIGLRIAGGATVWATPDHKVLTEYGWRAAGELRKG DRVAGPGGSGNSLALSALTADQMVSALLDAEPPILYSEYDPTSPFSEA SMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLCAWL EILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLL ATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH RALDKITDTLIHLMAKAGTLTQQHQRLAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADAL DDKFLHDMMLAEELRYSVIREVLPTRRARTFDLEVEELHTLVAEGVV VHNC (SEQ ID NO: 5)
37R3-1 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVV SWFDQGTRDVIGLRIAGGATVWATPDHKVLTEYGWRAAGELRKG DRVAGPGGSGNSLALSALTADQMVSALLDAEPPILYSEYNPTSPFSEA SMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLERAWL

	EILMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLL ATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIH RALDKITDTLIHLMAKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEH EHLYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADAL DDKFLHDMLAEGLRYSVIREVLPTRRARTFDLEVEELHTLVAEGVV VHNC ((SEQ ID NO: 6))
37R3-2 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVV SWFDQGTRDVIGLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGD RVAGPGGSGNSLALSITADQMVSALLDAEPPILYSEYDPTSPFSEAS MMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLEAWLEI LMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLLAT SSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRA LDKITDTLIHLMAKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADALDD KFLHDMLAEGLRYSVIREVLPTRRARTFDLEVEELHTLVAEGVVVH NC (SEQ ID NO: 7)
37R3-3 INTEIN	CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAADKDGTLLARPVVS WFDQGTRDVIGLRIAGGATVWATPDHKVLTEYGWRAAGELRKGD RVAGPGGSGNSLALSITADQMVSALLDAEPPILYSEYDPTSPFSEAS MMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQAHLLEAWLEI LMIGLVWRSMEHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDMLLAT SSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRA LDKITDTLIHLMAKAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEH LYSMKYKNVVPLYDLLLEMLDAHRLHAGGSGASRVQAFADALDD KFLHDMLAEGLRYSVIREVLPTRRARTFDLEVEELHTLVAEGVVVH NC (SEQ ID NO: 8)

napDNAbp

[0058] As used herein, the term “nucleic acid programmable DNA binding protein” or “napDNAbp,” of which Cas9 is an example, refer to a proteins which use RNA:DNA hybridization to target and bind to specific sequences in a DNA molecule. Each napDNAbp is associated with at least one guide nucleic acid (e.g., guide RNA), which localizes the napDNAbp to a DNA sequence that comprises a DNA strand (i.e., a target strand) that is complementary to the guide nucleic acid, or a portion thereof (e.g., the protospacer sequence of a guide RNA). In other words, the guide nucleic-acid “programs” the napDNAbp (e.g., Cas9 or equivalent) to localize and bind to a complementary sequence.

[0059] Without being bound by theory, the binding mechanism of a napDNAbp – guide RNA complex, in general, includes the step of forming an R-loop whereby the napDNAbp induces the unwinding of a double-strand DNA target, thereby separating the strands in the region bound by the napDNAbp. The guideRNA protospacer then hybridizes to the “target strand.” This displaces a “non-target strand” that is complementary to the target strand, which forms the single strand region of the R-loop. In some embodiments, the napDNAbp includes one or more nuclease activities, which then cut the DNA leaving various types of lesions. For

example, the napDNAbp may comprises a nuclease activity that cuts the non-target strand at a first location, and/ or cuts the target strand at a second location. Depending on the nuclease activity, the target DNA can be cut to form a “double-stranded break” whereby both strands are cut. In other embodiments, the target DNA can be cut at only a single site, i.e., the DNA is “nicked” on one strand. Exemplary napDNAbp with different nuclease activities include “Cas9 nickase” (“nCas9”) and a deactivated Cas9 having no nuclease activities (“dead Cas9” or “dCas9”). Exemplary sequences for these and other napDNAbp are provided herein.

Nickase

[0003] The term “nickase” refers to a Cas9 with one of the two nuclease domains inactivated. This enzyme is capable of cleaving only one strand of a target DNA. For example, a Cas9 nickase may have an inactivating mutation in an HNH nuclease domain, but with an unaltered RuvC nuclease domain. In another example, a Cas9 nickase may have an unaltered HNH nuclease domain, but have an inactivating mutation in the RuvC nuclease domain.

Nuclear localization sequence (NLS)

[0060] The term “nuclear localization sequence” or “NLS” refers to an amino acid sequence that promotes import of a protein into the cell nucleus, for example, by nuclear transport. Nuclear localization sequences are known in the art and would be apparent to the skilled artisan. For example, NLS sequences are described in Plank *et al.*, international PCT application, PCT/EP2000/011690, filed November 23, 2000, published as WO/2001/038547 on May 31, 2001, the contents of which are incorporated herein by reference for its disclosure of exemplary nuclear localization sequences. In some embodiments, a NLS comprises the amino acid sequence PKKKRKV (SEQ ID NO: 9) or MDSLLMNRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO: 10).

Linker

[0061] The term “linker,” as used herein, refers to a molecule linking two other molecules or moieties. The linker can be an amino acid sequence in the case of a linker joining two fusion proteins. For example, a Cas9 can be fused to an engineered ribozyme by an amino acid linker sequence. The linker can also be a nucleotide sequence in the case of joining two nucleotide sequences together. For example, in the instant case, the traditional guide RNA is linked via a spacer or linker nucleotide sequence to the RNA extension of an extended guide RNA which may comprise a RT template sequence and an RT primer binding site. In other embodiments, the linker is an organic molecule, group, polymer, or chemical moiety. In some embodiments, the linker is 5-100 amino acids in length, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 30-35, 35-40, 40-

45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-150, or 150-200 amino acids in length.

Longer or shorter linkers are also contemplated.

Nucleic acid molecule

[0062] The term “nucleic acid,” as used herein, refers to a polymer of nucleotides. The polymer may include natural nucleosides (i.e., adenosine, thymidine, guanosine, cytidine, uridine, deoxyadenosine, deoxythymidine, deoxyguanosine, and deoxycytidine), nucleoside analogs (e.g., 2-aminoadenosine, 2-thiothymidine, inosine, pyrrolo-pyrimidine, 3-methyl adenosine, 5-methylcytidine, C5 bromouridine, C5 fluorouridine, C5 iodouridine, C5 propynyl uridine, C5 propynyl cytidine, C5 methylcytidine, 7 deazaadenosine, 7 deazaguanosine, 8 oxoadenosine, 8 oxoguanosine, O(6) methylguanine, 4-acetylcytidine, 5-(carboxyhydroxymethyl)uridine, dihydrouridine, methylpseudouridine, 1-methyl adenosine, 1-methyl guanosine, N6-methyl adenosine, and 2-thiocytidine), chemically modified bases, biologically modified bases (e.g., methylated bases), intercalated bases, modified sugars (e.g., 2'-fluororibose, ribose, 2'-deoxyribose, 2'-O-methylcytidine, arabinose, and hexose), or modified phosphate groups (e.g., phosphorothioates and 5' N phosphoramidite linkages).

Promoter

[0063] The term “promoter” is art-recognized and refers to a nucleic acid molecule with a sequence recognized by the cellular transcription machinery and able to initiate transcription of a downstream gene. A promoter can be constitutively active, meaning that the promoter is always active in a given cellular context, or conditionally active, meaning that the promoter is only active in the presence of a specific condition. For example, a conditional promoter may only be active in the presence of a specific protein that connects a protein associated with a regulatory element in the promoter to the basic transcriptional machinery, or only in the absence of an inhibitory molecule. A subclass of conditionally active promoters are inducible promoters that require the presence of a small molecule “inducer” for activity. Examples of inducible promoters include, but are not limited to, arabinose-inducible promoters, Tet-on promoters, and tamoxifen-inducible promoters. A variety of constitutive, conditional, and inducible promoters are well known to the skilled artisan, and the skilled artisan will be able to ascertain a variety of such promoters useful in carrying out the instant invention, which is not limited in this respect.

Protospacer adjacent motif (PAM)

[0064] The genome editing system described herein may utilize any Cas9, Cas9 variant or equivalent thereof. Such proteins bind to DNA sites at associated PAM sites, or “protospacer adjacent sequences.” As used herein, the term “protospacer adjacent sequence” or “PAM”

refers to an approximately 2-6 base pair DNA sequence that is an important targeting component of a Cas9 nuclease. Typically, the PAM sequence is on either strand, and is downstream in the 5' to 3' direction of Cas9 cut site. The canonical PAM sequence (i.e., the PAM sequence that is associated with the Cas9 nuclease of *Streptococcus pyogenes* or SpCas9) is 5'-NGG-3' wherein "N" is any nucleobase followed by two guanine ("G") nucleobases. Different PAM sequences can be associated with different Cas9 nucleases or equivalent proteins from different organisms. In addition, any given Cas9 nuclease, e.g., SpCas9, may be modified to alter the PAM specificity of the nuclease such that the nuclease recognizes alternative PAM sequence.

[0065] For example, with reference to the canonical SpCas9 amino acid sequence is SEQ ID NO: 11, the PAM sequence can be modified by introducing one or more mutations, including (a) D1135V, R1335Q, and T1337R "the VQR variant", which alters the PAM specificity to NGAN or NGNG, (b) D1135E, R1335Q, and T1337R "the EQR variant", which alters the PAM specificity to NGAG, and (c) D1135V, G1218R, R1335E, and T1337R "the VRER variant", which alters the PAM specificity to NGCG. In addition, the D1135E variant of canonical SpCas9 still recognizes NGG, but it is more selective compared to the wild type SpCas9 protein.

[0066] It will also be appreciated that Cas9 enzymes from different bacterial species (i.e., Cas9 orthologs) can have varying PAM specificities. For example, Cas9 from *Staphylococcus aureus* (SaCas9) recognizes NGRRT or NGRRN. In addition, Cas9 from *Neisseria meningitis* (NmCas) recognizes NNNNGATT. In another example, Cas9 from *Streptococcus thermophilis* (StCas9) recognizes NNAGAAW. In still another example, Cas9 from *Treponema denticola* (TdCas) recognizes NAAAAC. These examples are not meant to be limiting. It will be further appreciated that non-SpCas9s bind a variety of PAM sequences, which makes them useful when no suitable SpCas9 PAM sequence is present at the desired target cut site. Furthermore, non-SpCas9s may have other characteristics that make them more useful than SpCas9. For example, Cas9 from *Staphylococcus aureus* (SaCas9) is about 1 kilobase smaller than SpCas9, so it can be packaged into adeno-associated virus (AAV). Further reference may be made to Shah et al., "Protospacer recognition motifs: mixed identities and functional diversity," *RNA Biology*, 10(5): 891-899 (which is incorporated herein by reference).

Ribozyme

[0067] The term "ribozyme" or "ribonucleic acid enzyme" describes a class of RNA molecules which have the ability to catalyze specific biochemical reactions, including, but

not limited to, RNA processing reactions (e.g., insertion, deletion, substitution, inversion of nucleotides in RNA), RNA splicing, viral replication, and transfer RNA biosynthesis.

Naturally occurring ribozymes include, but are not limited to, RNase P, ribosomal RNA (rRNA), hammerhead ribozyme, hairpin ribozyme, twister ribozyme, twister sister ribozyme, hatchet ribozyme, pistol ribozyme, GIR1 branching ribozyme, *glmS* ribozyme, and splicing ribozymes (e.g., Group I self-splicing intron and Group II self-splicing intron). The genome editing systems (e.g., complexes comprising napDNAbp, guide RNA, and a ribozyme), pharmaceutical compositions, kits, and methods of editing may utilize naturally occurring ribozymes (modified to act on DNA), variants thereof, or artificial or engineered ribozymes, such as those described herein. Exemplary ribozymes are discussed herein.

RNA-protein recruitment system

[0068] The genome editing system described herein may utilize RNA-protein recruitment systems to co-localize components of the editing system at a target DNA site (e.g., for achieving co-localization of napDNAbp/guide RNA complex with a ribozyme at a target DNA site). An exemplary system is the MS2 tagging technique, described herein.

PACE

[0069] In various embodiment, the polypeptide components of the genome editing system, e.g. the napDNAbp, can be further change through evolutionary processes. The term “phage-assisted continuous evolution (PACE),” as used herein, refers to continuous evolution that employs phage as viral vectors. The general concept of PACE technology has been described, for example, in International PCT Application, PCT/US2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Application, U.S. Patent No. 9,023,594, issued May 5, 2015, International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015, and International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, the entire contents of each of which are incorporated herein by reference.

Protein, peptide, and polypeptide

The terms “protein,” “peptide,” and “polypeptide” are used interchangeably herein, and refer to a polymer of amino acid residues linked together by peptide (amide) bonds. The terms refer to a protein, peptide, or polypeptide of any size, structure, or function. Typically, a protein, peptide, or polypeptide will be at least three amino acids long. A protein, peptide, or polypeptide may refer to an individual protein or a collection of proteins. One or more of the

amino acids in a protein, peptide, or polypeptide may be modified, for example, by the addition of a chemical entity such as a carbohydrate group, a hydroxyl group, a phosphate group, a farnesyl group, an isofarnesyl group, a fatty acid group, a linker for conjugation, functionalization, or other modification, etc. A protein, peptide, or polypeptide may also be a single molecule or may be a multi-molecular complex. A protein, peptide, or polypeptide may be just a fragment of a naturally occurring protein or peptide. A protein, peptide, or polypeptide may be naturally occurring, recombinant, or synthetic, or any combination thereof. Any of the proteins provided herein may be produced by any method known in the art. For example, the proteins provided herein may be produced via recombinant protein expression and purification, which is especially suited for fusion proteins comprising a peptide linker. Methods for recombinant protein expression and purification are well known, and include those described by Green and Sambrook, *Molecular Cloning: A Laboratory Manual* (4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2012)), the entire contents of which are incorporated herein by reference.

Protein splicing

[0004] The term “protein splicing,” as used herein, refers to a process in which a sequence, an intein (or split inteins, as the case may be), is excised from within an amino acid sequence, and the remaining fragments of the amino acid sequence, the exteins, are ligated via an amide bond to form a continuous amino acid sequence. The term “trans” protein splicing refers to the specific case where the inteins are split inteins and they are located on different proteins.

Spacer sequence

[0070] As used herein, the term “spacer sequence” in connection with a guide RNA refers to the portion of the guide RNA of about 20 nucleotides which contains a nucleotide sequence that matches the protospacer sequence in the target DNA sequence, and which anneals to the strand of the target DNA site that is complementary to the protospacer.

Split intein

[0071] Although inteins are most frequently found as a contiguous domain, some exist in a naturally split form. In this case, the two fragments are expressed as separate polypeptides and must associate before splicing takes place, so-called protein trans-splicing. In the context of the instant disclosure, split inteins may be utilized as a strategy to rejoin split portions of a complete protein, which of which are separately expressed and/or delivered to a cell. This can be utilized in the context of delivering smaller fragments of a genome editing system described herein wherein the polypeptide component(s) (e.g., the napDNAbp) is split into two half portions (of the same or different size, depending on the split site) which are

separately delivered to the same cell (e.g., by vector transfection and expressed in cell, or by nucleoprotein complexes for direct transfer of the half proteins into the same cell) and then which are reformed as a complete polypeptide through the process of trans-splicing.

[0072] An exemplary split intein is the *Ssp* DnaE intein, which comprises two subunits, namely, DnaE-N and DnaE-C. The two different subunits are encoded by separate genes, namely *dnaE-n* and *dnaE-c*, which encode the DnaE-N and DnaE-C subunits, respectively. DnaE is a naturally occurring split intein in *Synechocystis sp.* PCC6803 and is capable of directing trans-splicing of two separate proteins, each comprising a fusion with either DnaE-N or DnaE-C.

[0073] Additional naturally occurring or engineered split-intein sequences are known in the or can be made from whole-intein sequences described herein or those available in the art. Examples of split-intein sequences can be found in Stevens et al., “A promiscuous split intein with expanded protein engineering applications,” PNAS, 2017, Vol.114: 8538-8543; Iwai et al., “Highly efficient protein trans-splicing by a naturally split DnaE intein from *Nostoc punctiforme*, FEBS Lett, 580: 1853-1858, each of which are incorporated herein by reference. Additional split intein sequences can be found, for example, in WO 2013/045632, WO 2014/055782, WO 2016/069774, and EP2877490, the contents each of which are incorporated herein by reference.

[0074] In addition, protein splicing in trans has been described *in vivo* and *in vitro* (Shingledecker, et al., *Gene* 207:187 (1998), Southworth, et al., *EMBO J.* 17:918 (1998); Mills, et al., *Proc. Natl. Acad. Sci. USA*, 95:3543-3548 (1998); Lew, et al., *J. Biol. Chem.*, 273:15887-15890 (1998); Wu, et al., *Biochim. Biophys. Acta* 35732:1 (1998b), Yamazaki, et al., *J. Am. Chem. Soc.* 120:5591 (1998), Evans, et al., *J. Biol. Chem.* 275:9091 (2000); Otomo, et al., *Biochemistry* 38:16040-16044 (1999); Otomo, et al., *J. Biomol. NMR* 14:105-114 (1999); Scott, et al., *Proc. Natl. Acad. Sci. USA* 96:13638-13643 (1999)) and provides the opportunity to express a protein as to two inactive fragments that subsequently undergo ligation to form a functional product.

Subject

[0075] The term “subject,” as used herein, refers to an individual organism, for example, an individual mammal. In some embodiments, the subject is a human. In some embodiments, the subject is a non-human mammal. In some embodiments, the subject is a non-human primate. In some embodiments, the subject is a rodent. In some embodiments, the subject is a sheep, a goat, a cattle, a cat, or a dog. In some embodiments, the subject is a vertebrate, an amphibian, a reptile, a fish, an insect, a fly, or a nematode. In some embodiments, the subject

is a research animal. In some embodiments, the subject is genetically engineered, e.g., a genetically engineered non-human subject. The subject may be of either sex and at any stage of development.

Target site

[0076] The term “target site” refers to a sequence within a nucleic acid molecule that is edited by an editor composition disclosed herein. For example, a target site can refer to the nucleotide position at which the engineered ribozymes described herein may install an insertion or deletion.

Targeting moiety

[0077] The term “targeting moiety” refers to a structural element which binds to a targeting moiety receptor. For example, a ribozyme of the present disclosure may include one or more targeting moieties to facilitate the localization of the ribozyme to a target site bound by a napDNAbp (e.g., Cas9), wherein the napDNAbp comprises a targeting moiety receptor which interacts with and binds the targeting moiety. For example, a targeting moiety can include an MS2 hairpin structure integrated into the ribozyme. The MS2 hairpin structure binds to a bacteriophage coat protein, which can be fused or otherwise attached to the napDNAbp (e.g., Cas9).

Targeting moiety receptor

[0078] The term “targeting moiety receptor” refers to the structural feature that binds to a targeting moiety. In certain embodiments, the targeting moiety receptor can be fused or otherwise attached to the napDNAbp such that the ribozyme becomes localized to the the napDNAbp once bound to a target site. For example, a targeting moiety can include an MS2 hairpin structure integrated into the ribozyme. The MS2 hairpin structure binds to a bacteriophage coat protein, which can be fused or otherwise attached to the napDNAbp (e.g., Cas9).

Transitions

[0005] As used herein, “transitions” refer to the interchange of purine nucleobases ($A \leftrightarrow G$) or the interchange of pyrimidine nucleobases ($C \leftrightarrow T$). This class of interchanges involves nucleobases of similar shape. The compositions and methods disclosed herein are capable of inducing one or more transitions in a target DNA molecule. The compositions and methods disclosed herein are also capable of inducing both transitions and transversion in the same target DNA molecule. These changes involve $A \leftrightarrow G$, $G \leftrightarrow A$, $C \leftrightarrow T$, or $T \leftrightarrow C$. In the context of a double-strand DNA with Watson-Crick paired nucleobases, transversions refer to the following base pair exchanges: $A:T \leftrightarrow G:C$, $G:C \leftrightarrow A:T$, $C:G \leftrightarrow T:A$, or $T:A \leftrightarrow C:G$.

The compositions and methods disclosed herein are capable of inducing one or more transitions in a target DNA molecule. The compositions and methods disclosed herein are also capable of inducing both transitions and transversion in the same target DNA molecule, as well as other nucleotide changes, including deletions and insertions.

Transversions

[0079] As used herein, “transversions” refer to the interchange of purine nucleobases for pyrimidine nucleobases, or in the reverse and thus, involve the interchange of nucleobases with dissimilar shape. These changes involve $T \leftrightarrow A$, $T \leftrightarrow G$, $C \leftrightarrow G$, $C \leftrightarrow A$, $A \leftrightarrow T$, $A \leftrightarrow C$, $G \leftrightarrow C$, and $G \leftrightarrow T$. In the context of a double-strand DNA with Watson-Crick paired nucleobases, transversions refer to the following base pair exchanges: $T:A \leftrightarrow A:T$, $T:A \leftrightarrow G:C$, $C:G \leftrightarrow G:C$, $C:G \leftrightarrow A:T$, $A:T \leftrightarrow T:A$, $A:T \leftrightarrow C:G$, $G:C \leftrightarrow C:G$, and $G:C \leftrightarrow T:A$. The compositions and methods disclosed herein are capable of inducing one or more transversions in a target DNA molecule. The compositions and methods disclosed herein are also capable of inducing both transitions and transversion in the same target DNA molecule, as well as other nucleotide changes, including deletions and insertions.

Treatment

[0080] The terms “treatment,” “treat,” and “treating,” refer to a clinical intervention aimed to reverse, alleviate, delay the onset of, or inhibit the progress of a disease or disorder, or one or more symptoms thereof, as described herein. As used herein, the terms “treatment,” “treat,” and “treating” refer to a clinical intervention aimed to reverse, alleviate, delay the onset of, or inhibit the progress of a disease or disorder, or one or more symptoms thereof, as described herein. In some embodiments, treatment may be administered after one or more symptoms have developed and/or after a disease has been diagnosed. In other embodiments, treatment may be administered in the absence of symptoms, *e.g.*, to prevent or delay onset of a symptom or inhibit onset or progression of a disease. For example, treatment may be administered to a susceptible individual prior to the onset of symptoms (*e.g.*, in light of a history of symptoms and/or in light of genetic or other susceptibility factors). Treatment may also be continued after symptoms have resolved, for example, to prevent or delay their recurrence.

Ribozyme-mediated programmable editing system

[0081] As used herein, the term “ribozyme-mediated programmable editing system” or “ribozyme-mediated programmable editor” refers to a novel approach (and the compositions achieving said novel approach) for gene editing that is mediated by both an engineered ribozyme and one or more napDNAbs to carry out the direct installment of insertions or

deletions at a desired genome target site. In general, the napDNAbp component is programmed with a guide RNA to bind the napDNAbp to a target site for editing. The napDNAbp (e.g., Cas9) then forms an R-loop structure comprising the nucleotide site to be modified (e.g., the point of insertion or deletion by the ribozyme), and the engineered ribozyme then binds to the single-strand DNA region and installs the desired insertion or deletion. Following DNA repair and/or replication processes that occur naturally in the cell, the insertion or deletion becomes permanently installed at the target site. In embodiments, this insertion or deletion of a single nucleotide can correct a frameshift mutation.

Variant

[0082] As used herein the term “variant” should be taken to mean the exhibition of qualities that have a pattern that deviates from what occurs in nature, e.g., a variant Cas9 is a Cas9 comprising one or more changes in amino acid residues as compared to a wild type Cas9 amino acid sequence. The term “variant” encompasses homologous proteins having at least 75%, or at least 80%, or at least 85%, or at least 90%, or at least 95%, or at least 99% percent identity with a reference sequence and having the same or substantially the same functional activity or activities as the reference sequence. The term also encompasses mutants, truncations, or domains of a reference sequence, and which display the same or substantially the same functional activity or activities as the reference sequence.

Vector

[0083] The term “vector,” as used herein, refers to a nucleic acid that can be modified to encode a gene of interest and that is able to enter into a host cell, mutate and replicate within the host cell, and then transfer a replicated form of the vector into another host cell. Exemplary suitable vectors include viral vectors, such as retroviral vectors or bacteriophages and filamentous phage, and conjugative plasmids. Additional suitable vectors will be apparent to those of skill in the art based on the instant disclosure.

Wild Type

[0084] As used herein the term “wild type” is a term of the art understood by skilled persons and means the typical form of an organism, strain, gene or characteristic as it occurs in nature as distinguished from mutant or variant forms.

DETAILED DESCRIPTION OF CERTAIN EMBODIMENTS

[0085] Small genomic insertions or deletions are known to cause a wide variety of genetic diseases. Current methods to repair these mutations are inefficient, generally restricted to mitotic cells, and prone to result in the stochastic insertion or deletion of random nucleotides

(indels). No published method directly enables the insertion or deletion of a given nucleotide at a specified genetic locus. The development of such a technology would advance genome editing therapeutics by enabling the direct correction of frameshift mutations.

[0086] Base editing is a form of genome editing that enables the directed, targeted installation of certain classes of point mutations with greatly improved efficiency and reduced indel formation relative to other methods. This approach has been made possible by tethering base-modifying enzymes to RNA-guided endonucleases such as Cas9, targeting them to specific genetic loci.

[0087] The present specification relates to a genome editing system that is distinct from base editing in that it relies on the activity of ribozymes. The genome editing system provided herein is capable of directly installing an insertion or deletion of a given nucleotide at a specified genetic locus using a ribozyme in combination with a complex comprising a napDNAbp and a guide RNA.

[0088] The compositions and methods involve the novel combination of the use an engineered RNA enzyme (i.e., “ribozyme”) that is capable of site-specifically inserting or deleting a single nucleotide at a genetic locus and the use of a nucleic acid programmable DNA binding protein (napDNAbp) (e.g., Cas9) to target the engineered ribozyme to a specified genetic locus, thereby allowing for the direct installation of an insertion or deletion at the specified genetic locus by the engineered ribozyme.

[0089] In one embodiment of the present disclosure, as shown in the Figures and described in the Brief Description of the Figures, an RNA enzyme, or ribozyme, was engineered to site-specifically insert a single nucleotide at a genetic locus targeted by Cas9. A previously evolved version of the group I self-splicing intron was modified to site-specifically insert and subsequently ligate into place a single guanosine nucleotide into single-stranded DNA. Subsequently, the ability of this ribozyme to act on double-stranded DNA that was bound by a Cas9:guide RNA complex in vitro was demonstrated before its ability to function in human cells was examined. It was found that localizing the ribozyme to the same genetic locus as Cas9 enabled it to modify its genomic target.

[1] napDNAbp

[0090] The genome editing system described herein comprises a nucleic acid programmable DNA binding protein (napDNAbp), which becomes targeted to a DNA edit site by complexing with a guide RNA. In certain embodiments, the napDNAbp may modified to recruit a ribozyme to the DNA edit site. For example, an RNA-protein recruitment system may be used (e.g., an MS2 tagging system) wherein the napDNAbp is expressed as a fusion

with an MCP, and the ribozyme is cotranscribed with an MS2 hairpin structure, such that the ribozyme binds to the napDNAbp through the recruiting action of the MCP / MS2 hairpin interaction. In other embodiments, the napDNAbp can be further modified with additional functional domains, such as an NLS.

[0091] In one embodiment, the ribozyme can be the engineered ribozyme of FIG. 1A. FIG. 1A shows the sequence and secondary structure of (a) an exemplary engineered ribozyme based on the ribozyme of *Tetrahymena* group I intron with mutations identified in directed evolution that enable the ribozyme to bind and cleave ssDNA (blue and/or indicated with a “star”) and insertions and deletions that enable nucleotide (e.g., GTP) insertion (red boxes). For example, element (b) refers to the deletion of the terminal nucleotides (e.g., the terminal 4 nucleotides) of the ribozyme, which inactivates the self-insertion activity of the ribozyme for self-insertion into the DNA target or substrate with which the ribozyme is interacting. This is also shown in more details in FIG. 3B. Element (c) shows engineered changes in the active site which interacts with the substrate DNA, catalyzing the insertion of the nucleotide at the target site of the target DNA substrate. Element (d) refers to the location or site of insertion of an MS2 hairpin (AUCUU sequence is removed and replaced with the MS2 hairpin), which functions as a targeting moiety to localize the engineered ribozyme to a bound napDNAbp/guide RNA complex to a target DNA site, wherein the napDNAbp is modified to incorporate a cognate targeting moiety receptor. The nucleotide sequence of the ribozyme of FIG. 1A, as shown, is SEQ ID NO: 88.

[0092] A great variety of napDNAbp are known in the art at the time of this filing and all are contemplated for use in the genome editing system described herein. The napDNAbps can be associated with or complexed with at least one guide nucleic acid (e.g., guide RNA), which localizes the napDNAbp to a DNA sequence that comprises a DNA strand (i.e., a target strand) that is complementary to the guide nucleic acid, or a portion thereof (e.g., the spacer of a guide RNA which anneals to a complementary strand of the DNA target). In other words, the guide nucleic-acid “programs” the napDNAbp (e.g., Cas9 or equivalent) to localize and bind to the target DNA edit site.

[0093] Any suitable napDNAbp may be used in the genome editing system described herein. In various embodiments, the napDNAbp may be any Class 2 CRISPR-Cas system, including any type II, type V, or type VI CRISPR-Cas enzyme. Given the rapid development of CRISPR-Cas as a tool for genome editing, there have been constant developments in the nomenclature used to describe and/or identify CRISPR-Cas enzymes, such as Cas9 and Cas9 orthologs. This application references CRISPR-Cas enzymes with nomenclature that may be

old and/or new. The skilled person will be able to identify the specific CRISPR-Cas enzyme being referenced in this Application based on the nomenclature that is used, whether it is old (i.e., “legacy”) or new nomenclature. CRISPR-Cas nomenclature is extensively discussed in Makarova et al., “Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?,” *The CRISPR Journal*, Vol. 1. No. 5, 2018, the entire contents of which are incorporated herein by reference. The particular CRISPR-Cas nomenclature used in any given instance in this Application is not limiting in any way and the skilled person will be able to identify which CRISPR-Cas enzyme is being referenced.

[0094] For example, the following type II, type V, and type VI Class 2 CRISPR-Cas enzymes have the following art-recognized old (i.e., legacy) and new names. Each of these enzymes, and/or variants thereof, may be used with the genome editing system described herein:

Legacy nomenclature	Current nomenclature*
<i>type II CRISPR-Cas enzymes</i>	
Cas9	same
<i>type V CRISPR-Cas enzymes</i>	
Cpf1	Cas12a
CasX	Cas12e
C2c1	Cas12b1
Cas12b2	same
C2c3	Cas12c
CasY	Cas12d
C2c4	same
C2c8	same
C2c5	same
C2c10	same
C2c9	same
<i>type VI CRISPR-Cas enzymes</i>	
C2c2	Cas13a
Cas13d	same
C2c7	Cas13c
C2c6	Cas13b

* See Makarova et al., *The CRISPR Journal*, Vol. 1, No. 5, 2018

[0095] Without being bound by theory, the mechanism of action of certain napDNAbp contemplated herein includes the step of forming an R-loop whereby the napDNAbp induces the unwinding of a double-strand DNA target, thereby separating the strands in the region bound by the napDNAbp. The guide RNA spacer then hybridizes to the “target strand”, which is the complement of the protospacer sequence. This displaces a “non-target strand” that is complementary to the target strand, which forms the single strand region of the R-loop. In some embodiments, the napDNAbp includes one or more nuclease activities, which then

cut the DNA leaving various types of lesions. For example, the napDNABp may comprises a nuclease activity that cuts the non-target strand at a first location, and/ or cuts the target strand at a second location. Depending on the nuclease activity, the target DNA can be cut to form a “double-stranded break” whereby both strands are cut. In other embodiments, the target DNA can be cut at only a single site, i.e., the DNA is “nicked” on one strand. Exemplary napDNABp with different nuclease activities include “Cas9 nickase” (“nCas9”) and a deactivated Cas9 having no nuclease activities (“dead Cas9” or “dCas9”).

[0096] The below description of various napDNABps which can be used in connection with the presently disclose genome editing system is not meant to be limiting in any way. The genome editing system may comprise the canonical SpCas9, or any ortholog Cas9 protein, or any variant Cas9 protein—including any naturally occurring variant, mutant, or otherwise engineered version of Cas9—that is known or which can be made or evolved through a directed evolutionary or otherwise mutagenic process. In various embodiments, the Cas9 or Cas9 variants have a nickase activity, i.e., only cleave of strand of the target DNA sequence. In other embodiments, the Cas9 or Cas9 variants have inactive nucleases, i.e., are “dead” Cas9 proteins. Other variant Cas9 proteins that may be used are those having a smaller molecular weight than the canonical SpCas9 (e.g., for easier delivery) or having modified or rearranged primary amino acid structure (e.g., the circular permutant formats).

[0097] The genome editing system described herein may also comprise Cas9 equivalents, including Cas12a (Cpf1) and Cas12b1 proteins which are the result of convergent evolution. The napDNABps used herein (e.g., SpCas9, Cas9 variant, or Cas9 equivalents) may also may also contain various modifications that alter/enhance their PAM specificities. Lastly, the application contemplates any Cas9, Cas9 variant, or Cas9 equivalent which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% sequence identity to a reference Cas9 sequence, such as a references SpCas9 canonical sequence or a reference Cas9 equivalent (e.g., Cas12a (Cpf1)).

[0098] The napDNABp can be a CRISPR (clustered regularly interspaced short palindromic repeat)-associated nuclease. As outlined above, CRISPR is an adaptive immune system that provides protection against mobile genetic elements (viruses, transposable elements and conjugative plasmids). CRISPR clusters contain spacers, sequences complementary to antecedent mobile elements, and target invading nucleic acids. CRISPR clusters are transcribed and processed into CRISPR RNA (crRNA). In type II CRISPR systems correct processing of pre-crRNA requires a trans-encoded small RNA (tracrRNA), endogenous

ribonuclease 3 (*rnc*) and a Cas9 protein. The *tracrRNA* serves as a guide for ribonuclease 3-aided processing of pre-crRNA. Subsequently, Cas9/crRNA/*tracrRNA* endonucleolytically cleaves linear or circular dsDNA target complementary to the spacer. The target strand not complementary to crRNA is first cut endonucleolytically, then trimmed 3'-5' exonucleolytically. In nature, DNA-binding and cleavage typically requires protein and both RNAs. However, single guide RNAs ("sgRNA", or simply "gRNA") can be engineered so as to incorporate aspects of both the crRNA and *tracrRNA* into a single RNA species. See, e.g., Jinek M. et al., *Science* 337:816-821(2012), the entire contents of which is hereby incorporated by reference.

[0099] In some embodiments, the napDNAbp directs cleavage of one or both strands at the location of a target sequence, such as within the target sequence and/or within the complement of the target sequence. In some embodiments, the napDNAbp directs cleavage of one or both strands within about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 50, 100, 200, 500, or more base pairs from the first or last nucleotide of a target sequence. In some embodiments, a vector encodes a napDNAbp that is mutated to with respect to a corresponding wild-type enzyme such that the mutated napDNAbp lacks the ability to cleave one or both strands of a target polynucleotide containing a target sequence. For example, an aspartate-to-alanine substitution (D10A) in the RuvC I catalytic domain of Cas9 from *S. pyogenes* converts Cas9 from a nuclease that cleaves both strands to a nickase (cleaves a single strand). Other examples of mutations that render Cas9 a nickase include, without limitation, H840A, N854A, and N863A in reference to the canonical SpCas9 sequence, or to equivalent amino acid positions in other Cas9 variants or Cas9 equivalents.

[0100] As used herein, the term "Cas protein" refers to a full-length Cas protein obtained from nature, a recombinant Cas protein having a sequences that differs from a naturally occurring Cas protein, or any fragment of a Cas protein that nevertheless retains all or a significant amount of the requisite basic functions needed for the disclosed methods, i.e., (i) possession of nucleic-acid programmable binding of the Cas protein to a target DNA, and (ii) ability to nick the target DNA sequence on one strand. The Cas proteins contemplated herein embrace CRISPR Cas 9 proteins, as well as Cas9 equivalents, variants (e.g., Cas9 nickase (nC9) or nuclease inactive Cas9 (dCas9)) homologs, orthologs, or paralogs, whether naturally occurring or non-naturally occurring (e.g., engineered or recombinant), and may include a Cas9 equivalent from any Class 2 CRISPR system (e.g., type II, V, VI), including Cas12a (Cpf1), Cas12e (CasX), Cas12b1 (C2c1), Cas12b2, Cas12c (C2c3), C2c4, C2c8, C2c5, C2c10, C2c9 Cas13a (C2c2), Cas13d, Cas13c (C2c7), Cas13b (C2c6), and

Cas13b. Further Cas-equivalents are described in Makarova et al., “C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector,” *Science* 2016; 353(6299) and Makarova et al., “Classification and Nomenclature of CRISPR-Cas Systems: Where from Here?,” *The CRISPR Journal*, Vol. 1. No. 5, 2018, the contents of which are incorporated herein by reference.

[0101] The terms “Cas9” or “Cas9 nuclease” or “Cas9 moiety” or “Cas9 domain” embrace any naturally occurring Cas9 from any organism, any naturally-occurring Cas9 equivalent or functional fragment thereof, any Cas9 homolog, ortholog, or paralog from any organism, and any mutant or variant of a Cas9, naturally-occurring or engineered. The term Cas9 is not meant to be particularly limiting and may be referred to as a “Cas9 or equivalent.”

Exemplary Cas9 proteins are further described herein and/or are described in the art and are incorporated herein by reference. The present disclosure is unlimited with regard to the particular Cas9 that is employed in the genome editing system described herein.

[0102] As noted herein, Cas9 nuclease sequences and structures are well known to those of skill in the art (see, e.g., “Complete genome sequence of an M1 strain of *Streptococcus pyogenes*.” Ferretti et al., J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E., *Proc. Natl. Acad. Sci. U.S.A.* 98:4658-4663(2001); “CRISPR RNA maturation by trans-encoded small RNA and host factor RNase III.” Deltcheva E., Chylinski K., Sharma C.M., Gonzales K., Chao Y., Pirzada Z.A., Eckert M.R., Vogel J., Charpentier E., *Nature* 471:602-607(2011); and “A programmable dual-RNA-guided DNA endonuclease in adaptive bacterial immunity.” Jinek M., Chylinski K., Fonfara I., Hauer M., Doudna J.A., Charpentier E. *Science* 337:816-821(2012), the entire contents of each of which are incorporated herein by reference).

[0103] Examples of Cas9 and Cas9 equivalents are provided as follows; however, these specific examples are not meant to be limiting. The genome editing system of the present disclosure may use any suitable napDNAbp, including any suitable Cas9 or Cas9 equivalent. The following are exemplary napDNAbp that may be used.

A. Wild type canonical SpCas9

[0104] In one embodiment, the genome editing system described herein may comprise the “canonical SpCas9” nuclease from *S. pyogenes*, which has been widely used as a tool for genome engineering and is categorized as the type II subgroup of enzymes of the Class 2 CRISPR-Cas systems. This Cas9 protein is a large, multi-domain protein containing two

distinct nuclease domains. Point mutations can be introduced into Cas9 to abolish one or both nuclease activities, resulting in a nickase Cas9 (nCas9) or dead Cas9 (dCas9), respectively, that still retains its ability to bind DNA in a sgRNA-programmed manner. In principle, when fused to another protein or domain, Cas9 or variant thereof (e.g., nCas9) can target that protein to virtually any DNA sequence simply by co-expression with an appropriate sgRNA. As used herein, the canonical SpCas9 protein refers to the wild type protein from *Streptococcus pyogenes* having the following amino acid sequence:

Description	Sequence	SEQ ID NO:
SpCas9 <i>Streptococcus pyogenes</i> M1 SwissProt Accession No. Q99ZW2 Wild type	MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGN TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRR KNRICYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKH ERHPIFGNIVDEVAYHEKYPTIYHLRKKLV DSTDKADL RLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQ TYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQL PGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDI LRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQ PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEK MDGTEELLVKNREDLLRKQRTFDNGSIPHQIHLGELH AILRRQEDFYFPLKDNREKIEKILTRIPYYVGPLARGN SRFAWMTRKSEETITPWNFEVVDKGASQSFIERMTN FDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKI ECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEE NEDILEDIVLTTLTFEDREMIEERLKTYAHLFDDKVMK QLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDG FANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIA NLAGSPAIIKKGILQTVKVVDLVKVMGRHKPENIVIE ARENQTTQKGQKNSRERMKRIEELGSGILKEHPV ENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYD VDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEV VKMKKNYWRQLLNAKLITQRKFDNLTKAERGGLSEL DKAGFIKQRLVETRQITKHVAQILDSRMNTKYDENDK LIREVKVITLKSCLVSDFRKDFQFYKVREINNYHHAHD AYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVVRKMIA KSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLI ETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT VAYSVLVVAKEKGKSKKLKSVKELLGITIMERSSSF NPIDFLEAKGYKEVKKDLIIKLPKYSLENGRKRML ASAGELQKGNELALPSKYVNFLYLASHYEKLKGPED NEQKQLFVEQHKHYLDEIEQISEFSKRVLADANLDKV LSAYNKHRRDKPIREQAENIIHLFTLTNLGAPAAFKYFDT TIDRKRYTSTKEVLDTLHQSITGLYETRIDLSQLGGD	SEQ ID NO: 11
SpCas9	ATGGATAAAAAATATAGCATTGGCCTGGATATTGGC ACCAACAGCGTGGGCTGGGCGGTGATTACCGATGAA	SEQ ID NO: 12

Reverse translation of SwissProt Accession No. Q99ZW2 <i>Streptococcus pyogenes</i>	TATAAAGTGCCGAGCAAAAAATTTAAAGTGCTGGGC AACACCGATCGCCATAGCATTAAAAAAACCTGATT GGCGCGCTGCTGTTTGATAGCGGCGAAACCGCGGAA GCGACCCGCCTGAAACGCACCGCGCGCCGCCGCTAT ACCCGCCGCAAAAACCGCATTTGCTATCTGCAGGAA ATTTTATAGCAACGAAATGGCGAAAGTGGATGATAGC TTTTTTCATCGCCTGGAAGAAAGCTTTCTGGTGGAAAG AAGATAAAAAACATGAACGCCATCCGATTTTTGGCA ACATTGTGGATGAAGTGGCGTATCATGAAAAATATC CGACCATTTATCATCTGCGCAAAAAACTGGTGGATA GCACCGATAAAGCGGATCTGCGCCTGATTTATCTGG CGCTGGCGCATATGATTAAATTCGCGGCCATTTTCT GATTGAAGGCGATCTGAACCCGGATAACAGCGATGT GGATAAACTGTTTATTCAGCTGGTGCAGACCTATAA CCAGCTGTTTGAAGAAAACCCGATTAACGCGAGCGG CGTGGATGCGAAAGCGATTCTGAGCGCGCGCCTGAG CAAAAGCCGCCGCTGGAAAACCTGATTGCGCAGCT GCCGGGCGAAAAAAAACGGCCTGTTTGGCAACCT GATTGCGCTGAGCCTGGGCCTGACCCCGAACTTTAA AAGCAACTTTGATCTGGCGGAAGATGCGAAACTGCA GCTGAGCAAAGATACCTATGATGATGATCTGGATAA CCTGCTGGCGCAGATTGGCGATCAGTATGCGGATCT GTTTCTGGCGGCGAAAAACCTGAGCGATGCGATTCT GCTGAGCGATATTCTGCGCGTGAACACCGAAATTAC CAAAGCGCCGCTGAGCGCGAGCATGATTAAACGCTA TGATGAACATCATCAGGATCTGACCCTGCTGAAAGC GCTGGTGCGCCAGCAGCTGCCGGAAAAATATAAG AAATTTTTTTTGATCAGAGCAAAAACGGCTATGCGG GCTATATTGATGGCGGCGCGAGCCAGGAAGAATTTT ATAAATTTATTAACCGATTCTGGAAAAAATGGATG GCACCGAAGAACTGCTGGTGAAACTGAACCGCGAA GATCTGCTGCGCAACAGCGCACCTTTGATAACGGC AGCATTCCGCATCAGATTCATCTGGGCGAACTGCAT GCGATTCTGCGCCGCCAGGAAGATTTTTATCCGTTTC TGAAAGATAACCGCGCAAAAAATTGAAAAAATTCTG ACCTTTCGCATTCCGTATTATGTGGGCCCGCTGGCGC GCGGCAACAGCCGCTTTGCGTGGATGACCCGCAAAA GCGAAGAAACCATTACCCCGTGGAACCTTTGAAGAAG TGGTGGATAAAGGCGCGAGCGCGCAGAGCTTTATTG AACGCATGACCAACTTTGATAAAAACCTGCCGAACG AAAAAGTGCTGCCGAAACATAGCCTGCTGTATGAAT ATTTTACCGTGTATAACGAACCTGACCAAAGTGAAAT ATGTGACCGAAGGCATGCGCAAACCGGCGTTTCTGA GCGGCGAACAGAAAAAAGCGATTGTGGATCTGCTGT TTAAACCAACCGCAAAAGTGACCGTGAAACAGCTGA AAGAAGATTATTTTAAAAAAATTGAATGCTTTGATA GCGTGGAAATTAGCGGCGTGGAAGATCGCTTTAACG CGAGCCTGGGCACCTATCATGATCTGCTGAAAATTA TTAAAGATAAAGATTTTCTGGATAACGAAGAAAACG AAGATATTCTGGAAGATATTGTGCTGACCCTGACCC	
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TGTTTGAAGATCGCGAAATGATTGAAGAACGCCTGA
 AAACCTATGCGCATCTGTTTGATGATAAAGTGATGA
 AACAGCTGAAACGCCGCCGCTATACCGGCTGGGGCC
 GCCTGAGCCGCAAACCTGATTAACGGCATTTCGCGATA
 AACAGAGCGGCAAAACCATTTCTGGATTTTCTGAAAA
 GCGATGGCTTTGCGAACCGCAACTTTATGCAGCTGA
 TTCATGATGATAGCCTGACCTTTAAAGAAGATATTC
 AGAAAGCGCAGGTGAGCGGCCAGGGCGATAGCCTG
 CATGAACATATTGCGAACCTGGCGGGCAGCCCGGCG
 ATTAAAAAAGGCATTCTGCAGACCGTGAAAGTGGTG
 GATGAACTGGTGAAAGTGATGGGCGGCCATAAACCG
 GAAAACATTGTGATTGAAATGGCGCGCGAAAAACCA
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 GCATGAAACGCATTGAAGAAGGCATTAAAGAAGCTG
 GGCAGCCAGATTCTGAAAGAACATCCGGTGGA
 CACCCAGCTGCAGAACGAAAAACTGTATCTGTATTA
 TCTGCAGAACGGCCGCGATATGTATGTGGATCAGGA
 ACTGGATATTAACCGCCTGAGCGATTATGATGTGGA
 TCATATTGTGCCGCGAGAGCTTTCTGAAAGATGATAG
 CATTGATAACAAAGTGCTGACCCGCGAGCGATAAAAA
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 CTGGATAGCCGCATGAACACCAAATATGATGAAAAC
 GATAAACTGATTTCGCGAAGTGAAAGTGATTACCCTG
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 AAGGCTATAAAGAAGTGAAAAAAGATCTGATTATTA
 AACTGCCGAAATATAGCCTGTTTGAAGTGGAAAACG
 GCCGCAAACGCATGCTGGCGAGCGCGGGCGAACTG

	CAGAAAGGCAACGAACTGGCGCTGCCGAGCAAATA TGTGAACTTTCTGTATCTGGCGAGCCATTATGAAAA ACTGAAAGGCAGCCCGGAAGATAACGAACAGAAAC AGCTGTTTGTGGAACAGCATAAACATTATCTGGATG AAATTATTGAACAGATTAGCGAATTTAGCAAACGCG TGATTCTGGCGGATGCGAACCTGGATAAAGTGCTGA GCGCGTATAACAAACATCGCGATAAACCGATTTCGCG AACAGGCGGAAAACATTATTCATCTGTTTACCCTGA CCAACCTGGGCGCGCCGGCGGCGTTTAAATATTTTG ATACCACCATTGATCGCAAACGCTATAACCAGCACCA AAGAAGTGCTGGATGCGACCCTGATTCATCAGAGCA TTACCGGCCTGTATGAAACCCGCATTGATCTGAGCC AGCTGGGCGGCGAT	
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[0105] The genome editing system described herein may include canonical SpCas9, or any variant thereof having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity with a wild type Cas9 sequence provided above. These variants may include SpCas9 variants containing one or more mutations, including any known mutation reported with the SwissProt Accession No. Q99ZW2 (SEQ ID NO: 11 entry, which include:

SpCas9 mutation (relative to the amino acid sequence of the canonical SpCas9 sequence, SEQ ID NO: 11)	Function/Characteristic (as reported) (see UniProtKB – Q99ZW2 (CAS9_STRPT1) entry – incorporated herein by reference)
D10A	Nickase mutant which cleaves the protospacer strand (but no cleavage of non-protospacer strand)
S15A	Decreased DNA cleavage activity
R66A	Decreased DNA cleavage activity
R70A	No DNA cleavage
R74A	Decreased DNA cleavage
R78A	Decreased DNA cleavage
97-150 deletion	No nuclease activity
R165A	Decreased DNA cleavage
175-307 deletion	About 50% decreased DNA cleavage
312-409 deletion	No nuclease activity
E762A	Nickase
H840A	Nickase mutant which cleaves the non-protospacer strand but does not cleave the protospacer strand
N854A	Nickase
N863A	Nickase
H982A	Decreased DNA cleavage
D986A	Nickase
1099-1368 deletion	No nuclease activity
R1333A	Reduced DNA binding

1. Other wild type SpCas9 sequences that may be used in the present disclosure, include:

Description	Sequence	SEQ ID NO:
SpCas9 <i>Streptococcus pyogenes</i>	ATGGATAAGAAATACTCAATAGGCTTAGATATCGGCA CAAATAGCGTCGGATGGGCGGTGATCACTGATGATTA TAAGGTTCCGTCTAAAAAGTTCAAGGTTCTGGGAAAT	SEQ ID NO: 13

MGAS1882 wild type NC_017053.1	ACAGACCGCCACAGTATCAAAAAAAAAATCTTATAGGGG CTCTTTTATTTGGCAGTGGAGAGACAGCGGAAGCGAC TCGTCTCAAACGGACAGCTCGTAGAAGGTATACACGT CGGAAGAATCGTATTTGTTATCTACAGGAGATTTTTTC AAATGAGATGGCGAAAGTAGATGATAGTTTCTTTCATC GACTTGAAGAGTCTTTTTTTGGTGGAAGAAGACAAGAA GCATGAACGTCATCCTATTTTTTGGAAATATAGTAGATG AAGTTGCTTATCATGAGAAATATCCAACATCTATCAT CTGCGAAAAAAATTGGCAGATTCTACTGATAAAGCGG ATTTGCGCTTAATCTATTTGGCCTTAGCGCATATGATT AAGTTTCGTGGTCATTTTTTTGATTGAGGGAGATTTAAA TCCTGATAATAGTGATGTGGACAAACTATTTATCCAGT TGGTACAAATCTACAATCAATTATTTGAAGAAAACCT ATTAACGCAAGTAGAGTAGATGCTAAAGCGATTCTTTC TGCACGATTGAGTAAATCAAGACGATTAGAAAATCTC ATTGCTCAGCTCCCCGGTGAGAAGAGAAATGGCTTGTT TGGGAATCTCATTGCTTTGTCATTGGGATTGACCCCTA ATTTTAAATCAAATTTTGATTTGGCAGAAGATGCTAAA TTACAGCTTTCAAAGATACTTACGATGATGATTTAGA TAATTTATTGGCGCAAATTGGAGATCAATATGCTGATT TGTTTTTGGCAGCTAAGAATTTATCAGATGCTATTTTA CTTTCAGATATCCTAAGAGTAAATAGTGAAATAACTA AGGCTCCCCTATCAGCTTCAATGATTAAGCGCTACGAT GAACATCATCAAGACTTGACTCTTTTAAAAGCTTTAGT TCGACAACAACCTCCAGAAAAGTATAAAGAAATCTTT TTTGATCAATCAAAAAACGGATATGCAGGTTATATTGA TGGGGGAGCTAGCCAAGAAGAATTTTATAAATTTATC AAACCAATTTTAGAAAAAATGGATGGTACTGAGGAAT TATTGGTGAAACTAAATCGTGAAGATTTGCTGCGCAA GCAACGGACCTTTGACAACGGCTCTATTCCCATCAAA TTCACCTGGGTGAGCTGCATGCTATTTTGAGAAGACAA GAAGACTTTTATCCATTTTAAAAGACAATCGTGAGAA GATTGAAAAAATCTTGACTTTTCGAATTCCTTATTATG TTGGTCCATTGGCGCGTGGCAATAGTCGTTTTGCATGG ATGACTCGGAAGTCTGAAGAAACAATTACCCCATGGA ATTTTGAAGAAGTTGTCGATAAAGGTGCTTCAGCTCAA TCATTTATTGAACGCATGACAACTTTGATAAAAAATCT TCCAAATGAAAAAGTACTACCAAAACATAGTTTGCTTT ATGAGTATTTTACGGTTTATAACGAATTGACAAAGGTC AAATATGTTACTGAGGGAATGCGAAAACCAGCATTTC TTTCAGGTGAACAGAAGAAAGCCATTGTTGATTTACTC TTCAAAACAAATCGAAAAGTAACCGTTAAGCAATTAA AAGAAGATTATTTCAAAAAAATAGAATGTTTTGATAG TGTTGAAATTTAGGAGTTGAAGATAGATTTAATGCTT CATTAGGCGCCTACCATGATTTGCTAAAAATTATTTAA GATAAAGATTTTTTGGATAATGAAGAAAATGAAGATA TCTTAGAGGATATTGTTTTAACATTGACCTTATTTGAA GATAGGGGGATGATTGAGGAAAGACTTAAAACATATG CTCACCTCTTTGATGATAAGGTGATGAAACAGCTTAAA CGTCGCCGTTATACTGGTTGGGGACGTTTGTCTCGAAA
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 CAAAAAATATGGTGGTTTTGATAGTCCAACGGTAGC
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SpCas9 <i>Streptococcus</i> <i>pyogenes</i> MGAS1882 wild type NC_017053.1	MDKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNT DRHSIKKNLIGALLFGSGETAEATRLKRTARRRYTRRKN RICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHERHP IFGNIVDEVAYHEKYPTIYHLRKKLADSTDKADLRLIYLA LAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQIYNQLFE ENPINASRVDAKAILSARLSKSRRLENLIAQLPGEKRNG FGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDITYDDDL NLLAQIGDQYADLFLAAKNLSDAILSDILRVNSEITKAP LSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQS KNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLN REDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLK DNREKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITP WNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLL YEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLF KTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLG AYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDRGMIE ERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIR DKQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKA QVSGQGHSLSHEQIANLAGSPAIIKKGILQTVKIVDELVKV MGHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFIKDDSIDNKVLTRSDKNRGKSD NVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERG GLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDE NDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHHA HDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRKMI AKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLI ETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQ TGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVA YSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPID FLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGE LQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQLF VEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKHR DKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTST KEVLDATLIHQSIITGLYETRIDLSQLGGD	SEQ ID NO: 14
SpCas9 <i>Streptococcus</i> <i>pyogenes</i> wild type SWBC2D7W 014	ATGGATAAAAAGTATTCTATTGGTTTAGACATCGGCAC TAATTCCGTTGGATGGGCTGTCATAACCGATGAATACA AAGTACCTTCAAAGAAATTTAAGGTGTTGGGGAACAC AGACCGTCATTTCGATTAAAAAGAATCTTATCGGTGCCC TCCTATTTCGATAGTGGCGAAACGGCAGAGGCGACTCG CCTGAAACGAACCGCTCGGAGAAGGTATACACGTCGC AAGAACCGAATATGTTACTTACAAGAAATTTTATAGCA ATGAGATGGCCAAAGTTGACGATTCTTTCTTTCACCGT	SEQ ID NO: 15

TTGGAAGAGTCCTTTCCTTGTCGAAGAGGACAAGAAAC ATGAACGGCACCCCATCTTTGGAAACATAGTAGATGA GGTGGCATATCATGAAAAGTACCCAACGATTTATCAC CTCAGAAAAAAGCTAGTTGACTCAACTGATAAAGCGG ACCTGAGGTTAATCTACTTGGCTCTTGCCCATATGATA AAGTTCCGTGGGCACTTTCTCATTGAGGGTGATCTAAA TCCGGACAACCTCGGATGTCGACAACTGTTTCATCCAGT TAGTACAAACCTATAATCAGTTGTTTGAAGAGAACCCT ATAAATGCAAGTGGCGTGGATGCGAAGGCTATTCTTA GCGCCCGCCTCTCTAAATCCCGACGGCTAGAAAACCT GATCGCACAATTACCCGGAGAGAAGAAAAATGGGTTG TTCGGTAACCTTATAGCGCTCTCACTAGGCCTGACACC AAATTTTAAGTCGAACCTTCGACTTAGCTGAAGATGCCA AATTGCAGCTTAGTAAGGACACGTACGATGACGATCT CGACAATCTACTGGCACAATTGGAGATCAGTATGCG GACTTATTTTTGGCTGCCAAAAACCTTAGCGATGCAAT CCTCCTATCTGACATACTGAGAGTTAATACTGAGATTA CCAAGGCGCCGTTATCCGCTTCAATGATCAAAAGGTA CGATGAACATCACCAAGACTTGACACTTCTCAAGGCC CTAGTCCGTCAGCAACTGCCTGAGAAATATAAGGAAA TATTCTTTGATCAGTCGAAAAACGGGTACGCAGGTTAT ATTGACGGCGGAGCGAGTCAAGAGGAATTCTACAAGT TTATCAAACCCATATTAGAGAAGATGGATGGGACGGA AGAGTTGCTTGTAAACTCAATCGCGAAGATCTACTGC GAAAGCAGCGGACTTTTCGACAACGGTAGCATTCCACA TCAATCCACTTAGGGCAATTGCATGCTATACTTAGAA GGCAGGAGGATTTTTATCCGTTCTCAAAGACAATCGT GAAAAGATTGAGAAAATCCTAACCTTTTCGCATACCTTA CTATGTGGGACCCCTGGCCCGAGGGAACCTCTCGGTTTCG CATGGATGACAAGAAAGTCCGAAGAAACGATTACTCC ATGGAATTTTGAGGAAGTTGTCGATAAAGGTGCGTCA GCTCAATCGTTCATCGAGAGGATGACCAACTTTGACA AGAATTTACCGAACGAAAAAGTATTGCCTAAGCACAG TTTACTTTACGAGTATTTACAGTGTACAATGAACTCA CGAAAGTTAAGTATGTCACTGAGGGCATGCGTAAACC CGCCTTTCTAAGCGGAGAACAGAAGAAAGCAATAGTA GATCTGTTATTCAAGACCAACCGCAAAGTGACAGTTA AGCAATTGAAAGAGGACTACTTTAAGAAAATTGAATG CTTCGATTCTGTGCGAGATCTCCGGGGTAGAAGATCGAT TTAATGCGTCACTTGGTACGTATCATGACCTCCTAAAG ATAATTAAAGATAAGGACTTCCTGGATAACGAAGAGA ATGAAGATATCTTAGAAGATATAGTGTGACTCTTACC CTCTTTGAAGATCGGGAAATGATTGAGGAAAGACTAA AAACATACGCTCACCTGTTTCGACGATAAGGTTATGAA ACAGTTAAAGAGGCGTCGCTATACGGGCTGGGGACGA TTGTCGCGGAACTTATCAACGGGATAAGAGACAAGC AAAGTGGTAAAACTATTCTCGATTTTCTAAAGAGCGAC GGCTTCGCCAATAGGAACTTTATGCAGCTGATCCATGA TGACTCTTTAACCTTCAAAGAGGATATACAAAAGGCA CAGGTTTCCGGACAAGGGGACTCATTGCACGAACATA	
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TTGCGAATCTTGCTGGTTCGCCAGCCATCAAAAAGGGC ATACTCCAGACAGTCAAAGTAGTGGATGAGCTAGTTA AGGTCATGGGACGTCACAAACCGGAAAACATTGTAAT CGAGATGGCACGCGAAAATCAAACGACTCAGAAGGG GCAAAAAAACAGTCGAGAGCGGATGAAGAGAATAGA AGAGGGTATTAAAGAACTGGGCAGCCAGATCTTAAAG GAGCATCCTGTGGAAAATACCCAATTGCAGAACGAGA AACTTTACCTCTATTACCTACAAAATGGAAGGGACATG TATGTTGATCAGGAAGTGGACATAAACCGTTTATCTGA TTACGACGTCGATCACATTGTACCCCAATCCTTTTTGA AGGACGATTCAATCGACAATAAAGTGCTTACACGCTC GGATAAGAACCGAGGGGAAAAGTGACAATGTTCCAAGC GAGGAAGTCGTAAAGAAAATGAAGAACTATTGGCGGC AGCTCCTAAATGCGAACTGATAACGCAAAGAAAGTT CGATAACTTAACTAAAGCTGAGAGGGGTGGCTTGTCT GAACTTGACAAGGCCGGATTTATTAAACGTCAGCTCGT GGAAACCCGCCAAATCACAAAGCATGTTGCACAGATA CTAGATTCCCGAATGAATACGAAATACGACGAGAACG ATAAGCTGATTTCGGGAAGTCAAAGTAATCACTTTAAA GTCAAAATTGGTGTTCGGACTTCAGAAAGGATTTTCAAT TCTATAAAGTTAGGGAGATAAATAACTACCACCATGC GCACGACGCTTATCTTAATGCCGTCGTAGGGACCGCAC TCATTAAGAAATACCCGAAGCTAGAAAGTGAGTTTGT GTATGGTGATTACAAAGTTTATGACGTCCGTAAGATGA TCGCGAAAAGCGAACAGGAGATAGGCAAGGCTACAG CCAAATACTTCTTTTATTCTAACATTATGAATTTCTTTA AGACGGAAATCACTCTGGCAAACGGAGAGATACGCAA ACGACCTTTAATTGAAACCAATGGGGAGACAGGTGAA ATCGTATGGGATAAGGGCCGGGACTTCGCGACGGTGA GAAAAGTTTTGTCCATGCCCAAGTCAACATAGTAAA GAAAAGTGGGTGCAGACCGGAGGGTTTTCAAAGGAA TCGATTCTTCCAAAAAGGAATAGTGATAAGCTCATCGC TCGTAAAAAGGACTGGGACCCGAAAAAGTACGGTGGC TTCGATAGCCCTACAGTTGCCTATTCTGTCCTAGTAGT GGCAAAAGTTGAGAAGGGAAAATCCAAGAACTGAA GTCAGTCAAAGAATTATTGGGGATAACGATTATGGAG CGCTCGTCTTTTGAAAAGAACCCCATCGACTTCCTTGA GGCGAAAGGTTACAAGGAAGTAAAAAAGGATCTCATA ATTAACTACCAAAGTATAGTCTGTTTGAGTTAGAAAA TGGCCGAAAACGGATGTTGGCTAGCGCCGGAGAGCTT CAAAAGGGGAACGAACTCGCACTACCGTCTAAATACG TGAATTTCTGTATTTAGCGTCCCATTACGAGAAGTTG AAAGGTTACCTGAAGATAACGAACAGAAGCAACTTT TTGTTGAGCAGCACAAACATTATCTCGACGAAATCATA GAGCAAATTTTCGGAATTCAGTAAGAGAGTCATCCTAG CTGATGCCAATCTGGACAAAGTATTAAGCGCATACAA CAAGCACAGGGATAAACCACATACGTGAGCAGGCGGAA AATATTATCCATTTGTTTACTCTTACCAACCTCGGCGCT CCAGCCGCATTCAAGTATTTTGACACAACGATAGATCG CAAACGATACACTTCTACCAAGGAGGTGCTAGACGCG	
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	ACACTGATTACCAATCCATCACGGGATTATATGAAAC TCGGATAGATTTGTACAGCTTGGGGGTGACGGATCCC CCAAGAAGAAGAGGAAAGTCTCGAGCGACTACAAAG ACCATGACGGTGATTATAAAGATCATGACATCGATTA CAAGGATGACGATGACAAGGCTGCAGGA	
SpCas9 <i>Streptococcus</i> <i>pyogenes</i> wild type Encoded product of SWBC2D7W 014	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRILIYAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKS NFDLAEDAKLQLSKD TYDDDLN LLAQIGDQYADLFLAAKNLS DAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKKGILQTVKVVDELVKVM GRHKPENIVIE MARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKS KLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERS SFEKNPI DFLEAKGYKEVKKDLIIKLPKYS LFELNGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGS PEDNEQKQL FVEQHKHYLDEIIEQISEFSKR VILADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVL DATLIHQ SITGLYETRIDL SQLGGDGSPKKKRKVS SDYKDHDGDYKDHDIDYKDDDDKAAG	SEQ ID NO: 16
SpCas9 <i>Streptococcus</i> <i>pyogenes</i> M1GAS wild type NC_002737.2	ATGGATAAGAAATACTCAATAGGCTTAGATATCGGCA CAAATAGCGTCGGATGGGCGGTGATCACTGATGAATA TAAGGTTCCGTCTAAAAAGTTCAAGGTTCTGGGAAAT ACAGACCGCCACAGTATCAAAAAAATCTTATAGGGG CTCTTTTATTTGACAGTGGAGAGACAGCGGAAGCGAC TCGTCTCAAACGGACAGCTCGTAGAAGGTATACACGT CGGAAGAATCGTATTTGTATCTACAGGAGATTTTTC AAATGAGATGGCGAAAGTAGATGATAGTTTCTTTCATC GACTTGAAGAGTCTTTTTTGGTGGGAAGAAGACAAGAA	SEQ ID NO: 17

GCATGAACGTCATCCTATTTTTTGGAAATATAGTAGATG AAGTTGCTTATCATGAGAAATATCCAACTATCTATCAT CTGCGAAAAAAATTGGTAGATTCTACTGATAAAGCGG ATTTGCGCTTAATCTATTTGGCCTTAGCGCATATGATT AAGTTTCGTGGTCATTTTTTGATTGAGGGAGATTTAAA TCCTGATAATAGTGATGTGGACAAACTATTTATCCAGT TGGTACAAACCTACAATCAATTATTTGAAGAAAACCT ATTAACGCAAGTGGAGTAGATGCTAAAGCGATTCTTTC TGCACGATTGAGTAAATCAAGACGATTAGAAAATCTC ATTGCTCAGCTCCCCGGTGAGAAGAAAAATGGCTTATT TGGGAATCTCATTGCTTTGTCATTGGGTTTGACCCCTA ATTTTAAATCAAATTTTGATTTGGCAGAAGATGCTAAA TTACAGCTTTCAAAGATACTTACGATGATGATTTAGA TAATTTATTGGCGCAAATTGGAGATCAATATGCTGATT TGTTTTTGGCAGCTAAGAATTTATCAGATGCTATTTTA CTTTCAGATATCCTAAGAGTAAATACTGAAATAACTAA GGCTCCCCTATCAGCTTCAATGATTAAACGCTACGATG AACATCATCAAGACTTGACTCTTTTAAAAGCTTTAGTT CGACAACAACCTCCAGAAAAGTATAAAGAAATCTTTT TTGATCAATCAAAAAACGGATATGCAGGTTATATTGAT GGGGGAGCTAGCCAAGAAGAATTTTATAAATTTATCA AACCAATTTTAGAAAAAATGGATGGTACTGAGGAATT ATTGGTGAACTAAATCGTGAAGATTTGCTGCGCAAG CAACGGACCTTTGACAACGGCTCTATTCCCCATCAAAT TCACTTGGGTGAGCTGCATGCTATTTTGAGAAGACAAG AAGACTTTTATCCATTTTTTAAAAGACAATCGTGAGAAG ATTGAAAAAATCTTGACTTTTCGAATTCCTTATTATGTT GGTCCATTGGCGCGTGGCAATAGTCGTTTTGTCATGGAT GACTCGGAAGTCTGAAGAAACAATTACCCCATGGAAT TTTGAAGAAGTTGTGATAAAGGTGCTTCAGCTCAATC ATTTATTGAACGCATGACAACTTTGATAAAAAATCTTC CAAATGAAAAAGTACTACCAAAACATAGTTTGCTTTAT GAGTATTTTACGGTTTATAACGAATTGACAAAGGTCAA ATATGTTACTGAAGGAATGCGAAAACCAGCATTTCTTT CAGGTGAACAGAAGAAAGCCATTGTTGATTTACTCTTC AAAACAAATCGAAAAGTAACCGTTAAGCAATTAAAAG AAGATTATTTCAAAAAAATAGAATGTTTTGATAGTGTT GAAATTTGAGGAGTTGAAGATAGATTTAATGCTTCATT AGGTACCTACCATGATTTGCTAAAAATTATTAAAGATA AAGATTTTTTGGATAATGAAGAAAATGAAGATATCTT AGAGGATATTGTTTTAACATTGACCTTATTTGAAGATA GGGAGATGATTGAGGAAAGACTTAAAACATATGCTCA CCTCTTTGATGATAAGGTGATGAAACAGCTTAAACGTC GCCGTTATACTGGTTGGGGACGTTTGTCTCGAAAATTG ATTAATGGTATTAGGGATAAGCAATCTGGCAAAACAA TATTAGATTTTTTGAAATCAGATGGTTTTGCCAATCGC AATTTTATGCAGCTGATCCATGATGATAGTTTGACATT TAAAGAAGACATTCAAAAAGCACAAAGTGTCTGGACAA GGCGATAGTTTACATGAACATATTGCAAATTTAGCTGG TAGCCCTGCTATTAAAAAAGGTATTTTACAGACTGTAA	
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AAGTTGTTGATGAATTGGTCAAAGTAATGGGGCGGCA TAAGCCAGAAAATATCGTTATTGAAATGGCACGTGAA AATCAGACAACTCAAAAGGGCCAGAAAAATTCGCGAG AGCGTATGAAACGAATCGAAGAAGGTATCAAAGAATT AGGAAGTCAGATTCTTAAAGAGCATCCTGTTGAAAAT ACTCAATTGCAAAATGAAAAGCTCTATCTCTATTATCT CCAAAATGGAAGAGACATGTATGTGGACCAAGAATTA GATATTAATCGTTTAAAGTGATTATGATGTGCGATCACAT TGTTCCACAAAGTTTCCTTAAAGACGATTCAATAGACA ATAAGGTCTTAACGCGTTCTGATAAAAAATCGTGGTAA ATCGGATAACGTTCCAAGTGAAGAAGTAGTCAAAAAG ATGAAAAACTATTGGAGACAACTTCTAAACGCCAAGT TAATCACTCAACGTAAGTTTGATAATTTAACGAAAGCT GAACGTGGAGGTTTGAGTGAAGTTGATAAAGCTGGTT TTATCAAACGCCAATTGGTTGAAACTCGCCAAATCACT AAGCATGTGGCACAAATTTTGGATAGTCGCATGAATA CTAAATACGATGAAAATGATAAACTTATTCGAGAGGT TAAAGTGATTACCTTAAAATCTAAATTAGTTTCTGACT TCCGAAAAGATTTCCAATTCTATAAAGTACGTGAGATT ACAATTACCATCATGCCCATGATGCGTATCTAAATGC CGTCGTTGGAAGTCTTTGATTAAAGAAATATCCAAAAC TTGAATCGGAGTTTGTCTATGGTGATTATAAAGTTTAT GATGTTTCGTAAAATGATTGCTAAGTCTGAGCAAGAAA TAGGCAAAGCAACCGCAAAATATTTCTTTTACTCTAAT ATCATGAACTTCTTCAAAACAGAAATTACACTTGCAAA TGGAGAGATTCGCAAACGCCCTCTAATCGAAACTAAT GGGGAAACTGGAGAAATTGTCTGGGATAAAGGGCGAG ATTTTGCCACAGTGCGCAAAGTATTGTCCATGCCCCAA GTCAATATTGTCAAGAAAACAGAAGTACAGACAGGCG GATTCTCCAAGGAGTCAATTTTACCAAAAAGAAATTC GGACAAGCTTATTGCTCGTAAAAAAGACTGGGATCCA AAAAAATATGGTGGTTTTGATAGTCCAACGGTAGCTTA TTCAGTCCTAGTGGTTGCTAAGGTGGAAAAAGGGAAA TCGAAGAAGTTAAAATCCGTTAAAGAGTTACTAGGGA TCACAATTATGGAAAGAAGTTCCTTTGAAAAAAATCC GATTGACTTTTTAGAAAGCTAAAGGATATAAGGAAGTT AAAAAAGACTTAATCATTAACTACCTAAATATAGTCT TTTTGAGTTAGAAAACGGTCGTAAACGGATGCTGGCT AGTGCCGGAGAATTACAAAAGGAAATGAGCTGGCTC TGCCAAGCAAATATGTGAATTTTTTATATTTAGCTAGT CATTATGAAAAGTTGAAGGGTAGTCCAGAAGATAACG AACAAAAACAATTGTTTGTGGAGCAGCATAAGCATTA TTTAGATGAGATTATTGAGCAAATCAGTGAATTTTCTA AGCGTGTTATTTTAGCAGATGCCAATTTAGATAAAGTT CTTAGTGCATATAACAAACATAGAGACAAACCAATAC GTGAACAAGCAGAAAATATTATTCATTTATTTACGTTG ACGAATCTTGAGAGCTCCCGCTGCTTTTAAATATTTTGA TACAACAATTGATCGTAAACGATATACGTCTACAAAA GAAGTTTTAGATGCCACTCTTATCCATCAATCCATCAC	
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	TGGTCTTTATGAAACACGCATTGATTTGAGTCAGCTAG GAGGTGACTGA	
SpCas9 <i>Streptococcus</i> <i>pyogenes</i> M1GAS wild type Encoded product of NC_002737.2 (100% identical to the canonical Q99ZW2 wild type)	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRILIYAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASQAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	SEQ ID NO: 18

[0106] The genome editing system described herein may include any of the above SpCas9 sequences, or any variant thereof having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

B. Wild type Cas9 orthologs

[0107] In other embodiments, the genome editing system described herein may utilize a wild type Cas9 ortholog from another bacterial species different from the canonical Cas9 from *S. pyogenes*. For example, the following Cas9 orthologs can be used in connection with the genome editing system described in this specification. In addition, any variant Cas9 orthologs having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%

sequence identity to any of the below orthologs may also be used with the herein described editing system.

Description	Sequence
LfCas9 <i>Lactobacillus fermentum</i> wild type GenBank: SNX31424.1 1	MKEYHIGLDIGTSSIGWAVTDSQFKLMRIKGKTAIGVRLFEEGKTA AERR TFRTTRRLKRRKWRLHYLDEIFAPHLQEVDENFLRRLKQSNHPEDPTK NQAFIGKLLFPDLLKKNERGYPTLIKMRDELPVEQRAHYPVMNIYKLRE AMINEDRQFDLREVYLA VHHIVKYRGHFLNNASVDKFKVGRIDFDKSFN VLNEAYEELQNGEGSFTIEPSKVEKIGQLLLDTKMRKLD RQKAVAKLLE VKVADKEETKR NKQIATAMSKLV LGYKADFATVAMANGNEWKIDLSS ETSEDEIEKFREE LSDAQN DILTEITSLFSQIMLNEIVPNGMSISESMM DRY W THERQLAEVKEYLATQPASARKEFDQVYNKYIGQAPKERGF DLEKGL KKILSKKENWKEIDELLKAGDFLPKQRTSANGVIPHQMHQQELDRIIEKQ AKYYPWLATENPATGERDRHQAKYELDQLVSFRIPYYVGPLVTPEVQK ATSGAKFAWAKRKEDGEITPWNLWDKIDRAESAEAFIKRMTVKDTYLL NEDVLPANSLLYQKYNVLNELNNVRVNGRRLSVGIKQDIYTELFKKKKKT VKASDVASLVM AKTRGVNKP SVEGLSDPKKFNSNLATYLDLKSIVGDK VDDNRYQTDLENII EWRSVFEDGEIFADKLTEVEWLTDEQRSALVKKRY KGWGRLSKKLLTGIVDENGQRIIDLMWNTDQNFKEIVDQPVFKEQIDQL NQKAITNDGMTLRERVESVLDDAYTSPQNKKAIWQVVRVVEDIVKAVG NAPKSISIEFARNEG NKGEITRSRRTQLQKLFEDQAHEL VKDTSLTEELEK APDLSDRYYFYFTQGGKDMYTGD PINFDEISTKYDIDHILPQS FVKDNSL DNRVLT SRKENNKKSDQVPAKLYAAKM KPYWNQLLKQGLITQRKFEN LTKDVDQNIKYRSLGFVKRQLVETRQVIKLTANILGSMYQEAGTEIIE TR AGLTKQLREEFDLPKVREVNDYHHA VDAYLTTFAGQYLNRRYPKLRSF FVYGEYMKFKHGS DLKLRNFNFFHELMEGDKS QGKVVDQQTGELITTR DEVAKSFDRL LNMYMLVSKEVHDRSDQLYGATIVTAKESGKLTSP IEI KKNRLVDLYGAYTNGTSAFM TIIFKFTGNKPKYKVIGIPTTSAASLKRAGK PGSESYNQELHRII KSNPKVKKGFEIVVPHVSYGQLIVDGDCKFTLASPTV QHPATQLVLSKKSLETISSGYKILKDKPAIANERLIRVFDEVVGQMNRYF TIFDQRSNRQKVADARDKFLSLPTESKYEGAKKVQVGKTEVITNLLMGL HANATQGDLKVLGLATFGFFQSTTGLSLSED TMIVYQSPTGLFERRICKL DI (SEQ ID NO: 19)
SaCas9 <i>Staphylococcus aureus</i> wild type GenBank: AYD60528. 1	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFS NEMAKVDDSSFFH RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKA DLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEEN PINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIALSLGLTP NFKSNFDLAEDAKLQLSKD TYDDDLNLLAQIGDQYADLFLAAKNLSD AILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDL LRKQRTFDNGSIPHQIHLGELHAILRRQEDFY PFLKDNREKIEKILTRIPY YVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFD KNLPNEKVL PKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAI VDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDL LKI IKDKDFLDNEENEDILEDIVLTTLTFEDREMIEERLKYAHLFDDKVM KQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKS DGFANRNFMQLI HDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPA IKKGILQTVKVVDL VKVMGRHKPENIVIE MARENQTTQKGQKNSRERMKRIEEG IKELGSQIL KEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQ

Description	Sequence
	SFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNT KYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHHAHDAYLN AVVGTALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKATAKYFFY SNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLMS PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT VAYSVLVVAKEKKGSKKLKSVKELLGITIMERSSSFENPIDFLEAKGYK EVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFY LASHYEKLKGPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANL DKVLSAYNKHDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYT STKEVLDTLIHQSIITGLYETRIDLSQLGGD (SEQ ID NO: 20)
SaCas9 <i>Staphylococcus aureus</i>	MGKRNILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRS KRGARRLKRRRRHRIQRVKLLFDYNLLTDHSELGINPYEARVKGLSQ KLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEE KYVAELQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVKAYHQLDQ SFIDTYIDLLETRRTY YEGPGEPSFGWKDIKEWYEMLMGHCTYFPEELR SVKYAYNADLYNALNDLNNLVITRDENEKLEYEYEFQIENVFQKKKKP TLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIENA ELLDQIAKILTIYQSSEDIQEELTNLNSLTQEEIEQISNLKGYTGTHNLSL KAINLILDELWHTNDNQIAIFNRLKLVKKVDLSQQKEIPTTLVDDFILSP VVKRSFIQSIKVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQKRNR QTNERIEEIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNP FNYEVDHIIPRSVSFDNSFNKVLVKQEENSCKGNRTPFYLSSSDSKISY ETFKKHILNLAKEGGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRY ATRGLMNLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYK HHAEDALIINANADFIFKEWKKLDKAKKVMENQMFEKQAESMPEIETE EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGN TLIVNNLNGLYDKDNDKLKLINKSPEKLLMYHHDPPQTYQKLKLIMEQ YGDEKNPLYKYEEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDT DDYPNSRNKVVKLSLKPYPYFDVYLDNGVYKFVTVKNLDVIKENYYEV NSKCYEEAKKLKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIE VNMIDITYREYLENMNDKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSK KHPQIIKK (SEQ ID NO: 21)
StCas9 <i>Streptococcus thermophilus</i> UniProtKB/ Swiss-Prot: G3ECR1.2 Wild type	MLFNKCIISINLDFSNKEKCMTPYSIGLDIGTNSVGWAVITDNYKVPSK KMKVLGNTSKKYIKKNLLGVLLFDSGITAEGRRLKRTARRRYTRRRNRI LYLQEIFSTEMATLDDAFFQRLDDSFLLVPDDKRDSKYPIFGNLVEEKVYH DEFPTIYHLRKYLADSTKKADRLVYLALAHMIKYRGHFLIEGEFNSKN NDIQKNFQDFLDITYNAIFESDLSLENSKQLEEIVKDKISKLEKKDRILKLF PGEKNSGIFSEFLKLIVGNQADFRKCFNLDEKASLHFSKESYDEDETLT GYIGDDYSDVFLKAKKLYDAILLSGFLTVDNETEAPLSSAMIKRYNEH KEDLALLKEYIRNLSLKYTYNEVFKDDTKNGYAGYIDGKTNQEDFYVYLK NLLAEFEGADYFLEKIDREDFLRKQRTFDNGSIPYQIHLQEMRAILDKQA KFYPFLAKNKERIEKILTRIPYVVGPLARGNSDFAWSIRKRNKIPWNF EDVIDKESSAEAFINRMTSFDLYLPEEKVLPKHSLLYETFNVYNELTKVR FIAESMRDYQFLDSKQKKDIVRLYFKDKRKVTDKDIIEYLHAIYGYDGIE LKGIEKQFNSSLSTYHDLLNIINDKEFLDDSSNEAIIIEIIHTLTIFEDREMIK QRLSKFENIFDKSVLKKLSRRHYTGWGKLSAKLINGIRDEKSGNTILDYLI DDGISNRNFMQLIHDDALSFKKKIQKAQIIGDEDKGNIEVVKSLPGSPAI

Description	Sequence
	KKGILQSIKIVDELVKVMGGRKPESIVVEMARENQYTNQGKSNSQQRLLK RLEKSLKELGSKILKENIPAKLSKIDNNALQNDRLYLYYLQNGKDMYTG DDLDDIDRLSNYDIDHIIPQAFLKDNSIDNKVLVSSASNRGKSDDFPSLEV KKRKTFWYQLLKSKLISQRKFDNLTKAERGGLLPEDKAGFIQRQLVETR QITKHVARLLDEKFNKKDENNRAVRTVKIITLKSTLVSQFRKDFELYK VREINDFHHAHDAYLNAVIAASALLKKYPKLEPEFVYGDYPKYNSFRERK SATEKVYFYSNIMNIFKKSISLADGRVIERPLIEVNEETGESVWNKESDLA TVRRVLSYPQVNVVKKVEEQNHGLDRGKPKGLFNANLSSKPKPNSNEN LVGAKEYLDPKKYGGYAGISNSFAVLVKGTEIEGAKKKITNVLEFQGISI LDRINRDKDLNLFLEKGYKDIELIIELPKYSLEFSDGSRMLASILSTN NKRGEIHKGNQIFLSQKFVLLYHAKRISNTINENHRKYVENHKKKEFEEL FYYILEFNENYVGAKKNGKLLNSAFQSWQNHSEIDELCSSFIGPTGSEKRG LFELTSRGSAADEFELGVKIPRYRDYTPSSLLKDATLIHQSVTGLYETRID LAKLGEG (SEQ ID NO: 22)
LcCas9 <i>Lactobacillus crispatus</i> NCBI Reference Sequence: WP_133478 044.1 Wild type	MKIKNYNLALTPTS AVGHVEVDDDLNILEPVHHQKAIGVAKFGEGETA EARRLARSARRTTKRRANRINH YFNEIMKPEIDKVDPLMFDRIKQAGLSP LDERKEFRTVIFDRPNIASY YHNQFPTIWLHLQKYL MITDEKADIRLIYWA LHSLKHRGHFFNTTPMSQFKPGKLN LKDDMLALDDYNDLEGLSFAVA NSPEIEKVIKDRSMHKKEKIAELKKLIVNDVPDKDLAKRNNKIITQIVNAI MGNSFHLNFIFDMDLDKLT SKAWSFKLDDPELDTKFDAISGSMTDNQIGI FETLQKIYSAISLLDILNGSSNVVDAKNALYDKHKRDLNLYFKFLNTLPD EIAKTLKAGYTLYIGNRKKDL LAARKLLKVNVAKNFSQDDFYKLINKEL KSIDKQGLQTRFSEKVGELVAQNNFLPVQRSSDNVFIPYQLNAITFNKILE NQGKYYDFLVKPNPAKKDRKNAPYELS QLMQFTIPYYVGPLVTPEEQV KSGIPKTSRFAWMVRKDNGAITPWNFYDKVDIEATADKFIKRSIAKDSY LSELVLPKHSLLYEKYE VFNELSNVSLDGGKLSGGVKQILFNEVFKKTN KVNTSRILKALAKHNIPGSKITGLSNPEEFTSSLQTYNAWKKYFPNQIDNF AYQQDLEKMIEWSTVFEDHKILAKKLDEIEWLDDDQKKFVANTRLRGW GRLSKRLLTGLKDNYGKSIMQRLETTKANFQQIVYKPEFREIDKISQAA AKNQSLEDILANSYTS PSNRKAIRKTMSVVDEYIKLNHKGEPDKIFLMFQ RSEQEKGKQTEARSKQLNRILSQLKADKSANKLFSKQLADEFSNAIKKS KYKLNDKQYFYFQQLGRDAL TGEVIDYDELYKYTVLHIIPRSKLTDDSQ NNKVLTKYKIVDGSVALKFGNSYS DALGMPIKAFWTELNRKLIPKGL LNLTTDFSTLNKYQRDGYIARQLVETQQIVKLLATIMQSRFKHTKII VR NSQVANIRYQFDYFRIKNLNEY YRGFDAYLA AVVGTYLYKVYPKARRL FVYGQYLKPKKTNQENQDMHLDSEKKSQGFNFWNLLYGKQDQIFVN GTDVIAFNRKDLITKMNTVYNYKSQKISLAIDYHNGAMFKATLFPNRDR DTAKTRKLIPKKKDYDTDIYGGYTSNV DGYMLLAEIHKRDGNKQYGFY VPSRLVSELDTLKKTRYTEYEEKLKEIIP ELGVDLKKIKKIKILKNKVPF NQVIIDKGSKFFITSTS YRWNYRQLILSAESQQTMDLVVDPDFS NHKAR KDARKNADERLIKVYEEILYQVKNYMPMFVELHRCYEKLVD AQKTFKS LKISDKAMVLNQILILLHSNATSPVLEKLG YHTRFTLGKKHNLISENAVL VTQSITGLKENHVS IQML (SEQ ID NO: 23)
PdCas9 <i>Pedicoccus damnosus</i> NCBI Reference Sequence:	MTNEKYSIGLDIGTSSIGFA VVNDNNRVIRVKGKNAIGVRLFDEGKAAA DRRSFRTTTRSFR TTRRRLSRRRWRLKLLREIFDAYITPVDEAFFIRLKE NLSPKDSKKQYSGDILFNDRSDKDFYEKYPTIYHLRNALMTEHRKFDVR EIYLAIHIMKFRGHFLNATPANNFKVGR LNLLEEKFEELNDIYQRFVPE SIEFRDNLLEQIKEVLLDNKRSRADRQRTLVS DIYQSSDKDIEKRNKAV ATEILKASLGNKAKLNVITNVEVDKEAAKEWSITFDESIDDDLAKIEGQ

Description	Sequence
WP_062913 273.1 Wild type	MTDDGHEIIEVLRSLYSGITLSAIVPENHTLSQSMVAKYDLHKDHLKLFK KLINGMTDTKKAKNLRAAYDGYIDGVKGKVLQPQEDFYKQVQVNLDDS AEANEIQTIDQDIFMPKQRTKANGSIPHQLQQQELDQIIENQKAYYPWL AELNPNPDKKRQQLAKYKLDELVTFRVPYYVGPMITAKDQKNQSGAEF AWMIRKEPGNITPWNFDQKVDRMATANQFIKRMTTTDTYLLGEDVLP QSLLYQKFEVLNELNKRIDHKPISIEQKQQIFNDLQKQFKNVTIKHLQDY LVSQGGQYSKRPLIEGLADEKRFNSSLSTYSDLGIFGAKLVEENDRQEDL EKIIEWSTIFEDKKIYRAKLNDLTWLTDDQKEKLATKRYQGWGRLSRKL LVGLKNSEHRNIMDILWITNENFMQIQAEPDFAKLVTDANKGMLEKTD QDVINDLYTSPQNKKAIRQILLVVHDIQNAMHGQAPAKIHVEFARGEER NPRRSVQRQRQVEAAYEKVSNELVSAKVRQEFKEAINNKRDFKDRLFL YFMQGGIDIYTGKQLNIDQLSSYQIDHILPQAFVKDDSLTNRVLTNENQV KADSVPIDIFGKKMLS VWGRMKDQGLISKGKYRNLTMNPENISAHTENG FINRQLVETRQVIKLA VNILADEYGDSTQIISVKADLSHQMREDFELLKN RDVNDYHHAFDAYLA AFIGNYLLKRYPKLESYFVYGDFFKFTQKETKM RRFNFIYDLKHCDQVNVKETGEILWTKDEDIKYIRHLFAYKKILVSHEVR EKRGA LYNQTIYKAKDDKSGSQESKKLIRIKDDKETKIYGGYSGKSLAY MTIVQITKKNKVS YRVIGIPTLALARLNKLENDSTENNGELYKIIKPQFTH YKVDKKNGEIIE TTDDFKIVVSKVRFQQLIDDAGQFFMLASDTYKNNAQ QLVISNNALKAINNTNITDCPRDDLRLDLNLRLDSAFDEIVKKMDKYFSA YDANNFREKIRNSNLIFYQLPVEDQWENNKITELGKRTVLTRILQGLHAN ATTTDMSIFKIKTPFGQLRQRSGISLSENAQLIYQSPTGLFERRVQLNKK (SEQ ID NO: 24)
FnCas9 <i>Fusobacteriu m nucleatum</i> NCBI Reference Sequence: WP_060798 984.1	MKKQKFSDYYLGFDIGTNSVGWCVTDL DYNVLRFNKKDMWGSRLFEE AKTAAERRVQRNSRRRLKRRKWRLNLLEEIFSNEILKIDSNFFRRLKESSL WLEDKSSKEKFTLFNDNDYKDYDFYKQYPTIFHLRNLIELKNPEKKDIRLV YLAIHSIFKSRGHFLFEGQNLKEIKNFETLYNNLIAFLEDNGINKIIDKNNI EKLEKIVCDSKKGLKDKEKEFEKIFNSDKQLVAIFKLSVGSSVSLNDLFD TDEYKKGEVEKEKISFREQIYEDDKPIYYISILGEKIELLDIAKTFYDFMVL NNILADSQYISEAKVKLYEEHKKDLKNLKYIIRKYNKGN YDKLFDKNE NNYSAYIGLNKEKSKKEVIEKSRLKIDDLIKNIKGYLPKVEEIEEKDKAIF NKILNKIELKTILPKQRISDNGTLPYQIHEAELEKILENQSKYYDFLN YEE NGIITKDKLLMTFKFRIPYYVGPLNSYHKDKGGNSWIVRKEEGKILPWNF EQKVDIEKSAEEFIKRM TNKCTYLNGEDVIPKDTFLYSEYVILNELNKVQ VNDEFLNEENKRKIIDELFKENKKVSEKKFKEYLLVKQIVDGTIELKGVK DSFNSNYISYIRFKDIFGEKLNLDIYKEISEKSILWKCLYGD DKKIFEKKIK NEYGDILTKDEIKKINTFKFNWGR LSEKLLTGIEFINLETGECYSSVMDA LRRNTYNLMELLSSKFTLQESINNENKEMNEASYRDLIEESYVSPSLKRAI FQTLKIYEEIRKITGRVPK KVFIE MARGGDESMKNKKIPARQEQLKKLYD SCGNDIANFSIDIKEMKNSLISYDNNSLRQKKLYLYYLQFGKCMYTGREI DLDRLLQNNDTYDIDHIYPRSKVIKDDSF DNLVVLKNENA EKSNEYPV KKEIQEKMKSFWRFLKEKNFISDEKYKRLTGKDDFELRGFMARQLVNV RQTTKEVGKILQQIEPEIKIVYSKAEIASSFREMFDFIKVRELNDTHHAKD AYLNIVAGNVYNTKFTEKPYRYLQEIKENYDVKKIYN YDIKNAWDKEN SLEIVKKNMEKNTVNITRFI KEKKGQLFDLNPIKKGETSNEIISIKPKVYN GKDDKLNEKYGYYS LNPA YFLYVEHKEKNKRIKSFERVNLVDVNNIK DEKSLVKYLIENKKLVEPRVIKKVYKRQVILINDYPYSIVTLD SNKLMDF ENLKPLFLENKYEKILKNVIKFLEDNQGKSEENYKFIYLLKKKDRYEKNET LESVKDRYNLEFNEMYDKFLEKLD SKDYKNYMNNKKYQELLDVKEKFI

Description	Sequence
	KLNLFDKAFTLKSFLDLFNRKTMADFSKVGLTKYLGKIQKISSNVLSKNE LYLLEESVTGLFVKKIKL (SEQ ID NO: 25)
EcCas9 <i>Enterococcus cecorum</i> NCBI Reference Sequence: WP_047338 501.1 Wild type	RRKQRIQILQELLGEEVLKTDPGFFHRMKESRYVVEDKRTL D GKQVELP YALFVDKDYTDKEYYKQFPTINHLIVYLM TTS DTPDIRLVYLALHYMK NRGNFLHSGDINN VKDINDILEQLDNVLETFLD G WNLKLSYVEDIKNIY NRDLGRGERKKAFVNTLGAKTKAEKAFCSLISGGSTNLAELFDDSSLKEI ETPKIEFASSSLEDKIDG IQEAL EDRFAVIEAAKRLYDWKTLTDILGDSSS LAEARVNSYQMHHEQLLEL KSLVKEYLDRKVFQEVFVSLNVANNYPAY IGHTKINGKKKELEV KRTKRND FYSYVKKQVIEPIKKKVSDEAVLTKLSE IESLIEVDKYLPLQVNSDNGVIPYQVKLNELTRIFDNLENRIPVLREN RDK IIKTFKFRIPYYVGS L NGVVKNGKCTNWMVRKEEGKIYPWNFEDKVDLE ASAEQFIRRM TNKCTYL VNEDVLPKYSLLYSKYLV LSELNNLRIDGRPLD VKIKQDIYENVFKNRKVT LKKIKKYLLKEGIITDDDELSGLADDVKSSL TAYRDFKEKLGHLDLSEAQMENIILNITLFGDDK KLLKKRLAALYPFIDD KSLNRIATLNYRDWGR L SERFLSGITSVDQETGELRTIIQCMYETQANLM QLLAEPYHFVEAIEKENPKVDLESISYRIVNDLYVSPAVKRQIWQTLLVIK DIKQVMKHDPERIFIEMAREKQESKKT SRKQVLSEVYKKAKEYEHLFE KLNSLTEEQ LRSKKIYLYFTQLGKCMYSGEPIDFENLVSANSNYDIDHIYP QSKTIDDSFNNIVLVK KSLNAYKSNHYPIDKNIRDNEKVKTLWNTLVSK GLITKEKYERLIRSTPF SDEELAGFIARQLVETRQSTKAVAEILSNWFP ESE IVYSKAKNVSNFRQDFEILKVRELNDCHHAHDA YL NIVVGNA YHTKFTN SPYRFIKNKANQEYNLRKLLQKV NKIESNGVVAWVGQSENNPGTIATVK KVIRNTVLISRMVKEVDGQLFDLTLMKKGKGQVPIKSSDERLTDISKY GGYNKATGAYFTFVKS KRGKVVRSEFYVPLHLSKQFENNNELLKEYIE KDRGLTDVEILIPKVLINSLFRYNGSLVRITGRGDTRLLLVHEQPLYVSNS FVQQLKS VSSYKLK KSENDNAKLT KTATEKLSNIDELYDGLLRKLDLPY SYWFSSIKEYLVESRTKYIKLSIEEKALVIFEILHLFQSDAQVPNLKILGLS TKPSRIRIQKNLKD TDKMSIIHQSPSGIFEHEIELTSL (SEQ ID NO: 26)
AhCas9 <i>Anaerostipes hadrus</i> NCBI Reference Sequence: WP_044924 278.1 Wild type	MQNGFLGITVSSEQVGWAVTNPKYELERASRKDLWGVRLFDKAETAED RRMFRTNRRLNQRKKNR IHYLRDIFHEEVNQKDPNFFQQLDES NFCEDD RTVEFNFD TNLYKNQFPTVYHLRKYLMETKDKPDIRLVYLAFSKFMKN RGHFLYKGNLGEVMDFENS MKGFCESLEKFNIDFPTLSDEQVKEVRDIL CDHKIAKTVKKKNITITK VSKTAKAWIGLFCGCSVPVKVLFQDIDEEIV TDPEKISFEDASYDDY IANIEKGVG IY YEAI VSAKMLFDWSILNEILGDHQ LLSDAMIAEYNKHHDDL KRLQKIIKGTGSRELYQDIFINDVSGNYVCYV GHAKTMSSADQKQFY TFLKNRLKNVNGISSEDAEWIDTEIKNGTLLPKQ TKRDNSVIPHQ LQLREFELIDNMQEMYPFLKENREKLLKIFNFVIPYYV GPLKGVVRKGESTNWMVPK KDGVIHPWNFDEMVDKEASAECFISRMT GNCSYLFNEKVL PKNSLLYETFEVLNELNPLKINGEPISVELKQRIYEQLF LTGKKVTKKSLTKYLIKNGYDKDIELSGIDNEFHSNLKSHIDFEDYDNLS DEEVEQIILRITVFEDKQLL KDYLNREFVKLS EDERKQICSLSYKGWGNL SEMLLNGITVTD SNGVEVSVM DMLWNTNLNLMQILSKKYGYKAEIEHY NKEHEKTIYNREDLMDYLNIPPAQR RKVNQLITIVKSLKKT YGVPNKIFF KISREHQDDPKRTSSRKEQLKYLYKSLKSEDEKHLMKELDELNDHEL SN DKVYLYFLQKGRCIYSGKKL NLSRLRKS NYQNDIDYIYPLSAVNDRSMN NKVLTGIQENRADKYTYFPVDSEIQKKMKGFWMELVLQGFMTKEKYFR LSRENDFSKSELVSFIEREISDNQQSGRM IASVLQYYFPESKIVFVKEKLIS SFKRDFHLISSYGHNHLQA AKDAYITIVVGNVYHTKFTMDPAIYFKNHK RKDYDLNRLFLENISR DGQIAWESGPYGS IQTVRKEYAQN HIAVTKRVV

Description	Sequence
	EVKGGFLFKQMPLKKGHGEYPLKTNDPRFGNIAQYGGYTNTVTSYFVLV ESMEKGKKRISLEYVPVYLHERLEDDPGHKLLKEYLVDHRKLNHPKILL AKVRKNSLLKIDGFYRLNGRSGNALILTNAVELIMDDWQTKTANKISG YMKRRAIDKKARVYQNEFHIQELEQLYDFYLDKLNKVYKNRKNNA ELIHNEKEQFMELKTEDQCVLLTEIKKLFVCSPMQADLTIGGSKHTGMI AMSSNVTKADFAVIAEDPLGLRNKVIYSHKGEK (SEQ ID NO: 27)
KvCas9 <i>Kandleria vitulina</i> NCBI Reference Sequence: WP_031589 969.1 Wild type	MSQNNNKIYNIGLDIGDASVGWAVVDEHYNLLKRHGKHMWGSRLFTQ ANTAVERRSSSRSTRRRYNKRERIRLLREIMEDMVLDVDPTFFIRLANVS FLDQEDKKDYLKENYHSNYNLFIDKDFNDKTYDYKYPTIYHLRKHLCES KEKEDPRLIYLALHHIVKYRGNFLYEGQKFSMDVSNIEDKMIDVLRQFN EINLFEYVEDRKKIDEVLNVLKEPLSKKHKAFAFALDFTTKDNKAAYK ELCAALAGNKFNVTKMLKEAELHDEDEKDISFKFSDATFDDAFVEKQPL LGDCVEFIDLLHDIYSWVELQNILGSAHTSEPSISAAMIQRYEDHKNDLK LLKDVIRKYLPPKYFEVFRDEKSKKNYCNYNHPSKTPVDEFYKYIKK LIEKIDDPDVKTILNKIELESFMLKQNSRTNGAVPYQMQDELNKILENQ SVYYSDLKDNEDKIRSILTFRIPIYFGLNITKDRQFDWIKKKEGKENERIL PWNANEIVDVKTADEFIKMRNFCTYFPDEPVMAKNSLTVSKYEVLN EINKLRINDHLIKRDMKDKMLHTLFMDHKSISANAMKKWLKVNQYFSN TDDIKIEGFQKENACSTSLTPWIDFTKIFGKINESNYDFIEKIIYDVTVFED KKILRRRLKKEYDLDEEKIKKILKLKYSWGSRLSKKLLSGIKTKYKDSTR TPETVLEVMERTNMNLMQVINDEKLGFKKTIDDANSTSVSGKFSYAEVQ ELAGSPAIKRGIWQALLIVDEIKKIMKHEPAHVYIEFARNEDEKERKDSF VNQMLKLYKDYDFELETEKEANKHLKGEDAKSKIRSERLKLYYTQMG KCMYTGKSLDIDRLDTYQVDHIVPQSLLKDDSIDNKVLVLSSENQRKLD DLVIPSSIRNKMYGFWEKLFNNKIISPKKFYSLIKTEFNEKDQERFINRQIV ETRQITKHVAQIIDNHYENTKVVTVRADLSHQFRERYHIYKNRDINDFHH AHDAYIATILGTIYIGHRFESLDAKYIYGEYKRIFRNQKNKGKEMKKNNND GFILNSMRNIYADKDTGEIVWDPNYIDRIKKCFYKDCFVTKKLEENNG TFFNVTVLPNDTNSDKDNTLATVPVKNKYRSNVNKEYGGFSGVNSFIVA GKKKKGGKKVIEVNKLTGIPLMYKNADEEIKINYLKQAEDLEEYVQIGKEIL KNQLIEKDGGLYYIVAPTEIINAKQLILNESQTKLVCEIYKAMKYKNYDN LDSEKIIDLRLINKMELYYPEYRKQLVKKFEDRYEQLKVISIEEKCNI KQILATLHCNSSIGKIMYSDFKISTTIGRLNGRTISLDDISFIAESPTGMYSK KYKL (SEQ ID NO: 28)
EfCas9 <i>Enterococcus faecalis</i> NCBI Reference Sequence: WP_016631 044.1 Wild type	MRLFEEGHTAEDRRLKRTARRRISRRRNRLRYLQAFEEAMTDLDENFF ARLQESFLVPEDKKWHRHPIFAKLEDEVAYHETYPTIYHLRKKLADSSE QADLRLIYLALAHIVKYRGHFLIEGKLSTENTS VKDQFQQFMVIYNQTFV NGESRLVSAPLPESVLEEELTEKASRTKKSEKVLQQFPQEKANGLFGQF LKLMMVGNAADFKKVFGLEEEAKITYASESYEEDLEGILAKVGDEYSDVF LAAKNVYDAVELSTILADSDKKSHAKLSSSMIVRFTEHQEDLKKFKRFIR ENCPDEYDNLFKNEQKDG YAGYIAHAGKVSQKLFYQYVKKIQQDIAGAE YFLEKIAQENFLRKQRTFDNGVIPHQIHLAELQAIHRQAAYYPFLKENQE KIEQLVTFRIPIYVVGPLSKGDASTFAWLKRQSEPIRPWNLQETVDLDQS ATAFIERMTNFDTYLPSEKVLPHSLLYEKFMVFNELTKISYTD DRGIKA NFSGKEKEKIFDYLFKTRRKVKKKDIIQFYRNEYNTEIVTLGLEEDQFN ASFSTYQDLLKCGLTRAELDHPDNAEKLEDIIKILTFEDRQRIRTLSTFK GQFSAEVLKKLERKH YTGWRSLSKKLINGIYDKESGKTILDYLVKDDGV SKHYNRNFMQLINDSQLSFKNAIQKAQSSEHEETLSETVNELAGSPAIAIKK

Description	Sequence
	GIYQSLKIVDELVAIMGYAPKRIVVEMARENQTTSTGKRRSIQRLKIVEK AMAEIGSNLLKEQPTTNEQLRDTRLFLYYMQNGKDMYTGDLSLHRLS HYDIDHIIPQSFMKDDSLDNLVLVGSTENRGKSDDVPSKEVVKDMKAY WEKLYAAGLISQRKFQRLTKGEQGGTLLEDKAHFQIRQLVETRQITKNV AGILDQRYNAKSKEKKVQIITLKASLTSQFRSIFGLYKVREVNDYHHGQD AYLNCVVATTLLKVYPNLAPEFVYGEYPKFQTFKENKATAKAIITYNLL RFFTEDEPRFTKDGEILWSNSYLKTIKKELNYHQMNIVKKVEVQKGGFS KESIKPKGSPSNKLIPVKNGLDPQKYGGFDSPVVA YTVLFTHEKGKKPLIK QEILGITIMEKTRFEQNPILFLEEKGFLRPRVLMKLPKYTL YEFPEGRRRL LASAKEAQKGNQMVLPEHLLTLLYHAKQCLLPNQSESLAYVEQHQP QEILERVVDFAEVHTLAKSKVQQIVKLFEANQTADVKEIAASFIQLMQFN AMGAPSTFKFFQKDIERARYTSIKEIFDATIIYQSPTGLYETRRKVVD (SEQ ID NO: 29)
<i>Staphylococcus aureus</i> Cas9	KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKR GARRLKRRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKL SEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKY VAEQLERLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQLDQSF DTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSV KYAYNADLYNALNDLNNLVITRDENEKLEYEYEFQIENVFKQKKKPTL KQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIENAE LDQIAKILTIYQSSEDIQEELTNLNSLTQEEIEQISNLKGYTGTHNLSLKA NLILDELWHTNDNQIAIFNRLKLVKKVDLSQQKEIPTTLVDDFILSPVVK RSFIQSIKVINAIKKYGLPNDIIELAREKNSKDAQKMINEMQKRNRQTN ERIEEIIRTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNPNFY EVDHIIPRSVSFDNSFNKVLVKQEENSCKGNRTPFQYLSSSDSKISYETF KKHILNLA KGKGRISKTKKEYLLEERDINRFSVQKDFINRLVDTRYATR GLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHA EDALIANADFIKWKLDKAKKVMENQMFEKQAESMPEIETE QEYK EIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLLKLINKSPEKLLMYHHDPTQYQKLKLIMEQYGD KNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYP NSRNKVVKLSLKPYPFDVYLDNGVYKFVTVKNLDVIKKENY YEVNSKC YEEAKKKKISNQAEFIASFYNNDLIKINGEL YRVGVNNDLLNRIEVNMI DITYREYLENMNDKRPPRIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQ IIKKG (SEQ ID NO: 30)
<i>Geobacillus thermodenitificans</i> Cas9	MKYKIGLDIGITSIGWAVINLDIPRIEDLGVRIFDRAENPKTGESLALPRRL ARSARRRLRRRKHRLERIRRLFVREGILTKEELNKLFEKKHEIDVWQLRV EALDRKLNDELARILLHLAKRRGFRSNRK SERTNKENSTMLKHIEENQ SILSSYRTVAEMVVKDPKFSLHKRNKEDNYTNTVARDDLEREIKLIFAKQ REYGNIVCTEAFEHEYISIWASQRPFASKDDIEKKVGFCTFEPKEKRAPK ATYTFQSFTVWEHINKLRLVSPGGIRALTDDERRLIYKQAFHKNKITFHD VRTLLNLPDDTRFKGLLYDRNTTLKENEKVRFLELGAYHKIRKAIDSVY GKGAAKSFRPIDFDTFGYALTMFKDDTDIRS YLRNEYEQNGKR MENLA DKVYDEELIEELLNLSFSKFGHLSLKALRNILPYMEQGEVYSTACERAGY TFTGPKKKQKTVLLPNIPPIANPVVMRALTQARKVVNAIKKY GSPVSIHI ELARELSQSFDERRKMQKEQEGNRKKNETAIRQLVEYGLTLNPTGLDIV KFKLWSEQNGKCAYS LQPIEIERLLEPGYTEVDHVIPYSRSLDDSYTNKV LVLTKENREKGNRTPAEYLGLG SERWQQFETFVL TNKQFSKKKRDRLLR

Description	Sequence
	LHYDENEENEFKNRNLNDTRYISRFLANFIREHLKFADSDDKQKVYTVN GRITAHLSRWNFNKNREESNLHHA VDAAIVACTTPSDIARVTA FYQRR EQNKELSKKTDPPQFPQPWPHFADELQARLSKNPKESIKALNLGNYDNEK LESLQPVFVSRMPKRSITGA AHQETLRRYIGIDERSGKIQT VVKKKLSEIQ LDKTGHFPMY GKESDPRTYEAIRQRLLEHNNDPKKAFQEPLYKPKKNGE LGPIIRTIKIIDTTNQVIPLNDGKTVA YNSNIVRVDFEKGDKYYCVPIYTI DMMKGILPNKAIEPNKPYSEWKEMTEDYTFRFSLYPNDLIRIEFPREKTIK TAVGEEIKIKDLFAYYQTIDSSNGGLSLVSHDNNFSLRSIGSRTLKRFEKY QVDVLGNIYKVRGEKRVGVASSSHSKAGETIRPL (SEQ ID NO: 31)
ScCas9 <i>S. canis</i> 1375 AA 159.2 kDa	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLM GALLFDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKLDDSF FQRLEESFLVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPE KADRLIYLALAHIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEE SPLDEIEVDAKGILSARLSKSKRLEKLI AVFPNEKKNGLFGNIIALALGLTP NFKSNFDLTEDAKLQLSKD TYDDDLDEL LGQIGDQYADLFSAAKNLSDA ILLSDLRSNSEVTKAPLSASMVKRYDEHHQDLALLKTLVRQQFPEKYAE IFKDDTKNGYAGYVGIGIKHRKRTTKLATQEEFYKFIKPILEKMDGAEEL LAKLNRDDLLRKQRTFDNGSIPHQIHLKELHAILRRQEEFYFPLKENREKI EKILTFRIPIYYVGPLARGNSRFAWLTRKSEEAITPWNFEEVVDKGASAQ SIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNELTKVKYVTERMRKPEF LSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEIIGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYA HLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKSDGF SNRNFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIIKKGIL QTVKIVDELVKVMGHKPENIVIMARENQTTTKGLQQSRERKKRIEEGIK ELESQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDV DHIVPQSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLL NAKLITQRKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDS RMNTKRDKNDKPIREVKVITLKS KLVSDFRKDFQLYKVRDINNYHHAH DAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKAT AKRFFYSNIMNFFKTEVKLANGEIRKRPLIETNGETGEVVWNKEKDFAT VRKVLAMPQVNIVKKTEVQTGGFSKESILSKRESAKLIPRKKGWDRKY GGFGSPTVAYSILVVAKEKGKAKKLKSVKVLVGITIMEKGSYEKDPIGF LEAKGYKDIKKELIFKLPKYS LFELENGRRRMLASATELQKANELVLPQ HLVRLLYYTQNISATTGSNNLG YIEQHREEFKEIFEKIIDFSEKYILKNKV NSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFTFLDL DVKQGR LYQTVTEVL DATLIYQSITGLYETRTDLSQLGGD (SEQ ID NO: 32)

[0108] The genome editing system described herein may include any of the above Cas9

ortholog sequences, or any variants thereof having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

[0109] The napDNAbp may include any suitable homologs and/or orthologs or naturally occurring enzymes, such as, Cas9. Cas9 homologs and/or orthologs have been described in various species, including, but not limited to, *S. pyogenes* and *S. thermophilus*. Preferably, the Cas moiety is configured (e.g, mutagenized, recombinantly engineered, or otherwise

obtained from nature) as a nickase, i.e., capable of cleaving only a single strand of the target double-stranded DNA. Additional suitable Cas9 nucleases and sequences will be apparent to those of skill in the art based on this disclosure, and such Cas9 nucleases and sequences include Cas9 sequences from the organisms and loci disclosed in Chylinski, Rhun, and Charpentier, “The tracrRNA and Cas9 families of type II CRISPR-Cas immunity systems” (2013) RNA Biology 10:5, 726-737; the entire contents of which are incorporated herein by reference. In some embodiments, a Cas9 nuclease has an inactive (e.g., an inactivated) DNA cleavage domain, that is, the Cas9 is a nickase. In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 80% identical to the amino acid sequence of a Cas9 protein as provided by any one of the variants of Table 3. In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a Cas9 protein as provided by any one of the Cas9 orthologs in the above tables.

C. Dead Cas9 variant

[0110] In certain embodiments, the genome editing system described herein may include a dead Cas9, e.g., dead SpCas9, which has no nuclease activity due to one or more mutations that inactivate both nuclease domains of Cas9, namely the RuvC domain (which cleaves the non-protospacer DNA strand) and HNH domain (which cleaves the protospacer DNA strand). The nuclease inactivation may be due to one or more mutations that result in one or more substitutions and/or deletions in the amino acid sequence of the encoded protein, or any variants thereof having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto. As used herein, the term “dCas9” refers to a nuclease-inactive Cas9 or nuclease-dead Cas9, or a functional fragment thereof, and embraces any naturally occurring dCas9 from any organism, any naturally-occurring dCas9 equivalent or functional fragment thereof, any dCas9 homolog, ortholog, or paralog from any organism, and any mutant or variant of a dCas9, naturally-occurring or engineered. The term dCas9 is not meant to be particularly limiting and may be referred to as a “dCas9 or equivalent.” Exemplary dCas9 proteins and method for making dCas9 proteins are further described herein and/or are described in the art and are incorporated herein by reference. In other embodiments, dCas9 corresponds to, or comprises in part or in whole, a Cas9 amino acid sequence having one or more mutations that inactivate the Cas9 nuclease activity. In other embodiments, Cas9 variants having mutations other than D10A and H840A are provided which may result in the full or partial inactivation of the endogenous Cas9 nuclease activity.

(e.g., nCas9 or dCas9, respectively). Such mutations, by way of example, include other amino acid substitutions at D10 and H820, or other substitutions within the nuclease domains of Cas9 (e.g., substitutions in the HNH nuclease subdomain and/or the RuvC1 subdomain) with reference to a wild type sequence such as Cas9 from *Streptococcus pyogenes* (NCBI Reference Sequence: NC_017053.1 (SEQ ID NO: 14)). In some embodiments, variants or homologues of Cas9 (e.g., variants of Cas9 from *Streptococcus pyogenes* (NCBI Reference Sequence: NC_017053.1 (SEQ ID NO: 14))) are provided which are at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to NCBI Reference Sequence: NC_017053.1 (SEQ ID NO: 14). In some embodiments, variants of dCas9 (e.g., variants of NCBI Reference Sequence: NC_017053.1 (SEQ ID NO: 14)) are provided having amino acid sequences which are shorter, or longer than NC_017053.1 (SEQ ID NO: 14) by about 5 amino acids, by about 10 amino acids, by about 15 amino acids, by about 20 amino acids, by about 25 amino acids, by about 30 amino acids, by about 40 amino acids, by about 50 amino acids, by about 75 amino acids, by about 100 amino acids or more.

[0111] In one embodiment, the dead Cas9 may be based on the canonical SpCas9 sequence of Q99ZW2 and may have the following sequence, which comprises a D10X and an H810X, wherein X may be any amino acid, substitutions (underlined and bolded), or a variant be variant of SEQ ID NO: 11 having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

[0112] In one embodiment, the dead Cas9 may be based on the canonical SpCas9 sequence of Q99ZW2 and may have the following sequence, which comprises a D10A and an H810A substitutions (underlined and bolded), or be a variant of SEQ ID NO: 11 having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

Description	Sequence	SEQ ID NO:
dead Cas9 or dCas9	MDKKYSIGL X IGTNSVGWAVITDEYKVPSKKFKVLGNTD	SEQ ID NO: 33
<i>Streptococcus pyogenes</i> Q99ZW2	RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI	
Cas9 with D10 X and H810 X	CYLQEIFSNEMAKVDDSFHRLVESFLVEEDKKHERHPIF	
	GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRILIYAL	
	AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE	
	NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF	
	GNLIALSLGLTPNFKSFDLAEDAKLQLSKDITYDDDLN	
	LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS	
	ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN	
	GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE	

Description	Sequence	SEQ ID NO:
Where "X" is any amino acid	DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDXIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDENEQKQL FVEQHKHYLDEIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
dead Cas9 or dCas9 <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with D10A and H810A	MDKKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLLESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNFDAEDAKLQLSKD TYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDXIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD	SEQ ID NO: 34

Description	Sequence	SEQ ID NO:
	ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGITALIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEKKGSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	

D. Cas9 nickase variant

[0113] In one embodiment, the genome editing system described herein comprise a Cas9 nickase. The term “Cas9 nickase” or “nCas9” refers to a variant of Cas9 which is capable of introducing a single-strand break in a double strand DNA molecule target. In some embodiments, the Cas9 nickase comprises only a single functioning nuclease domain. The wild type Cas9 (e.g., the canonical SpCas9) comprises two separate nuclease domains, namely, the RuvC domain (which cleaves the non-protospacer DNA strand) and HNH domain (which cleaves the protospacer DNA strand). In one embodiment, the Cas9 nickase comprises a mutation in the RuvC domain which inactivates the RuvC nuclease activity. For example, mutations in aspartate (D) 10, histidine (H) 983, aspartate (D) 986, or glutamate (E) 762, have been reported as loss-of-function mutations of the RuvC nuclease domain and the creation of a functional Cas9 nickase (e.g., Nishimasu et al., “Crystal structure of Cas9 in complex with guide RNA and target DNA,” *Cell* 156(5), 935–949, which is incorporated herein by reference). Thus, nickase mutations in the RuvC domain could include D10X, H983X, D986X, or E762X, wherein X is any amino acid other than the wild type amino acid. In certain embodiments, the nickase could be D10A, or H983A, or D986A, or E762A, or a combination thereof. In various embodiments, the Cas9 nickase can having a mutation in the RuvC nuclease domain and have one of the following amino acid sequences, or a variant thereof having an amino acid sequence that has at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

Description	Sequence	SEQ ID NO:
Cas9 nickase	MDKKYSIGLXIGTNSVGWAVITDEYKVPSKKFKVLGNTD	SEQ ID NO: 35
<i>Streptococcus pyogenes</i> Q99ZW2	RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI	
Cas9 with D10X,	CYLQEIFSNEMAKVDDSFHRLSEFLVEEDKKHERHPIF	
	GNIVDEVAYHEKYPTIYHLRKKLV DSTDKADLR LIYLAL	
	AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE	
	NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF	
	GNLIALSLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLN	

Description	Sequence	SEQ ID NO:
wherein X is any alternate amino acid	LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASQAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVHDHVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with E762X, wherein X is any alternate amino acid	MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLDN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASQAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIXMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL	SEQ ID NO: 36

Description	Sequence	SEQ ID NO:
	DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLHQSITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with H983X, wherein X is any alternate amino acid	MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSSTKADLRILIYAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLRKKQRTFDNGSIPHQIHLGELHAILRRQEDFYPLKDN REKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMNTNFDKNLPNEKVLPHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKKIHKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEIEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYH X AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLHQSITGLYETRIDLSQLGGD	SEQ ID NO: 37

Description	Sequence	SEQ ID NO:
Cas9 nickase	MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGNTD	SEQ ID NO:
<i>Streptococcus pyogenes</i> Q99ZW2	RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI	38
Cas9 with D986X, wherein X is any alternate amino acid	CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRILIYAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKKIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHXAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase	MDKKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTD	SEQ ID NO:
<i>Streptococcus pyogenes</i> Q99ZW2	RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI	39
Cas9 with D10A	CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRILIYAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK	

Description	Sequence	SEQ ID NO:
	TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVM GRHKPENIVIEAMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with E762A	MDKKYSIGLDIGTNSVGWAVITDEYKVPSSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASQAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVM GRHKPENIVIA<u>M</u>ARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEV	SEQ ID NO: 40

Description	Sequence	SEQ ID NO:
	QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPI DFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with H983A	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASASQSIERMTNFDKNLPNEKVLPHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKKIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHA AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPI DFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	SEQ ID NO: 41
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with D986A	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKSNDLAEDAKLQLSKDTYDDDLN	SEQ ID NO: 42

Description	Sequence	SEQ ID NO:
	LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEAMARENQTTQKGQKNSRERMKRIEIGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVL DATLIHQSI TGLYETRIDLSQLGGD	

[0114] In another embodiment, the Cas9 nickase comprises a mutation in the HNH domain which inactivates the HNH nuclease activity. For example, mutations in histidine (H) 840 or asparagine (R) 863 have been reported as loss-of-function mutations of the HNH nuclease domain and the creation of a functional Cas9 nickase (e.g., Nishimasu et al., “Crystal structure of Cas9 in complex with guide RNA and target DNA,” *Cell* 156(5), 935–949, which is incorporated herein by reference). Thus, nickase mutations in the HNH domain could include H840X and R863X, wherein X is any amino acid other than the wild type amino acid. In certain embodiments, the nickase could be H840A or R863A or a combination thereof.

[0115] In various embodiments, the Cas9 nickase can have a mutation in the HNH nuclease domain and have one of the following amino acid sequences, or a variant thereof having an amino acid sequence that has at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

Description	Sequence	SEQ ID NO:
Cas9 nickase	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI	SEQ ID NO: 43

Description	Sequence	SEQ ID NO:
<i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with H840 <u>X</u> , wherein X is any alternate amino acid	CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIASLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVD <u>X</u> IVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKQQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSEFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVILADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with H840 <u>A</u>	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIASLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKIIKDKDFLDNEENEDILEDIVLTTLTLFEDREMIEE	SEQ ID NO: 44

Description	Sequence	SEQ ID NO:
	RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVD <u>A</u> IVPQSFLKDDSIDNKVLTRSDKNRGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPI DFLEAKGYKEVKKDLIIKLPKYSLEENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLKGSPEDEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVLDTLIHQSIITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus</i> <i>pyogenes</i> Q99ZW2 Cas9 with R863X, wherein X is any alternate amino acid	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFSNEMAKVDDSFHRLSEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLV DSTDKADRLIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLF GNLIASLGLTPNFKS NFDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLEPKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASQAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDLKKIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPAIIKGILQTVKVVDELVKVM GRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDV D HIVPQSFLKDDSIDNKVLTRSDKN <u>X</u> GKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVLSPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTV AYSVLVVAKEVGKSKKLKSVKELLGITIMERSSSFENPI	SEQ ID NO: 45

Description	Sequence	SEQ ID NO:
	DFLEAKGYKEVKKDLIIKLPKYSLEFLENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVL DATLIHQ SITGLYETRIDLSQLGGD	
Cas9 nickase <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with R863A	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTD RHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRI CYLQEIFS NEMAKVDDSFHRLEESFLVEEDKKHERHPIF GNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLR LIYLAL AHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEE NPINASGVDAKAILSARLSKSRRLLENLIAQLPGEKKNGLF GNLIALSLGLTPNFKS NFDLAEDAKLQLSKD TYDDDLN LLAQIGDQYADLFLAAKNLSDAILSDILRVNTEITKAPLS ASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNRE DLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDN REKIEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPW NFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLY EYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFK TNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT YHDL LKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRD KQSGKTILDFLKSDGFANRNF MQLIHDDSLTFKEDIQKAQ VSGQGDSLHEHIANLAGSPA IKKGILQTVKVVDELVKVM GRHKPENIV IEMARENQTTQKGQKNSRERMKRIEEGIKE LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQEL DINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNAGKS DNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKS KLVSDFRKDFQFYKVREINNYHH AHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRK MIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRP LIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWD PKKYGGFDSPTV AYSVLVVAKVEKGKSKKLKSVKELLGITIMERS SFEKNPI DFLEAKGYKEVKKDLIIKLPKYSLEFLENGRKRMLASAG ELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQL FVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTS TKEVL DATLIHQ SITGLYETRIDLSQLGGD	SEQ ID NO: 46

[0116] In some embodiments, the N-terminal methionine is removed from a Cas9 nickase, or from any Cas9 variant, ortholog, or equivalent disclosed or contemplated herein. For example, methionine-minus Cas9 nickases include the following sequences, or a variant thereof having an amino acid sequence that has at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

Description	Sequence
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Cas9 nickase (Met minus)	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSF FHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV DST
<i>Streptococcus pyogenes</i> Q99ZW2	DKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQ LFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIAL SLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLNLLAQIGDQYADLFLA
Cas9 with H840 <u>X</u> , wherein X is any alternate amino acid	AKNLS DAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELL VKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDNREK IEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEVVVDKGASA QSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMR KPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILD FLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAG SPAIKKGILQTVKVVDLKVVMGRHKPENIVIEMARENQTTQKGQKNS RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYV DQELDINRLSDYDVD <u>X</u> IVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKR QLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR KDFQFYKVREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYK VYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIE TNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEVQTGGFSKESILP KRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEVGKSKKLLK SVKELLGITIMERSSEKNPIDFLEAKGYKEVKKDLIILPKYSLFELEN GRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQK QLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKH RDKPIRE QAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQ SITG LYETRIDLSQLGGD (SEQ ID NO: 47)
Cas9 nickase (Met minus)	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSF FHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV DST
<i>Streptococcus pyogenes</i> Q99ZW2	DKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQ LFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIAL SLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLNLLAQIGDQYADLFLA
Cas9 with H840 <u>A</u>	AKNLS DAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELL VKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDNREK IEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEVVVDKGASA QSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMR KPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTTLTFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILD FLKSDGFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAG SPAIKKGILQTVKVVDLKVVMGRHKPENIVIEMARENQTTQKGQKNS RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYV DQELDINRLSDYDVD <u>A</u> IVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKR QLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR KDFQFYKVREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYK

	VYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIE TNGETGEIVWDKGRDFATVRKVLSPQVNVIVKKTEVQTGGFSKESILP KRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEVEGKSKKLK SVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIILPKYSLFELEN GRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQK QLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKHHRDKPIRE QAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITE LYETRIDLSQLGGD (SEQ ID NO: 48)
Cas9 nickase (Met minus) <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with R863X, wherein X is any alternate amino acid	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEAKVDDSF FHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDST DKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQ LFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIAL SLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLNLLAQIGDQYADFLA AKNLSAAILSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELL VKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREK IEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEVVDKGA QSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMR KPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILD FLKSDGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAG SPAIIKGILQTVKVVDLKVLMGRHKPENIVIEMARENQTTQKGQKNS RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYV DQELDINRLSDYDVHIVPQSFLKDDSIDNKVLTRSDKNXGKSDNVPS EEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKR QLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR KDFQFYKVINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYK VYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIE TNGETGEIVWDKGRDFATVRKVLSPQVNVIVKKTEVQTGGFSKESILP KRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEVEGKSKKLK SVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIILPKYSLFELEN GRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQK QLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSAYNKHHRDKPIRE QAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITE LYETRIDLSQLGGD (SEQ ID NO: 49)
Cas9 nickase (Met minus) <i>Streptococcus pyogenes</i> Q99ZW2 Cas9 with R863A	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIG ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEAKVDDSF FHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDST DKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQ LFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFGNLIAL SLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLNLLAQIGDQYADFLA AKNLSAAILSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELL VKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREK IEKILTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEVVDKGA QSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMR KPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVE DRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEE

	RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILD FLKSDGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAG SPAIKKGILQTVKVVDLVKVMGRHKPENIVIEMARENQTTQKGQKNS RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYV DQELDINRLSDYDVHIVPQSFLKDDSIDNKVLTRSDKNAGKSDNVPS EEVVKMKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDAKAGFIKR QLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR KDFQFYKVRINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYK VYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIE TNGETGEIVWDKGRDFATVRKVLSPQVNVKKTEVQTGGFSKESILP KRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEKGKSKKLK SVKELLGITIMERSSEKKNPIDFLEAKGYKEVKKDLIIKLPKYSLELEN GRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQK QLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYNKHDKPIRE QAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITE LYETRIDLSQLGGD (SEQ ID NO: 50)
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E. Other Cas9 variants

[0117] Besides dead Cas9 and Cas9 nickase variants, the Cas9 proteins used herein may also include other “Cas9 variants” having at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to any reference Cas9 protein, including any wild type Cas9, or mutant Cas9 (e.g., a dead Cas9 or Cas9 nickase), or fragment Cas9, or circular permutant Cas9, or other variant of Cas9 disclosed herein or known in the art. In some embodiments, a Cas9 variant may have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50 or more amino acid changes compared to a reference Cas9. In some embodiments, the Cas9 variant comprises a fragment of a reference Cas9 (e.g., a gRNA binding domain or a DNA-cleavage domain), such that the fragment is at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to the corresponding fragment of wild type Cas9. In some embodiments, the fragment is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, 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% identical, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% of the amino acid length of a corresponding wild type Cas9 (e.g., SEQ ID NO: 11).

[0118] In some embodiments, the disclosure also may utilize Cas9 fragments which retain their functionality and which are fragments of any herein disclosed Cas9 protein. In some embodiments, the Cas9 fragment is at least 100 amino acids in length. In some embodiments, the fragment is at least 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, or at least 1300 amino acids in length.

[0119] In various embodiments, the genome editing system disclosed herein may comprise one of the Cas9 variants described as follows, or a Cas9 variant thereof having at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to any reference Cas9 variants.

F. Small-sized Cas9 variants

[0120] In some embodiments, the genome editing system contemplated herein can include a Cas9 protein that is of smaller molecular weight than the canonical SpCas9 sequence. In some embodiments, the smaller-sized Cas9 variants may facilitate delivery to cells, e.g., by an expression vector, nanoparticle, or other means of delivery. In certain embodiments, the smaller-sized Cas9 variants can include enzymes categorized as type II enzymes of the Class 2 CRISPR-Cas systems. In some embodiments, the smaller-sized Cas9 variants can include enzymes categorized as type V enzymes of the Class 2 CRISPR-Cas systems. In other embodiments, the smaller-sized Cas9 variants can include enzymes categorized as type VI enzymes of the Class 2 CRISPR-Cas systems.

[0121] The canonical SpCas9 protein is 1368 amino acids in length and has a predicted molecular weight of 158 kilodaltons. The term “small-sized Cas9 variant”, as used herein, refers to any Cas9 variant—naturally occurring, engineered, or otherwise—that is less than at least 1300 amino acids, or at least less than 1290 amino acids, or than less than 1280 amino acids, or less than 1270 amino acid, or less than 1260 amino acid, or less than 1250 amino acids, or less than 1240 amino acids, or less than 1230 amino acids, or less than 1220 amino acids, or less than 1210 amino acids, or less than 1200 amino acids, or less than 1190 amino acids, or less than 1180 amino acids, or less than 1170 amino acids, or less than 1160 amino acids, or less than 1150 amino acids, or less than 1140 amino acids, or less than 1130 amino acids, or less than 1120 amino acids, or less than 1110 amino acids, or less than 1100 amino acids, or less than 1050 amino acids, or less than 1000 amino acids, or less than 950 amino acids, or less than 900 amino acids, or less than 850 amino acids, or less than 800 amino

acids, or less than 750 amino acids, or less than 700 amino acids, or less than 650 amino acids, or less than 600 amino acids, or less than 550 amino acids, or less than 500 amino acids, but at least larger than about 400 amino acids and retaining the required functions of the Cas9 protein. The Cas9 variants can include those categorized as type II, type V, or type VI enzymes of the Class 2 CRISPR-Cas system.

[0122] In various embodiments, the genome editing system disclosed herein may comprise one of the small-sized Cas9 variants described as follows, or a Cas9 variant thereof having at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to any reference small-sized Cas9 protein.

Description	Sequence	SEQ ID NO:
SaCas9 <i>Staphylococcus aureus</i> 1053 AA 123 kDa	MGKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEA NVENNEGRRSKRGARRLKRRRRHRIQRVKKLLFDYNLL TDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRG VHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLE RLKKDGEVRGSINRFKTSYVKEAKQLLKVQKAYHQLD QSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEML MGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDE NEKLEYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIK GYRVTSTGKPEFTNLKVYHDIKDITARKEIENAELLDQIA KILTIYQSSEDIQEELTNLNSLTQEEIEQISNLKGYTGTHN LSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQK EIPTTLVDDFILSPVVKRSFIQSIKVINAIKKYGLPNDIIE AREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENA KYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDH IIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQYLSSSDS KISYETFKKHILNLAAGKGRISKTKKEYLLEERDINRFSV QKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKS I NGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFI F KEWKKLDKAKKVMENQMFEKQAESMPEIETEQEYKEI FITPHQIKHIKDFKDYKYSHRVDKKNRKLINDTLYSTRK DDKGNTLIVNNLNGLYDKDNDKLKLINKSPEKLLMYH HDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYS KKDNGPVIKKIKYYGNKLNAHLDDYDYPNSRNKVVKLS LKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKC YEEAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNN DLLNRIEVMIDITYREYLENMNDKRPPHIIKTIASKTQSI KKYSTDILGNLYEVKSKKHPQIIKK	SEQ ID NO: 51
NmeCas9 <i>N. meningitidis</i>	MAAFKPNSINYILGLDIGIASVGWAMVEIDEEENPIRLIDL GVRVFERAEPKTGDSLAMARRLARSVRRLTRRRRAHRL LRTRRLKREGVLQAANFDENGLIKSLPNTPWQLRAAAL DRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELGA LLKGVAGNAHALQTGDFRTPAELALNKFESGHIRNQR	SEQ ID NO: 52

Description	Sequence	SEQ ID NO:
1083 AA 124.5 kDa	SDYSHTFSRKDLQAELILLFEKQKEFGNPHVSGGLKEGIE TLLMTQRPALSGDAVQKMLGHCTFEPAEPKAAKNTYTA ERFIWLTCLNNLRILEQGSRPLTDTTERATLMDEPYRKS LTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKA YHAISRALEKEGLKDKKSPLNLSPELQDEIGTAFSLFKTD EDITGRLKDRIQPEILEALLKHISFDKFVQISLKALRRIVPL MEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIR NPVVLRAALSQARKVINGVVRRYGSPARIHIETAREVGKSF KDRKEIEKRQEENRKDREKAAAKFREYFPNFVGEPSKD ILKLRLYEQQHGKCLYSGKEINLGRLENEKGYVEIDAALPF SRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSR EWQEFKARVETSRFPRSKKQRILLQKFDEDEGFKERNLND TRYVNRFLCQFVADRMRLTGKGKKRVFASNGQITNLLR GFWGLRKVRAENDRHHALDAVVVACSTVAMQQKITRF VRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQE VMIRVFGKPDGKPEFEEADTLEKLRTLLAEKLSSRPEAVH EYVTPLFVSRAPNRKMSGQGHMETVKSARKLDEGVSVL RVPLTQLKLDLEKMNREREPPLYEALKARLEAHKDD PAKAFAPFYKYDKAGNRTQQVKAVRVEQVQKTGVWV RNHNGIADNATMVRVDVFEKGDKYYLVPIYSWQVAKGI LPDRAVVQGKDEEDWQLIDDSFNFKFSLHPNDLVEVITK KARMFYGFASCHRGTTGNINIRIHDLDHKIGKNGILEGIGV KTALSFKYQIDELGKEIRPCRLKKRPPVR	
CjCas9 <i>C. jejuni</i> 984 AA 114.9 kDa	MARILAFDIGISSIGWAFSENDELKDCGVRIFTKVENPKT GESLALPRRLARSARKRLARRKARLNHLKHLIANEFKLN YEDYQSFDSESLAKAYKGSLSIPYELRFRALNELLSKQDFA RVILHIAKRRGYDDIKNSDDKEKGAILKAIKQNEEKLAN YQSVGEYLYKEYFQKFKEKSKEFTNVRNKKESYERCIAQ SFLKDELKLIFKKQREFGFSFSKKFEEVLSVAFYKRALK DFSHLVGNCSFFTDEKRAPKNSPLAFMFVALTRIINLLNN LKNTGILYTKDDLNALLNEVLKNGTLTYKQTKKLLGLS DDYEFKGEKGTIFYEFKKYKEFIKALGEHNLSQDDLNEIA KDITLIKDEIKLKKALAKYDLNQNQIDSLSKLEFKDHLNIS FKALKLVTPLMLEGKKYDEACNELNLKVAINEDKKDFLP AFNETYYKDEVTPNPVVLRAIKEYRKVLNALLKKYGVH KINIELAREVGKNHSQRAKIEKEQNENYKAKKDAELECE KLGLKINSKNILKLRLFKEQKEFCAYSGEKIKISDLQDEK MLEIDHIYPYSRFSFDDSYMKNKVLVFTKQNQEKLNQTPFE AFGNDSAKWQKIEVLAKNLPTKKQKRILDKNYKDKEQK NFKDRNLNDTRYIARLVNLYTKDYLDLPLSDDENTKLN DTQKGSKVHVEAKSGMLTSALRHTWGFSKDRNNHLH HAIDAVIIAYANNSIVKAFSDFKKEQESNSAELYAKKISEL DYKNKRKFFEPFSGFRQKVLDKIDEIFVSKPERKKPSGAL HEETFRKEEFYQSYGGKEGVLKALELGKIRKVNKGIVK NGDMFRVDIFKHKKTNKFYAVPIYTMDFALKVLPNKAV ARSKKGEIKDWILMDENYEFCSLYKDSLILIQTKDMQEP EFVYYNAFTSSTVSLIVSKHDNKFETLSKNQKILFKNANE KEVIAKSIGIQNLKVFEKYIVSALGEVTKAEFRQREDFKK	SEQ ID NO: 53

Description	Sequence	SEQ ID NO:
GeoCas9	MRYKIGLDIGITSVGWAVMNLDIPRIEDLGVRIFDRAENP QTGESLALPRRLARSARRRLRRRKHRLERIRRLVIREGILT KEELDKLFEEKHEIDVWQLRVEALDRKLNDELARVLL HLAKRRGFKSNRKSERSNKENSTMLKHIEENRAILSSYRT VGEMIVKDPKFALHKRNGENYNTNTIARDDLREIRLIFS KQREFGNMSCTEEFENEYITIWASQRPVASKDDIEKKVGF CTFEPKEKRAPKATYTFQSFIWEHINKLRLISPSGARGLT DEERRLLYEQAFQKNKITYHDIRTLLHLPDDTYFKGIVYD RGESRKQENIRFLELDAYHQIRKAVDKVYGKGKSSSFL PIDFDTFGYALTFLKDDADIHSYLRNEYEQNGKRMPNLA NKVYDNELIEELLNLSFTKFGHLSLKALRSILPYMEQGEV YSSACERAGYTFTGPKKKQKTMLLPNIPPIANPVVMRAL TQARKVVNAIIKKYGPVSIHIELARDLSQTFDERRKTKK EQDENRKKNETAIRQLMEYGLTLNPTGHDIVKFKLWSEQ NGRCAYSLQPIEIERLLEPGYVEVDHVIPYSRSLDDSYTN KVLVLTRENREKGNRIPAEYLGVGTERWQQFETFVLTNK QFSKKKRDRLLRLHYDENEETEFKNRNLNDTRYISRFFA NFIREHLKFAESDDKQKVYTVNGRVT AHLRSRWEFNKN REESDLHHA VDAVIVACTTPSDIAKVTA FYQRREQNKEL AKKTEPHFPQPWPHFADELRARLSKHPKESIKALNLGNY DDQKLESLQPVFVSRMPKRSVTGA AHQETLRRYVGIDER SGKIQT VVKTKLSEIKLDASGHFPMY GKESDPRTYE AIRQ RLLEHNNDPKKAFQEPLYKPKKNGEPGPVIRTVKIIDTKN QVIPLNDGKTVA YNSNIVRVDFEKGDKYYCVPVYTMD IMKGILPNKAIEPNKPYSEWKEMTEDYTFRFSLYPNDLIRI ELPREKTVKTAAGEEINVKDV FVYYKTIDSANGGLELISH DHRFSLRGVGSRTLKRFEKYQVDVLGNIYKVRGEKRVG LASSAHSKPGKTIRPLQSTRD	SEQ ID NO: 54
<i>G. stearothermophilus</i>		
1087 AA 127 kDa		
LbaCas12a	MSKLEKFTNCYSLSKTLRFKAIPVGKTQENIDNKRLLED EKRAEDYKGVKKLLDRYLSFINDVLHSIKLKNLNNYIS LFRKKTRTEKENKELENLEINLRKEIAKAFKGNEGYKSLF KKDIIETILPEFLDDKDEIALVNSFNGFTTAFTGFFDNREN MFSEEAKSTSIAFRCINENLTRYISNMDIFEKVDAIFDKHE VQEIKEKILNSDYDVEDFFEGEFFNFVLTQEGIDVYNAIIG GFVTESGEKIKGLNEYINLYNQKTKQKLPKFKPLYKQVL SDRESLSFYGEGYTSDEEVLEVFRNTLNKNSEIFSSIKKLE KLKKNFDEYSSAGIFVKNGPAISTISKDIFGEWNVIRDKW NAEYDDIHLKKKAVVTEKEYEDDRKSFKKIGSFSLEQLQ EYADADLSVVEKLKEIIQKVDEIYKVYGSSEKLFDAFV LEKSLKKND AVVAIMKDLLDSVKS FENYIKAFFGEGKET NRDES FYGDFV LAYDILLKVDHIYDAIRNYVTQKPYSKD KFKLYFQNPQFMGGWDKDKETDYRATILRYGSKYYLAI MDKKYAKCLQKIDKDDVNGNYEKINYKLLPGPNKMLPK VFFSKKWMAYYNPSEDIQKIYKNGTFKKGDMFNLNDCH KLIDFFKDSISRYPKWSNAYDFNFSETEKYKDIAGFYREV EEQGYKVSFESASKKEVDKLVEEGKLYMFQIYNKDFSDK SHGTPNLHTMYFKLLFDENN H GQIRLSGGAELFMRRASL KKEELV VHPANSPIANKNPDPKKT T TSLSYDVYKDKRFS EDQYELHIPIAINKCPKNIFKINTEVRVLLKHDDNPYVIGI	SEQ ID NO: 55
<i>L. bacterium</i>		
1228 AA 143.9 kDa		

Description	Sequence	SEQ ID NO:
	DRGERNLLYIVVVDGKGNIVEQYSLNEIINNFNNGIRIKTD YHSLDDKKEKERFEARQNWTSIENIKELKAGYISQVVHKI CELVEKYDAVIALEDLNSGFKNSRVKVEKQVYQKFEKM LIDKLNMYVDKKSNPCATGGALKGYQITNKFESFKSMST QNGFIFYIPAWLTSKIDPSTGFVNLLKTKYTSIADSKKFIS FDRIMYVPEEDLFEFALDYKNFSRTDADYIKKWKLYSYG NRIRIFRNPKNNVFDWEEVCLTSAYKELFNKYGINYQQ GDIRALLCEQSDKAFYSSFMALMSLMLQMRNSITGRTDV DFLISPVKNSDGIFYDSRNYEAQENAILPKNADANGAYNI ARKVLWAIGQFKKADEKLDKVKIAISNKEWLEYAQT SKH	
BhCas12b <i>B. hisashii</i> 1108 AA 130.4 kDa	MATRSFILKIEPNEEVKKGLWKTHEVLNHGIAYYMNILK LIRQEAIYEHHEQDPKNPKKVSKEIQAEWDFVLKMQK CNSFTHEVDKDEVFNILRELYEELVPSSVEKKGEANQLSN KFLYPLVDPNSQSGKGTASSGRKPRWYNLKIAGDPSWEE EKKKWEEDKKKDPKILGKLAEYGLIPLFIPYTDSEPI VKEIKWMEKSRNQSVRRDKDMFIQALERFLSWESWNL KVKEEYKVEKEYKTLEERIKEDIQALKALEQYKERQE QLLRDTLNTNEYRLSKRGLRGWREIIQKWLKMDENEPSE KYLEVFKDYQRKHPREAGDYSVYEFLSKKENHFIWRNH PEYPYLYATFCEIDKKKKDAKQATFTLADPINHPLWVR FEERSGSNLNKYRILTEQLHTEKLKKKLTVQLDRLIYPT SGGWEEKGKVDIVLLPSRQFYNQIFLDIEEKGKHAFTYK DESIKFPKGTLLGGARVQFDRDHLRRYPHKVESGNVGR YFNMTVNIEPTESPVSKSLKIHRDDFPKVVNFKPKELTEW IKDSKGGKKLKSIESLEIGLRVMSIDLGQRQAAAASIFEV VDQKPDIEGKLFPIKGTLEYAVHRASFNIKLPGETLVKS REVLKAREDNLKL MNQKLNFLRNVLHFQQFEDITEREK RVTKWISRQENS DVPLVYQDELIQIRELMYKPYKDWVAF LKQLHKRLEVEIGKEVKHWRKSLSDGRKGLYGISLKNID EIDRTRKFLLRWSLRPTEPGEVRRLEPGQRFAIDQLNHLN ALKEDRLKKMANTIIMHALGYCYDVRKKKWQAKNPAC QIILFEDLSNYPYEERSRFENSKLMKWSRREIPRQVALQ GEIYGLQVGEVGAQFSSRFHAKTGSPGIRCSVVTKEKLQ DNRFFKNLQREGRLTLDKIAVLKEGDLYPDKGGEKFISLS KDRKCVTTHADINAAQNLQKRFWTRTHGFYKVYCKAY QVDGQTVYIPESKDQKQKIIIEFGEGYFILKDGVEYEWVN AGKLKIKKGSSKQSSSELVDSILKDSFDLASELKGEKLM LYRDPNGNVFSPDKWMAAGVFFGKLERILISKLTNQYSIS TIEDSSKQSM	SEQ ID NO: 56

G. Cas9 equivalents

[0123] In some embodiments, the genome editing system described herein can include any Cas9 equivalent. As used herein, the term “Cas9 equivalent” is a broad term that encompasses any nDNA protein that serves the same function as Cas9 in the present genome editing system despite that its amino acid primary sequence and/or its three-

dimensional structure may be different and/or unrelated from an evolutionary standpoint. Thus, while Cas9 equivalents include any Cas9 ortholog, homolog, mutant, or variant described or embraced herein that are evolutionarily related, the Cas9 equivalents also embrace proteins that may have evolved through convergent evolution processes to have the same or similar function as Cas9, but which do not necessarily have any similarity with regard to amino acid sequence and/or three dimensional structure. The genome editing system described here embrace any Cas9 equivalent that would provide the same or similar function as Cas9 despite that the Cas9 equivalent may be based on a protein that arose through convergent evolution. For instance, if Cas9 refers to a type II enzyme of the CRISPR-Cas system, a Cas9 equivalent can refer to a type V or type VI enzyme of the CRISPR-Cas system.

[0124] For example, Cas12e (CasX) is a Cas9 equivalent that reportedly has the same function as Cas9 but which evolved through convergent evolution. Thus, the Cas12e (CasX) protein described in Liu et al., “CasX enzymes comprises a distinct family of RNA-guided genome editors,” *Nature*, 2019, Vol.566: 218-223, is contemplated to be used with the genome editing system described herein. In addition, any variant or modification of Cas12e (CasX) is conceivable and within the scope of the present disclosure.

[0125] Cas9 is a bacterial enzyme that evolved in a wide variety of species. However, the Cas9 equivalents contemplated herein may also be obtained from archaea, which constitute a domain and kingdom of single-celled prokaryotic microbes different from bacteria.

[0126] In some embodiments, Cas9 equivalents may refer to Cas12e (CasX) or Cas12d (CasY), which have been described in, for example, Burstein et al., “New CRISPR–Cas systems from uncultivated microbes.” *Cell Res.* 2017 Feb 21. doi: 10.1038/cr.2017.21, the entire contents of which is hereby incorporated by reference. Using genome-resolved metagenomics, a number of CRISPR–Cas systems were identified, including the first reported Cas9 in the archaeal domain of life. This divergent Cas9 protein was found in little-studied nanoarchaea as part of an active CRISPR–Cas system. In bacteria, two previously unknown systems were discovered, CRISPR–Cas12e and CRISPR–Cas12d, which are among the most compact systems yet discovered. In some embodiments, Cas9 refers to Cas12e, or a variant of Cas12e. In some embodiments, Cas9 refers to a Cas12d, or a variant of Cas12d. It should be appreciated that other RNA-guided DNA binding proteins may be used as a nucleic acid programmable DNA binding protein (napDNAbp), and are within the scope of this disclosure. Also see Liu et al., “CasX enzymes comprises a distinct family of

RNA-guided genome editors,” *Nature*, 2019, Vol.566: 218-223. Any of these Cas9 equivalents are contemplated.

[0127] In some embodiments, the Cas9 equivalent comprises an amino acid sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to a naturally-occurring Cas12e (CasX) or Cas12d (CasY) protein. In some embodiments, the napDNAbp is a naturally-occurring Cas12e (CasX) or Cas12d (CasY) protein. In some embodiments, the napDNAbp comprises an amino acid sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to a wild-type Cas moiety or any Cas moiety provided herein.

[0128] In various embodiments, the nucleic acid programmable DNA binding proteins include, without limitation, Cas9 (*e.g.*, dCas9 and nCas9), Cas12e (CasX), Cas12d (CasY), Cas12a (Cpf1), Cas12b1 (C2c1), Cas13a (C2c2), Cas12c (C2c3), Argonaute, , and Cas12b1. One example of a nucleic acid programmable DNA-binding protein that has different PAM specificity than Cas9 is Clustered Regularly Interspaced Short Palindromic Repeats from *Prevotella* and *Francisella* 1 (*i.e.*, Cas12a (Cpf1)). Similar to Cas9, Cas12a (Cpf1) is also a Class 2 CRISPR effector, but it is a member of type V subgroup of enzymes, rather than the type II subgroup. It has been shown that Cas12a (Cpf1) mediates robust DNA interference with features distinct from Cas9. Cas12a (Cpf1) is a single RNA-guided endonuclease lacking tracrRNA, and it utilizes a T-rich protospacer-adjacent motif (TTN, TTTN, or YTN). Moreover, Cpf1 cleaves DNA via a staggered DNA double-stranded break. Out of 16 Cpf1-family proteins, two enzymes from *Acidaminococcus* and *Lachnospiraceae* are shown to have efficient genome-editing activity in human cells. Cpf1 proteins are known in the art and have been described previously, for example Yamano *et al.*, “Crystal structure of Cpf1 in complex with guide RNA and target DNA.” *Cell* (165) 2016, p. 949-962; the entire contents of which is hereby incorporated by reference.

[0129] In still other embodiments, the Cas protein may include any CRISPR associated protein, including but not limited to, Cas12a, Cas12b1, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas10, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, homologs thereof, or modified versions thereof, and preferably

comprising a nickase mutation (e.g., a mutation corresponding to the D10A mutation of the wild type Cas9 polypeptide of SEQ ID NO: 11).

[0130] In various other embodiments, the napDNAbp can be any of the following proteins: a Cas9, a Cas12a (Cpf1), a Cas12e (CasX), a Cas12d (CasY), a Cas12b1 (C2c1), a Cas13a (C2c2), a Cas12c (C2c3), a GeoCas9, a CjCas9, a Cas12g, a Cas12h, a Cas12i, a Cas13b, a Cas13c, a Cas13d, a Cas14, a Csn2, an xCas9, an SpCas9-NG, a circularly permuted Cas9, or an Argonaute (Ago) domain, or a variant thereof.

[0131] Exemplary Cas9 equivalent protein sequences can include the following:

Description	Sequence
AsCas12a (previously known as Cpf1)	MTQFEGFTNLYQVSKTLRFELIPQGKTLKHIQEQGFIEEDKARNDHYKEL KPIIDRIYKTYADQCLQLVQLDWENLSAAIDSYRKEKTEETRNLALIEEQA TYRNAIHDYFIGRTDNLDAINKRHAIEYKGLFKAELFNGKVLKQLGTV TTTEHENALLRSFDKFTTYFSGFYENRKNVFSADISTAIPHRIVQDNFPK FKENCHIFTRLITA VPSLREHFENVKKAIGIFVSTSIEEVFSFPFYNQLLTQ
<i>Acidaminococcus</i> <i>sp.</i> (strain BV3L6)	TQIDLYNQLLGGISREAGTEKIKGLNEVLNLAIQKNDETAHIIASLPHRFIP LFKQILSDRNTLSFILEEFKSDEEVIQSFCYKKTLLRNENVLETAEALFNE LNSIDLTHIFISHKKLETISSALCDHWDTLRNALYERRISELTGKITKSAKE KVQRSLKHEDINLQEIIAAGKELSEAFKQKTSEILSHAHAAALDQPLPTTL KKQEEKEILKSQLDSSLGLYHLLDWFAVDESNEVDPEFSARLTGIKLEM
UniProtKB U2UMQ6	EPSLSFYNKARNYATKKPYSVEKFKLNFQMPTLASGWDVNKEKNNGAI LFVKNGLYYLGIMPKQKGRYKALSFEPTSEKTSSEGFDMYYDYFPDAK MIPKCSTQLKAVTAHFQTHTPILLSNNFIEPLEITKEIYDLNNPEKEPKKF QTAYAKKTGDQKGYREALCKWIDFTRDFLSKYTKTTSIDLSSLRPSSQY KDLGEYYAELNPLLYHISFQRIAEKEIMDAVETGKLYLFQIYNKDFAKG HHGKPNLHTLYWTGLFSPENLAKTSIKLNGQAELFYRPKSRMKRMAHR LGEKMLNKKLKDQKTPIDTLYQELYDYVNHRLSHDLSDEARALLPNVI TKEVSHEIHKDRRFTSDKFFFHVPITLNYQAANSPSKFNQVRVNAYLKEHP ETPIIGIDRGERNLIYITVIDSTGKILEQRSNTIQQFDYQKKLDNREKERV AARQAWSVVGTIKDLKQGYLSQVIHEIVDLMIHQAVVLENLNFQFK SKRTGIAEKAVYQQFEKMLIDKLNCLVLKDYPAEKVGGVLNPPYQLTDQ FTSFAKMGTQSGFLFYVPAPYTSKIDPLTGFVDPFVWKTIKNHESRKHFL EGFDLHYDVKTGDFILHFKMNRNLSFQRGLPGFMPAWDIVFEKNETQF DAKGTPFIAGKRIVPVIENTHRFTGRYRDLYPANELIALLEEKGIVFRDGSN ILPKLLENDSSHAIDTMVALIRSVLQMRNSNAATGEDYINSPVRDLNGV CFDSRFQNPWPMDADANGAYHIALKGQLLLNHLKESKDLKLQNGISN QDWLAYIQELRN (SEQ ID NO: 57)
AsCas12a nickase (e.g., R1226A)	MTQFEGFTNLYQVSKTLRFELIPQGKTLKHIQEQGFIEEDKARNDHYKEL KPIIDRIYKTYADQCLQLVQLDWENLSAAIDSYRKEKTEETRNLALIEEQA TYRNAIHDYFIGRTDNLDAINKRHAIEYKGLFKAELFNGKVLKQLGTV TTTEHENALLRSFDKFTTYFSGFYENRKNVFSADISTAIPHRIVQDNFPK FKENCHIFTRLITA VPSLREHFENVKKAIGIFVSTSIEEVFSFPFYNQLLTQ TQIDLYNQLLGGISREAGTEKIKGLNEVLNLAIQKNDETAHIIASLPHRFIP LFKQILSDRNTLSFILEEFKSDEEVIQSFCYKKTLLRNENVLETAEALFNE LNSIDLTHIFISHKKLETISSALCDHWDTLRNALYERRISELTGKITKSAKE KVQRSLKHEDINLQEIIAAGKELSEAFKQKTSEILSHAHAAALDQPLPTTL KKQEEKEILKSQLDSSLGLYHLLDWFAVDESNEVDPEFSARLTGIKLEM

	EPSLSFYNKARNYATKKPYSVEKFKLNFQMPTLASGWDVNKEKNNGAIFLVKNGLYYLGIMPKQKGRYKALSFEPTSEKTFDGMYYDYFPDAAMIPKCSTQLKAVTAHFQTHTPILLSNNFIEPLEITKEIYDLNNPEKEPKKFQTAYAKKTGDQKGYREALCKWIDFTRDFLSKYTKTTSIDLSSLRPSSQYKDLGEYYAELNPLLYHISFQRIAEKEIMDAVETGKLYLFQIYNKDFAKGHHGKPNLHTLYWTGLFSPENLAKTSIKLNGQAELFYRPSRMKRMALHRLGEKMLNKKLKDQKTPIDTLYQELYDYVNHRLSHDLSDEARALLPNVITKEVSHEIHKDRRFTSDKFFFHVPITLNYQAANSPSKFNQRVNAYLKEHPETPIIGIDRGERNLIYITVIDSTGKILEQRSNTIQQFDYQKKLDNREKERV AARQAWSVVGTIKDLKQGYLSQVIHEIVDLMIHQYAVVLENLNFQFKSKRTGIAEKAVYQQFEKMLIDKLNLCLVLKDYPAEKVGGVLNYPQLTDQFTSFAKMGTSQSGFLFYVPAPYTSKIDPLTGFVDPFVWKTIKNHESRKHFL EGFDFLHYDVKTGDFILHFKMNRNLSFQRGLPGFMPAWDIVFEKNETQF DAKGTPFIAGKRIVPVIENTHRFTGRYRDLYPANELIALLEEKGIVFRDGSN ILPKLLENDSDHAIDTMVALIRSVLQMANSNAATGEDYINSPVRDLNGV CFDSRFQNPWPMDADANGAYHIALKGQLLLNLHLESKDLKLQNGISN QDWLAYIQELRN (SEQ ID NO: 58)
LbCas12a (previously known as Cpf1) <i>Lachnospir aceae</i> <i>bacterium</i> <i>GAM79</i> Ref Seq. WP_11962 3382.1	MNYKTGLEDFIGKESLSKTLRNALIPTESTKIHMEEMGVIRDDELRAEKQ QELKEIMDDYYRTFIEEKLGGIQQGIQWNSLQKMEETMEDISVRKDLDKI QNEKRKEICCYFTSDKRFKDLFNAKLITDILPNFIKDNKEYTEEEKAEKE QTRVLFQRFATAFTNYFNQRRNNFSEDNISTAISFRIVNENSEIHLQNM AFQRIEQQYPEEVCGMEEYKDMLEQWQMKHIYSVDFYDRELTPQIE YYNGICGKINEHMNQFCQKNRINKNDFRMKKLHKQILCKKSSYYEIPFR FESDQEVYDALNEFIKTMKKKEIIRRCVHLGQECDDYDLGKIYISSNKYE QISNALYGSWDITRKICKEEYMDALPGKGEKKEEKAEAAAKKEEYRSIA DIDKISLYGSEMDRTISAKKCITEICDMAGQISIDPLVCNSDIKLLQNEK TTEIKTILDSFLHVVYQWGQTFIVSDIIEKDSYFYSELEDVLEDFEGITTLN HVRSYVTQKPYSTVKFKLHFGSPTLANGWSQSKEYDNNAILLMRDQKF YLGIFNVRNPKDKQIKGHEKEEKGDYKKMIYNLLPGPSKMLPKVFITSR SGQETYKPSKHILDGYNEKRHIKSSPKFDLGYCWDLDYKCEIHKHPD WKNYDFHFSDTKDYEDISGFYREVEMQGYQIKWTYISADEIQKLDEKG QIFLFQIYNKDFS VHSTGKDNLHTMYLKNLFSEENLKDVLKLNGEAELEF FRKASIKTPIVHKKGSVLVNRSYTQTVGNKEIRVSIPEEYTYEINYLNHI GKGKLSSEAQRYLDEGKIKSFTATKDIVKNYRYCCDHFLHLPITINFKA KSDVAVNERTLAYIAKKEDIHIGIDRGERNLLYISVVDVHGNIREQRSFN IVNGYDYQQKLKDREKSRDAARKNWEEIEKIKELKEGYLSMVIHYIAQL VVKYNAVAMEDLNYGFKTGRFKVERQVYQKFETMLIEKLHYLVFKD REVCEEGLRGYQLTYIPESLKKVGKQCGFIFYVPAGYTSKIDPTTGFV NLFSFKNLTNRESRQDFVGKFDEIRYDRDKKMFESFDYNNYIKKGTLA STKWKVYTNGTRLKRIVVNGKYTSQSMEVELTDAMEKMLQRAGIEYH DGKDLKGQIVEKGIEAEIIFRLTVQMRNSRSESEDREYDRLISPVLNDK GEFFDTATADKTLPQDADANGAYCIAKGLYEYVKQIKENWKENEQFPR NKLVDNKTWDFDMQKKRYL (SEQ ID NO: 59)
PcCas12a – previously known as Cpf1 <i>Prevotella</i> <i>copri</i>	MAKNFEDFKRLYLSKTLRFEAKPIGATLDNIVKSGLLDEDEHRAASYV KVKKLIDEYHKVFIDRVLDDGCLPLENKGNNNSLAEEYYESYVSRAQDE DAKKKFKEIQQLRSVIAKKLTEDKAYANLFGNKLIESYKDKEDKKKII DSDLIQFINTAESTQLDSMSQDEAKELVKEFWGFVTFYFYGFFDNRNKMY TAAEKSTGIAYRLVNENLPKFDINIEAFNRAITRPEIQENMGVLYSDFSEY LNVESIQEMFQLDYNNMLLTQKQIDVYNAIIGGKTDDDEHDVKIKGINEYI NLYNQHQHKDDKLPKLKALFKQILSDRNAISWLPEEFNSDQEVLNAIKDC

Ref Seq. WP_11922 7726.1	YERLAENVLGDKVLKSLGSLADYSLDGIFIRNDLQLTDISQKMFGNWG VIQNAIMQNIKRVPARKHKESEEDYEKRIAGIFKKADSFSISYINDCLNE ADPNNAYFVENYFATFGAVNTPTMQRENLFALVQNAYTEVAALLHSDY PTVKHLAQDKANVSKIKALLDAIKSLQHFVKPLLGGKGDSESKDERFYGE LASLWAEELDTVTPLYNMIRNYMTRKPYSQKKIKLNFENPQLLGGWDAN KEKDYATIILRRNGLYYLAIMDKDSRKLKGKAMPDGECEYKEMVYKFF KDVTTMIPKCSTQLKDVQAYFKVNTDDYVLNSKAFNKPLTITKEVFDLN NVLYGKYKKFQKGYLTATGDNVGYTHAVNVWIKFCMDFLNSYDSTCI YDFSSLKPESYLSLDAFYQDANLLLYKLSFARASVSYINQLVEEGKMYL FQIYNKDFSEYSKGTPTNMHTLYWKALFDERNLADVYKLNQAEMFY RKKSIENTHPTHPANHPILNKNKDNKKKESLFDYDLIKDRRYTVDKFMF HVPITMNFKSVGSEINQDVKAYLRHADDMMHIGIDRGERHLLYLVIDL QGNIKEQYSLNEIVNEYNGNTYHTNYHDLLDVREEERLKRQSWQTEN IKELKEGYLSQVIHKITQLMVRYHAIVVLEDLSKGFMRSRQKVEKQVYQ KFEKMLIDKLNLYLVDKKTVDVSTPGGLLNAYQLTCKSDSSQKLKGKQSGF LFYIPAWNTSKIDPVTGFVNLLDTHSLNSKEKIKAFFSKFDAIRYNKDKK WFEFNLDYDKFGKKAEDTRTKWTLCTRGMRIDTFRNKEKNSQWDNQE VDLTTEMKSLLEHYIYIDIHGNLKDASQAQTDKAFFTGLLHILKLTQMRN SITGTETDYLVPVADENGIFYDSRSCGNQLPENADANGAYNIARKGLM LIEQIKNAEDLNNVKFDISNKAWLNFAQQKPYKNG (SEQ ID NO: 60)
ErCas12a – previously known at Cpf1 <i>Eubacteriu m rectale</i>	MFSAKLISDILPEFVIHNNNYSASEKEEKTQVIKLSRFATSFKDYFKNRA NCFSSANDISSSSCHRIVNDNAEIFFSNALVYRRIVKNLSNDDINKISGDMK DSLKEMSLEEIYSYEKYGEFITQEGISFYNDICGKVNLFMNLVCQKNKEN KNLYKLRKLHKQILCIADTSYEVYPYKFESDEEVYQSVNGFLDNISSKHIV ERLRKIGENYNGYNLDKIYIVSKFYESVSQKTYRDWETINTALEIHYNNI LPGNGKSKADKVKKAVKNDLQKSITEINELVSNYKLCPPDDNIKAETYIH EISHILNNFEAQELKYNPEIHLVESELKASELKNVLDVIMNAFWCSVFM TEELVDKDNNFYAELEEIYDEIYPVISLYNLVRNYVTQKPYSTKKIKLNF GIPTLADGWSKSKEYSNNAIILMRDNLYYLGIFNAKNKPKDKKIIEGNTSE NKGDYKKMIYNLLPGPNKMIPKVFLSSKTGVETYKPSAYILEGYKQNKH LKSSKDFDITFCHDLIDYFKNCIAIHPEWKNFGFDFSDTSTYEDISGFYRE VELQGYKIDWTYISEKDIDLLQEKGQLYLFQIYNKDFSKKSSGNDNLHT MYLKNLFSEENLKDIVLKLNGEAEIFFRKSIIKNPIHKKGSILVNRTYEA EEKDQFGNIQIVRKTIPENIYQELYKYFNDKSDKELSDEAAKLKNVVGH HEAATNIVKDYRYTYDKYFLHMPITINFKANKTSFINDRILQYIAKEKDL HVGIDRGERNLIYVSVIDTCGNIVEQKSFNIVNGYDYQIKLKQQEGARQI ARKEWKEIGKIKEIKEGYLSLVIHEISKMVIKYNAIAMEDLSYGFKKGRF KVERQVYQKFETMLINKLNLYLVFKDISITENGGLLKGYQLTYIPDKLKN VGHQCGCIFYVPAAYTSKIDPTTGFVNIFKFKDLTVDAKREFIKKFDSIRY DSDKNLFCFTFDYNNFITQNTVMSKSSWSVYTYGVRIKRRFVNGRFSNE SDTIDITKMEKTLEMTDINWRDGHDLRQDIIDYEIVQHIFEIFKLTVMQ RNSLSELED RDYDRLISPVLNENNIFYDSAKAGDALPKDADANGAYCIA LKGLYEIKQITENWKEDGKFSRDKLKISNKDWFDIQNKRYL (SEQ ID NO: 61)
CsCas12a – previously known at Cpf1	MNYKTGLEDFIGKESLSKTLRNALIPTESTKIHMEEMGVIRDDELRAEKQ QELKEIMDDYYRAFIEEKLGGIQQGIQWNSLFQKMEETMEDISVRKDLDKI QNEKRKEICCYFTSDKRFKDLFNAKLITDILPNFIKDNKEYTEEEKAEKE QTRVLFQRFATAFTNYFNQRRNNFSEDNISTAISFRIVNENSEIHLQNM AFQRIEQQYPEEVCGMEEYKDMQLQEWQMKHIYLVDFYDRVLTQPGIE YYNGICGKINEHMNQFCQKNRINKNDFRMKKLHKQILCKKSSYYEIPFR

<i>Clostridium</i> <i>sp. AF34-10BH</i> Ref Seq. WP_11853 8418.1	FESDQEVYDALNEFIKTMKEKEIICRCVHLGQKCDDYDLGKIYISSNKYE QISNALYGSWDITIRKCIKEEYMDALPGKGEKKEEKAEEAAKKEEYRSIA DIDKIISLYGSEMDRTISAKKCITEICDMAGQISTDPLVCNSDIKLLQNKE KTTEIKTILDSFLHVYQWGQTFIVSDIIEKDSYFYSELEDVLEDFEGITTLY NHVRSYVTQKPYSTVKFKLHFGSPTLANGWSQSKEYDNNAILLMRDQK FYLGFNVRNPKDPKQIIKGHEKEEKGDYKKMIYNLLPGPSKMLPKVFITS RSGQETYKPSKHILDGYNEKRHIKSSPKFDLGYCWDLDIDYYKECIHKHP DWKNYDFHFSDTKDIEDISGFYREVEMQGYQIKWTYISADEIQKLDEK GQIFLFQIYNKDFS VHSTGKDNLHTMYLKNL FSEENLKDIVLKLNGEAE FFRKASIKTPVVHKKGSVLVNRSYTQTVGDKEIRVSIPEEYYTEIYNLYN HIGRGKLSTE AQRYLEERKIKSFTATKDIVKNYRYCCDHYFLHLPITINFK AKSDIAVNERTLAYIAKKEDIHIGIDRGERNLLYISVVDVHGNIREQSRF NIVNGYDYQQKLKDREKSRDAARKNWEEIEKIKELKEGYLSMVIHYIAQ LVVKYN AVVAMEDLNYGFKTGRFKVERQVYQKFETMLIEKLHYLVFK DREVCEE GVLRGYQLTYIPESLKKVGKQCGFIFYVPAGYTSKIDPTTGF VNLFSFKNLTNRESRQDFVGKFDEIRYDRDKKMFESFDYNNYIKKGT LASTKWKVYTNGTRLKRIVVNGKYTSQSMEVELTDAMEKMLQRAGIE YHDGKDLKGQIVEKGIEAEIIDIFRLTVQMRNSRSESEDREYDRILSPVLN DKGEFFDTATADKTLPQDADANGAYCIALKGLYEVKQIKENWKENEQF PRNKLVDNKTWDFDMQKKRYL (SEQ ID NO: 62)
BhCas12b <i>Bacillus</i> <i>hisashii</i> Ref Seq. WP_09514 2515.1	MATRSFILKIEPNEEVKGLWKTHEVLNHGIAYYMNLKLRQEAIYEH EQDPKNPKKVS KAELWDFVLKMQKCNSFTHEVDKDEVFNILREL YEELVPSSVEKKGEANQLSNKFLYPLVDPNSQSGKGTASSGRKPRWYNL KIAGDPSWEEKKKWEEDKKKDPLAKILGKLA EYGLIPLFIPYTD SNEPI VKEIKWMEKSRNQSVRRLDKDMFIQALERFLSWESWNLKVKEEYKVE KEYKTLEERIKEDIQALKALEQYEKERQEQLLRDTLNTNEYRLSKRGLR GWREIIQKWLKMDENEPSEKYLEVFKDYQRKHPREAGDYSVYEFLSKK ENHFIWRNHPEYPYLYATFCEIDKKKKDAKQQTFTLADPINHPLWVRF EERSGSNLNKYRILTEQLHTEKLKKKLT VQLDRLIYPTESGGWEEKGKV DIVLLPSRQFYNQIFLDIEEKGKHAFTYKDESIKFPLKGT LGGARVQFDR DHLRRYPHKVESGNVGRIFYNMTVNIEPTESPVSKSLKIHRDDFPKVVNF KPKELTEWIKDSKGKKLKSGIESLEIGLRVMSIDLGQRQAAAASIFEVVD QKPDIEGKLFPIKGT ELYAVHRASFNIKLPGETLVKSREVLRKAREDNL KLMNQKLNFLRNVLFHFQQFEDITEREKRVTKWISRQENS DVPLVYQDEL IQIRELMYKPYKDWV AFLKQLHKRLEVEIGKEVKHWRKSLSDGRKGLY GISLKNIDEIDRTRKFLLRWSLRPTEPGEVRRLEPGQRFAIDQLNHLNALK EDRLKKMANTIIMHALGYCYDVRKKKWQAKNPACQIILFEDLSNYPY EERSRFENSKLMKWSRREIPRQVALQGEIYGLQVGEVGAQFSSRFHAKT GSPGIRCSVVTKEKLQDNRRFFKNLQREGRLTDKIAVLKEGDLYPD KGG EKFISLSKDRKCVTTHADINAAQNLQKRFWTRTHGFYKVYCKAYQVDG QTVYIPESKDQKQKIIIEFGEGYFILKDG VYEWVNAGKLKIKKGSSKQSS SELVDS DILKDSFDLASELKGEKLMLYRDP SGNVFPSDKWMAAGVFFG KLERILISKLTNQYSISTIEDDSSKQSM (SEQ ID NO: 63)
ThCas12b <i>Thermomonas</i> <i>hydrothermalis</i>	MSEKTTQRAYTLRLNRASGECAVCQNNSCDCWHDALWATHKAVNRG AKAFGDWLLTLRGGLCHTLVEMEVP AKGNPPQRPTDQERRDRRVLLA LSWLSVEDEHGAPKEFIVATGRDSADDRACKVEEKLREILEKRDFQEHEI DAWLQDCGPSLKAHIREDAVWVNRRALFDA AVERIKTLTWEEAWDFL EPFFGTQYFAGIGDGKDKDDAEGPARQGEKAKDLVQKAGQWLSARFGI GTGADFMSMAEAYEKIAK WASQAQNGDNGKATIEKLACALRPSEPPTL DTVLCISGPGHKSATREYLKTLDDKKSTVTQEDLNQLRKLAD EDARNC

Ref Seq. WP_07275 4838	RKKVGKKKGKKPWAVEVLKDVENSCELTYLQDNSPARHREFSVMLDHA ARRVSMASWIKKAEQRRRQFESDAQKLKNLQERAPS AVEWLDRFCES RSMTTGANTGSGYRIRKRAIEGWSYVVQAWAEASCDTE DKRIA AARKV QADPEIEKFGDIQLFEALAADEAICVWRDQEGTQNP SILIDYVTGKTA EH NQKRFKVPAYRHPDEL RHPVFCDFGNSRWSIQFAIHKEIRDRDKGAKQD TRQLQNRHGLKMRLWNGRSM TDVNLHWSSKRLTADLALDQNP NPNT EVTRADRLGRAASSAFDHVKIKNVFNEKEWNGRLQAPRAELDRIAKLE EQGKTEQAEKLRKRLRWYVSFSPCLSPSGPFIVYAGQHNIQPKRSGQYA PHAQANKGRARLAQLILSRLPDLRILSVDLGHRFAAACAVWETLSSDAF RREIQGLNVLAGGSGEGDLFLHVEMTGDDGKRRTVVYRRIGPDQLLDN TPHPAPWARLDRQFLIKLQGEDEGVREASNEELWTVHKLEVEVGRTVP LIDRMVRSFGFKTEKQKERLKKLRELGWISAMPNEPSAETDEKEGEIRSI SRSVDELMSSALGTLRLALKRHGNRARIAFAMTADYKPMPPGGQKYFHH EAKEASKNDDETKRRDNQIEFLQDALSLWHDLFSSPDWEDNEAKKLWQ NHIALTPNYQTPEEISAEKLRVERNKKRKENRDKLRTAAKALAENDQLR QHLHDTWKERWESDDQQWKERLRS LKDWIFPRGKAEDNPSIRHVGGLS ITRINTISGLYQILKAFKMRPEPDDL RKNIPQKGDDLENFNRRLLEARDR LREQRVKQLASRIIEAALGVGRIKIPKNGKLPKRPRTTVDT PCHAVVIESL KTYRPDDLRTREN RQLMQWSSAKVRKYLKEGCELYGLHFLEVPANYT SRQCSRTGLPGIRCDDVPTGDFLKAPWWRRRAINTAREKNGGDAKDRFL VDLYDHLNNLQSKGEALPATVRVPRQGGNLFIAQAQLDDTNKERRAIQ ADLNAAANIGLRALLDPDWRGRWWYVPCKDGTSEPALDRIEGSTAFND VRS LPTGDNSSRRAPREIENLWRDPSGDSLES GTWSPTRAYWDTVQSRV IELLRRHAGLPTS (SEQ ID NO: 64)
LsCas12b <i>Laceyella sacchari</i> WP_13222 1894.1	MSIRSFKLKLKTKSGVNAEQLRRGLWRTHQLINDGIAYYMNWLVL LRQ EDLFIRNKETNEIEKRSKEEIQAVLLERVHKQQQRNQWSGEVDEQ TLLQ ALRQLYEEIVPSVIGKSGNASLKARFFLGPLVDPNNKTTKD VSKSGPTPK WKKMKDAGDPNWWVQEYKEYMAERQTLVRLEEMGLIPLFPMY TDEVG DIHWLPQASGYTRTWDRDMFQQA IERLLSWESWNRRVRERRA QFEKKT HDFASRFESDVQWMNKLREYEAQQEKSLEENAFAPNEPYALT KKA LR GWERVYHSWMRLDSAASEEAYWQEVATCQTAMRGEFGDPAIYQFLAQ KENHDIWRGYPERVIDFAELNHLQRELRRAKEDATFTLPDSVDHPLWVR YEAPGGTNIHGYDLVQDTRKNLTLILDKFILPDENG SWHEVKKVPFSLA KSKQFHRQVWLQEEQKQKKREVVFYDYSTNLPHLGLTAGAKLQWDRN FLNKRTQQQIEETGEIGKVFFNISVDVRPAVEVKNGRLQNGLGKALT VL THPDGTKIVTGWKAEQLEKWVGESGRVSSLGLDSLSEGLRVMSIDL GQ RTSATVSVFEITKEAPDNPKFFYQLEGTEMF AVHQRSFLLALPGENPPQ KIKQMREIRWKERNRIKQQVDQLSAILRLHKKVNEDERIQAIDKLLQKV ASWQLNEEIATAWNQALSQLYSKAKENDLQWNQA IKNAAHHQLEPVVG KQISLWRKDLSTGRQGIAGLSLWSIEELEATKLLTRWSKRSREPGVVK RIERFETFAKQIQHHINQVKENRLKQLANLIVMTALGYKYDQE QKKWIE VYPACQVVL FENLRSYRFSFERSRRENKKLMEWSHRSIPKL VQM QGELF GLQVADVYAA YSSRYHGRTGAPGIRCHALTEADLRNETNIIHELIEAGFI KEEHRPYLQQGDLVPWSGGELFATLQKPYDNPRIL TLHADINAAQNIQK RFWHPMSMWFRVNCESVMEGEIVTYVPKNKTVHKKQGKTFRFVKVEGS DVYEWAKWSKNRNKNTFSSITERKPPSSMILFRDPSGTFFKEQE WVEQK TFWGKVQSMIQA YMKKTIVQRMEE (SEQ ID NO: 65)
DtCas12b	MVLGRKDDTAELRRALWTTHEHVNLAVAEVERVLLRCRGRSYWTLDR RGDPVHVPESQVAEDALAMAREAQRRNGWPVVGED EELLALRYLYEQ IVPSCLLDDL GKPLKGDAQKIGTNYAGPLFDS DTCRRDEGKDVACCGPF

<i>Dsulfonatobium thiodismutans</i> WP_031386437	HEVAGKYL GALPEWATPISKQEFDGKDASHLRFKATGGDDAFFRVSIEK ANAWYEDPANQDALKNKAYNKDDWKKEKDKGISSWAVKYIQKQLQL GQDPRTEVRRKLWLELGLLPLFIPVFDKTMVGNLWNRLAVRLALAHLL SWESWNHRAVQDQALARAKRDELAALFLGMEDGFAGLREYELRRNESI KQHAFEPVDRPYVVSGRALRSWTRVREEWLRHGDTQESRKNICNRLQD RLRGKFGDPDVFWHLAEDGQEALWKERDCVTSFSLNDADGLLEKRK GYALMTFADARLHPRWAMYEA PGGSNLRTYQIRKTENGLWADVLLS PRNESAAVEEKT FNVR LAPSGQLSNVSFDQIQKGSKMVGRCRYQSANQ QFEGLLGGAEILFDRKRIANEQH GATDLASKPGHVWFKLTLDVRPQAPQ GWL DGKGR PALPPEAKHFKTALS NKSKFADQVRPGLRVLSVDLGVR SF AACSVFELVRGGPDQGT YFPAADGRTVDDPEKLWAKHERSFKITLPGEN PSRKEEIARRAAMEELRSLNGDIRRLKAILRLSVLQEDDPRTEHLRLFME AIVDDPAKSALNAELFKGFGDDRFRSTPDLWKQHCHFFHDKAEKVVAE RFSRWRTETRPKSSSWQDWRERRGYAGGKSYWAVTYLEAVRGLILRW NMRGR TYGEVNRQDKKQFGTVASALLHHINQLKEDRIKTGADMIIQAA RGFVPRKNGAGWVQVHEPCRLILFEDLARYRFR TDRSRRENSRLMRWS HREIVNEVGMQGELYGLHVD TTEAGFSSRYLASSGAPGVRCRHLVEEDF HDGLPGMHLVGELDWLLPKDKDRTANEARRLLGGMVRPGMLVPWDG GELFATLNAASQLHVIHADINAAQNLQRRFWGRCGEAIRVCNQLSVDG STRYEMAKAPKARLLGALQQLKNGDAPFHLTSIPNSQKPENS YVMTPTN AGKKYRAGPGEKSSGEEDELALDIVEQAEELAQGRKTFFRDPSGVFFAP DRWLPSEIYWSRIRRRIWQVT LERNSSGRQERAEMDEMPY (SEQ ID NO: 66)
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[0132] The genome editing system described herein may also comprise Cas12a (Cpf1) (dCpf1) variants that may be used as a guide nucleotide sequence-programmable DNA-binding protein domain. The Cas12a (Cpf1) protein has a RuvC-like endonuclease domain that is similar to the RuvC domain of Cas9 but does not have a HNH endonuclease domain, and the N-terminal of Cas12a (Cpf1) does not have the alpha-helical recognition lobe of Cas9. It was shown in Zetsche *et al.*, *Cell*, 163, 759–771, 2015 (which is incorporated herein by reference) that, the RuvC-like domain of Cas12a (Cpf1) is responsible for cleaving both DNA strands and inactivation of the RuvC-like domain inactivates Cas12a (Cpf1) nuclease activity.

[0133] In some embodiments, the napDNAbp is a single effector of a microbial CRISPR-Cas system. Single effectors of microbial CRISPR-Cas systems include, without limitation, Cas9, Cas12a (Cpf1), Cas12b1 (C2c1), Cas13a (C2c2), and Cas12c (C2c3). Typically, microbial CRISPR-Cas systems are divided into Class 1 and Class 2 systems. Class 1 systems have multisubunit effector complexes, while Class 2 systems have a single protein effector. For example, Cas9 and Cas12a (Cpf1) are Class 2 effectors. In addition to Cas9 and Cas12a (Cpf1), three distinct Class 2 CRISPR-Cas systems (Cas12b1, Cas13a, and Cas12c) have been described by Shmakov *et al.*, “Discovery and Functional Characterization of Diverse Class 2 CRISPR Cas Systems”, *Mol. Cell*, 2015 Nov 5; 60(3): 385–397, the entire contents of which are hereby incorporated by reference.

[0134] Effectors of two of the systems, Cas12b1 and Cas12c, contain RuvC-like endonuclease domains related to Cas12a. A third system, Cas13a contains an effector with two predicated HEPN RNase domains. Production of mature CRISPR RNA is tracrRNA-independent, unlike production of CRISPR RNA by Cas12b1. Cas12b1 depends on both CRISPR RNA and tracrRNA for DNA cleavage. Bacterial Cas13a has been shown to possess a unique RNase activity for CRISPR RNA maturation distinct from its RNA-activated single-stranded RNA degradation activity. These RNase functions are different from each other and from the CRISPR RNA-processing behavior of Cas12a. See, e.g., East-Seletsky, et al., “Two distinct RNase activities of CRISPR-Cas13a enable guide-RNA processing and RNA detection”, *Nature*, 2016 Oct 13;538(7624):270-273, the entire contents of which are hereby incorporated by reference. *In vitro* biochemical analysis of Cas13a in *Leptotrichia shahii* has shown that Cas13a is guided by a single CRISPR RNA and can be programmed to cleave ssRNA targets carrying complementary protospacers. Catalytic residues in the two conserved HEPN domains mediate cleavage. Mutations in the catalytic residues generate catalytically inactive RNA-binding proteins. See e.g., Abudayyeh et al., “C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector”, *Science*, 2016 Aug 5; 353(6299), the entire contents of which are hereby incorporated by reference.

[0135] The crystal structure of *Alicyclobacillus acidoterrastris* Cas12b1 (AacC2c1) has been reported in complex with a chimeric single-molecule guide RNA (sgRNA). See e.g., Liu et al., “C2c1-sgRNA Complex Structure Reveals RNA-Guided DNA Cleavage Mechanism”, *Mol. Cell*, 2017 Jan 19;65(2):310-322, the entire contents of which are hereby incorporated by reference. The crystal structure has also been reported in *Alicyclobacillus acidoterrestris* C2c1 bound to target DNAs as ternary complexes. See e.g., Yang et al., “PAM-dependent Target DNA Recognition and Cleavage by C2C1 CRISPR-Cas endonuclease”, *Cell*, 2016 Dec 15;167(7):1814-1828, the entire contents of which are hereby incorporated by reference. Catalytically competent conformations of AacC2c1, both with target and non-target DNA strands, have been captured independently positioned within a single RuvC catalytic pocket, with C2c1-mediated cleavage resulting in a staggered seven-nucleotide break of target DNA. Structural comparisons between C2c1 ternary complexes and previously identified Cas9 and Cpf1 counterparts demonstrate the diversity of mechanisms used by CRISPR-Cas9 systems.

[0136] In some embodiments, the napDNAbp may be a C2c1, a C2c2, or a C2c3 protein. In some embodiments, the napDNAbp is a C2c1 protein. In some embodiments, the napDNAbp is a Cas13a protein. In some embodiments, the napDNAbp is a Cas12c protein. In some

embodiments, the napDNAbp comprises an amino acid sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to a naturally-occurring Cas12b1 (C2c1), Cas13a (C2c2), or Cas12c (C2c3) protein. In some embodiments, the napDNAbp is a naturally-occurring Cas12b1 (C2c1), Cas13a (C2c2), or Cas12c (C2c3) protein.

H. Cas9 circular permutants

[0137] In various embodiments, the genome editing system disclosed herein may comprise a circular permutant of Cas9.

[0138] The term “circularly permuted Cas9” or “circular permutant” of Cas9 or “CP-Cas9”) refers to any Cas9 protein, or variant thereof, that occurs or has been modified to engineered as a circular permutant variant, which means the N-terminus and the C-terminus of a Cas9 protein (e.g., a wild type Cas9 protein) have been topically rearranged. Such circularly permuted Cas9 proteins, or variants thereof, retain the ability to bind DNA when complexed with a guide RNA (gRNA). See, Oakes et al., “Protein Engineering of Cas9 for enhanced function,” *Methods Enzymol*, 2014, 546: 491–511 and Oakes et al., “CRISPR-Cas9 Circular Permutants as Programmable Scaffolds for Genome Modification,” *Cell*, January 10, 2019, 176: 254-267, each of which are incorporated herein by reference. The instant disclosure contemplates any previously known CP-Cas9 or use a new CP-Cas9 so long as the resulting circularly permuted protein retains the ability to bind DNA when complexed with a guide RNA (gRNA).

[0139] Any of the Cas9 proteins described herein, including any variant, ortholog, or naturally occurring Cas9 or equivalent thereof, may be reconfigured as a circular permutant variant.

[0140] In various embodiments, the circular permutants of Cas9 may have the following structure:

[0141] N-terminus-[original C-terminus] – [optional linker] – [original N-terminus]-C-terminus.

[0142] As an example, the present disclosure contemplates the following circular permutants of canonical *S. pyogenes* Cas9 (1368 amino acids of UniProtKB - Q99ZW2 (CAS9_STRP1) (numbering is based on the amino acid position in SEQ ID NO: 11)):

[0143] N-terminus-[1268-1368]-[optional linker]-[1-1267]-C-terminus;

[0144] N-terminus-[1168-1368]-[optional linker]-[1-1167]-C-terminus;

[0145] N-terminus-[1068-1368]-[optional linker]-[1-1067]-C-terminus;

[0146] N-terminus-[968-1368]-[optional linker]-[1-967]-C-terminus;

[0147] N-terminus-[868-1368]-[optional linker]-[1-867]-C-terminus;

[0148] N-terminus-[768-1368]-[optional linker]-[1-767]-C-terminus;

[0149] N-terminus-[668-1368]-[optional linker]-[1-667]-C-terminus;

[0150] N-terminus-[568-1368]-[optional linker]-[1-567]-C-terminus;

[0151] N-terminus-[468-1368]-[optional linker]-[1-467]-C-terminus;

[0152] N-terminus-[368-1368]-[optional linker]-[1-367]-C-terminus;

[0153] N-terminus-[268-1368]-[optional linker]-[1-267]-C-terminus;

[0154] N-terminus-[168-1368]-[optional linker]-[1-167]-C-terminus;

[0155] N-terminus-[68-1368]-[optional linker]-[1-67]-C-terminus; or

[0156] N-terminus-[10-1368]-[optional linker]-[1-9]-C-terminus, or the corresponding circular permutants of other Cas9 proteins (including other Cas9 orthologs, variants, etc).

[0157] In particular embodiments, the circular permuant Cas9 has the following structure (based on *S. pyogenes* Cas9 (1368 amino acids of UniProtKB - Q99ZW2 (CAS9_STRP1) (numbering is based on the amino acid position in SEQ ID NO: 11):

[0158] N-terminus-[102-1368]-[optional linker]-[1-101]-C-terminus;

[0159] N-terminus-[1028-1368]-[optional linker]-[1-1027]-C-terminus;

[0160] N-terminus-[1041-1368]-[optional linker]-[1-1043]-C-terminus;

[0161] N-terminus-[1249-1368]-[optional linker]-[1-1248]-C-terminus; or

[0162] N-terminus-[1300-1368]-[optional linker]-[1-1299]-C-terminus, or the corresponding circular permutants of other Cas9 proteins (including other Cas9 orthologs, variants, etc).

[0163] In still other embodiments, the circular permuant Cas9 has the following structure (based on *S. pyogenes* Cas9 (1368 amino acids of UniProtKB - Q99ZW2 (CAS9_STRP1) (numbering is based on the amino acid position in SEQ ID NO: 11):

[0164] N-terminus-[103-1368]-[optional linker]-[1-102]-C-terminus;

[0165] N-terminus-[1029-1368]-[optional linker]-[1-1028]-C-terminus;

[0166] N-terminus-[1042-1368]-[optional linker]-[1-1041]-C-terminus;

[0167] N-terminus-[1250-1368]-[optional linker]-[1-1249]-C-terminus; or

[0168] N-terminus-[1301-1368]-[optional linker]-[1-1300]-C-terminus, or the corresponding circular permutants of other Cas9 proteins (including other Cas9 orthologs, variants, etc).

[0169] In some embodiments, the circular permutant can be formed by linking a C-terminal fragment of a Cas9 to an N-terminal fragment of a Cas9, either directly or by using a linker, such as an amino acid linker. In some embodiments, The C-terminal fragment may correspond to the C-terminal 95% or more of the amino acids of a Cas9 (e.g., amino acids about 1300-1368), or the C-terminal 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%,

45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% or more of a Cas9 (e.g., any one of SEQ ID NOs: 77-86). The N-terminal portion may correspond to the N-terminal 95% or more of the amino acids of a Cas9 (e.g., amino acids about 1-1300), or the N-terminal 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, or 5% or more of a Cas9 (e.g., of SEQ ID NO: 11).

[0170] In some embodiments, the circular permutant can be formed by linking a C-terminal fragment of a Cas9 to an N-terminal fragment of a Cas9, either directly or by using a linker, such as an amino acid linker. In some embodiments, the C-terminal fragment that is rearranged to the N-terminus, includes or corresponds to the C-terminal 30% or less of the amino acids of a Cas9 (e.g., amino acids 1012-1368 of SEQ ID NO: 11). In some embodiments, the C-terminal fragment that is rearranged to the N-terminus, includes or corresponds to the C-terminal 30%, 29%, 28%, 27%, 26%, 25%, 24%, 23%, 22%, 21%, 20%, 19%, 18%, 17%, 16%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% of the amino acids of a Cas9 (e.g., the Cas9 of SEQ ID NO: 11). In some embodiments, the C-terminal fragment that is rearranged to the N-terminus, includes or corresponds to the C-terminal 410 residues or less of a Cas9 (e.g., the Cas9 of SEQ ID NO: 11). In some embodiments, the C-terminal portion that is rearranged to the N-terminus, includes or corresponds to the C-terminal 410, 400, 390, 380, 370, 360, 350, 340, 330, 320, 310, 300, 290, 280, 270, 260, 250, 240, 230, 220, 210, 200, 190, 180, 170, 160, 150, 140, 130, 120, 110, 100, 90, 80, 70, 60, 50, 40, 30, 20, or 10 residues of a Cas9 (e.g., the Cas9 of SEQ ID NO: 11). In some embodiments, the C-terminal portion that is rearranged to the N-terminus, includes or corresponds to the C-terminal 357, 341, 328, 120, or 69 residues of a Cas9 (e.g., the Cas9 of SEQ ID NO: 11).

[0171] In other embodiments, circular permutant Cas9 variants may be defined as a topological rearrangement of a Cas9 primary structure based on the following method, which is based on *S. pyogenes* Cas9 of SEQ ID NO: 11: (a) selecting a circular permutant (CP) site corresponding to an internal amino acid residue of the Cas9 primary structure, which dissects the original protein into two halves: an N-terminal region and a C-terminal region; (b) modifying the Cas9 protein sequence (e.g., by genetic engineering techniques) by moving the original C-terminal region (comprising the CP site amino acid) to precede the original N-terminal region, thereby forming a new N-terminus of the Cas9 protein that now begins with the CP site amino acid residue. The CP site can be located in any domain of the Cas9 protein, including, for example, the helical-II domain, the RuvCIII domain, or the CTD domain. For example, the CP site may be located (relative the *S. pyogenes* Cas9 of SEQ ID

NO: 18) at original amino acid residue 181, 199, 230, 270, 310, 1010, 1016, 1023, 1029, 1041, 1247, 1249, or 1282. Thus, once relocated to the N-terminus, original amino acid 181, 199, 230, 270, 310, 1010, 1016, 1023, 1029, 1041, 1247, 1249, or 1282 would become the new N-terminal amino acid. Nomenclature of these CP-Cas9 proteins may be referred to as Cas9-CP¹⁸¹, Cas9-CP¹⁹⁹, Cas9-CP²³⁰, Cas9-CP²⁷⁰, Cas9-CP³¹⁰, Cas9-CP¹⁰¹⁰, Cas9-CP¹⁰¹⁶, Cas9-CP¹⁰²³, Cas9-CP¹⁰²⁹, Cas9-CP¹⁰⁴¹, Cas9-CP¹²⁴⁷, Cas9-CP¹²⁴⁹, and Cas9-CP¹²⁸², respectively. This description is not meant to be limited to making CP variants from SEQ ID NO: 18, but may be implemented to make CP variants in any Cas9 sequence, either at CP sites that correspond to these positions, or at other CP sites entirely. This description is not meant to limit the specific CP sites in any way. Virtually any CP site may be used to form a CP-Cas9 variant.

[0172] Exemplary CP-Cas9 amino acid sequences, based on the Cas9 of SEQ ID NO: 11, are provided below in which linker sequences are indicated by underlining and optional methionine (M) residues are indicated in bold. It should be appreciated that the disclosure provides CP-Cas9 sequences that do not include a linker sequence or that include different linker sequences. It should be appreciated that CP-Cas9 sequences may be based on Cas9 sequences other than that of SEQ ID NO: 11 and any examples provided herein are not meant to be limiting. Exemplary CP-Cas9 sequences are as follows:

CP name	Sequence	SEQ ID NO:
CP1012	DYKVYDVRKMIKSEGEIGKATAKYFFYSNIMNFFKTE ITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLS MPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDW DPKKYGGFDSPTVAYSVLVVAKEKGKSKKLKSVKEL LGITIMERSSSFENPIDFLEAKGYKEVKKDLIKLPKYSL FELENGRKRMLASAGELQKGNELALPSKYVNFLYLAS HYEKLKGPEDNEQKQLFVEQHKHYLDEIIEQISEFSKR VILADANLDKVLSAYNKHDKPIREQAENIIHLFTLTNL GAPAAFKYFDTTIDRKRYTSTKEVLDTLIHQSTGLYE TRIDLSQLGGDGGSGGSGGSGGSGGSGGSGGDKKYSIG LAIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKN LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEI FSNEMAKVDDSFHRLEESFLVEEDKKHERHPIFGNIVD EVAYHEKYPTIYHLRKKLVDSTDKADLRILIYALAHMI KFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPI NASGVDAKAILSARLSKSRLENLIAQLPGEKKNGLFG NLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLN LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAP LSASMIKRYDEHHQDLTLLKALVRQQLPKEYKEIFFDQ SKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVK LNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYF FLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSE	SEQ ID NO: 67

CP name	Sequence	SEQ ID NO:
	ETITPWNFEVVDKGSASQSFIERMTNFDKNLPNEKVL PKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQK KAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGV EDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLT LTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGW GRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFQMQLIH DDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAICKGI LQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQ KNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYL YYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDD SIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLL NAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETR QITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVS DFRKDFQFYKVREINNYHHAHDAYLNAVVGITALIKKY PKLESEFVYG	
CP1028	EIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNG ETGEIVWDKGRDFATVRKVLSPQVNIVKKTEVQTGG FSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKVEKGKSKKLKSVKELLGITIMERSSEKPNIDF LEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAGE LQKGNELALPSKYVNFLYLASHYEKLKGGSPEDNEQKQ LFVEQHKHYLDEIIEQISEFSKRVLADANLDKVL SAYN KHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRK RYTSTKEVLDATLIHQSTGLYETRIDLSQLGGDGGSGG <u>SGGSGGSGGSGGSGGMDKKYSIGLAIGTNSVGWAVIT</u> DEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAE ATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSF HRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYH LRKKLV DSTDKADLR LIYLALAHMIKFRGHFLIEGDLN PDNSDV DKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRLENLIAQLPGEKKNGLFGNLIASLSGLTPNF KSNFDLAEDAKLQLSKD TYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEH HQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDG GASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQR TFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKI LTRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEV VDKGSASQSFIERMTNFDKNLPNEKVL PKHSLLYEYFT VYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTN RKVTVKQLKEDYFKKIECFDSVEISGV EDRFNASLGTY HDLLKIIKDKDFLDNEENEDILEDIVLT LTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIR DKQSGKTILDFLKSDGFANRNFQMQLIHDDS LTFKEDIQ KAQVSGQGDSLHEHIANLAGSPAICKGILQTVKVVDEL VKVMGRHKPENIVIAMARENQTTQKGQKNSRERMKRI EEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD MYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTR SDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQR KFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQ	SEQ ID NO: 68

CP name	Sequence	SEQ ID NO:
	ILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQ FYKVVREINNYHHAHDAYLNAVVGTAIIKKYPKLESEF VYGDYKVYDVRKMIKSEQ	
CP1041	NIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD FATVRKVLSPQVNIVKKTEVQTGGFSKESILPKRNSD KLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEVGK SKKLKSVKELLGITIMERSSEKKNPIDFLEAKGYKEVKK DLIILPKYSLFELENGRKRMLASAGELQKGNELALPS KYVNFLYLASHYEKLKGSPEDEQKQLFVEQHKHYLD EIIIEQISEFSKRVLADANLDKVL SAYNKHDKPIREQA ENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA TLIHQSITGLYETRIDLSQLGGDGGSGGSGGSGGSGGSGG GGSGGDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVL GNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYT RRKNRICYLQEIFSNEMAKVDDSFHRLSEESFLVEEDK KHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKA DLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQL VQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIA QLPGEKKNGLFGNLIALSLGLTPNFKSNDLAEDAKLQ LSKDTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLS DILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPI EKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGE LHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLAR GNSRFAWMTRKSEETITPWNFEVVDKGASAQSFIER MTNFDKNLPNEKVLPHSLLEYFTVYNELTKVKYVT EGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDY FKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFL DNEENEDILEDIVLTTLTFEDREMIEERLKTYAHLFDDK VMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFL KSDGFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSL HEHIANLAGSPAIIKKGILQTVKVVDLVKVMGRHKPE NIVIEMARENQTTQKGQKNSRERMKRIIEGKELGSQIL KEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINR LSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNV PSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERG GLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYD ENDKLIREVKVITLKSCLVSDFRKDFQFYKVVREINNYH HAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDV RKMIKSEQEIGKATAKYFFYS	SEQ ID NO: 69
CP1249	PEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVLADANL DKVL SAYNKHDKPIREQAENIIHLFTLTNLGAPAAFK YFDTTIDRKRYTSTKEVLDA TLIHQSITGLYETRIDLSQL GGDGGSGGSGGSGGSGGSGGSGGMDKKYSIGLAIGT NSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALL FDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFHRLSEESFLVEEDKKHERHPIFGNIVDEVAY HEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRG HFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASG	SEQ ID NO: 70

CP name	Sequence	SEQ ID NO:
	VDAKAILSARLSKSRRLLENLIAQLPGEKKNGLFGNLI SLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLDNLLAQI GDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN GYAGYIDGGASQE EFYKFIKPILEKMDGTEELLVKLN REDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFY PFLKDNREKIEKILTRIPYYVGPLARGNSRFAWMTRK SEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEK VLPKHSLLEYFTVYNELTKVKYVTEGMRKPAFLS GEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS VEISGVEDRFNASLGTYHDLLKIKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKT YAHLFDDKVMK QLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSD GFANRNF MQLIHDDSLTFKEDIQKAQVSGQGDSLHE HIANLAGSPAIIKKGILQTVKVVDELVKVMGRHKPEN IVIAMARENQTTQKGQKNSRERMKRIEEGIKELGSQIL KEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRL SDYDV DHIVPQSFLKDDSIDNKVLTRSDKNRGKSDN VPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER GGLSELDAKAGFIKRQLVETRQITKHVAQILDSRMNT KYDENDKLIREVKVITLKS LVSDFRKDFQFYKVR EINNYHHAHDAYLNAVVG TALIKKYPKLESEFVY GDYKVYDVRKMIAKSEQEIGKATAYFFYSNIMNFF KTEITLANGEIRKRPLIETNGETGEIVWDKGRDFAT VRKVL SMPQVNIVKKTEVQTGGFSKESILPKRNSD KLIARKKDWD PKKYGGFDSPTVAYSVLVVAKEK GKSKKLKSVKELLGITIMERS SFEKNPIDFLEAKGY KEVKKDLI IKLPKYSLFELENG RKRLASAGELQK GNE LALPSKYVNFLYLASHYEKLKGS	
CP1300	KPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTST KEVL DATLIHQ SITGLYETRIDLSQLGGDGGSGGSGGS GGSGGSGGSGGDKKYSIGLAIGTNSVGWAVITDEYKV PSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLK RTARRRYTRRKNRICYLQEIFS NEMAKVDD SFFHRL EESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKK LVDSTDKADLR LIYLALAHMIKFRGHFLIEGDLNPDNS DVDKLF IQLVQTYNQLFEENPINASGVDAKAILSARLS KSRRLLENLIAQLPGEKKNGLFGNLIASLGLTPNFKSNF DLAEDAKLQLSKD TYDDDLDNLLAQIGDQYADLFLAA KNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDL TLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQE EFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNG SIPHQIHLGELHAILRRQEDFY PFLKDNREKIEKILTRIP YYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKG ASAQSFIERMTNFDKNLPNEK VLPKHSLLEYFTVYNEL TKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVT VKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLK IKDKDFLDNEENE DILEDIVLTLTLFEDREMIEERLKT YAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSG KTILDFLKSDGFANRNF MQLIHDDSLTFKEDIQKAQVS	SEQ ID NO: 71

CP name	Sequence	SEQ ID NO:
	GGGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVM GRHKPENIVIAMARENQTTQKGQKNSRERMKRIIEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQ ELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNR GKSDNVPSEEVVKMKMKNYWRQLLNAKLITQRKFDNL TKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSR MNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKV REINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGD YKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEI TLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLS MPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDW DPKKYGGFDSPTVAYSVLVVAKEVEKGKSKKLKSVKEL LGITIMERSSSFENPIDFLEAKGYKEVKKDLIIKLPKYS LELENGRKRMLASAGELQKGNELALPSKYVNFLYLAS HYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKR VILADANLDKVLSAYNKHHRD	

[0173] The Cas9 circular permutants that may be useful in the genome editing system described herein. Exemplary C-terminal fragments of Cas9, based on the Cas9 of SEQ ID NO: 11, which may be rearranged to an N-terminus of Cas9, are provided below. It should be appreciated that such C-terminal fragments of Cas9 are exemplary and are not meant to be limiting. These exemplary CP-Cas9 fragments have the following sequences:

CP name	Sequence	SEQ ID NO:
CP1012 C-terminal fragment	DYKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKT EITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKD WDPKKYGGFDSPTVAYSVLVVAKEVEKGKSKKLKSVK ELLGITIMERSSSFENPIDFLEAKGYKEVKKDLIIKLPKY SLFELENGRKRMLASAGELQKGNELALPSKYVNFLYL ASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFS KRVILADANLDKVLSAYNKHHRDKPIREQAENIIHLFTLT NLGAPAAFKYFDTTIDRKRYTSTKEVLDTLIHQSTGL YETRIDLSQLGGD	SEQ ID NO: 72
CP1028 C-terminal fragment	EIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNG ETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGG FSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYS VLVVAKEVEKGKSKKLKSVKELLGITIMERSSSFENPIDF LEAKGYKEVKKDLIIKLPKYSLELENGRKRMLASAGE LQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQ LFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYN KHHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRK RYTSTKEVLDTLIHQSTGLYETRIDLSQLGGD	SEQ ID NO: 73
CP1041 C-terminal fragment	NIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRD FATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSD KLIARKKDWDPKKYGGFDSPTVAYSVLVVAKEVEKGK SKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKK DLIIKLPKYSLELENGRKRMLASAGELQKGNELALPS	SEQ ID NO: 74

CP name	Sequence	SEQ ID NO:
	KYVNFLYLASHYEKLKKGSPEDNEQKQLFVEQHKHYLD EIIIEQISEFSKRVLADANLDKVLSAYNKHHRDKPIREQA ENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA TLIHQSITGLYETRIDLSQLGGD	
CP1249 C-terminal fragment	PEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVLADANL DKVLSAYNKHHRDKPIREQAENIIHLFTLTNLGAPAAFK YFDTTIDRKRYTSTKEVLDA TLIHQSITGLYETRIDLSQL GGD	SEQ ID NO: 75
CP1300 C-terminal fragment	KPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTST KEVLDA TLIHQSITGLYETRIDLSQLGGD	SEQ ID NO: 76

I. Cas9 variants with modified PAM specificities

[0174] The genome editing system of the present disclosure may also comprise Cas9 variants with modified PAM specificities. Some aspects of this disclosure provide Cas9 proteins that exhibit activity on a target sequence that does not comprise the canonical PAM (5'-NGG-3', where N is A, C, G, or T) at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NGG-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NNG-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NNA-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NNC-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NNT-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NGT-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NGA-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NGC-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NAA-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NAC-3' PAM sequence at its 3'-end. In some embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NAT-3' PAM sequence at its 3'-end. In still other embodiments, the Cas9 protein exhibits activity on a target sequence comprising a 5'-NAG-3' PAM sequence at its 3'-end.

[0175] It should be appreciated that any of the amino acid mutations described herein, (e.g., A262T) from a first amino acid residue (e.g., A) to a second amino acid residue (e.g., T) may

also include mutations from the first amino acid residue to an amino acid residue that is similar to (e.g., conserved) the second amino acid residue. For example, mutation of an amino acid with a hydrophobic side chain (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, or tryptophan) may be a mutation to a second amino acid with a different hydrophobic side chain (e.g., alanine, valine, isoleucine, leucine, methionine, phenylalanine, tyrosine, or tryptophan). For example, a mutation of an alanine to a threonine (e.g., a A262T mutation) may also be a mutation from an alanine to an amino acid that is similar in size and chemical properties to a threonine, for example, serine. As another example, mutation of an amino acid with a positively charged side chain (e.g., arginine, histidine, or lysine) may be a mutation to a second amino acid with a different positively charged side chain (e.g., arginine, histidine, or lysine). As another example, mutation of an amino acid with a polar side chain (e.g., serine, threonine, asparagine, or glutamine) may be a mutation to a second amino acid with a different polar side chain (e.g., serine, threonine, asparagine, or glutamine). Additional similar amino acid pairs include, but are not limited to, the following: phenylalanine and tyrosine; asparagine and glutamine; methionine and cysteine; aspartic acid and glutamic acid; and arginine and lysine. The skilled artisan would recognize that such conservative amino acid substitutions will likely have minor effects on protein structure and are likely to be well tolerated without compromising function. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to a threonine may be an amino acid mutation to a serine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to an arginine may be an amino acid mutation to a lysine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to an isoleucine, may be an amino acid mutation to an alanine, valine, methionine, or leucine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to a lysine may be an amino acid mutation to an arginine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to an aspartic acid may be an amino acid mutation to a glutamic acid or asparagine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to a valine may be an amino acid mutation to an alanine, isoleucine, methionine, or leucine. In some embodiments, any amino of the amino acid mutations provided herein from one amino acid to a glycine may be an amino acid mutation to an alanine. It should be appreciated, however, that additional conserved amino acid residues would be recognized by the skilled artisan and any of the amino acid mutations to other conserved amino acid residues are also within the scope of this disclosure.

[0176] In some embodiments, the Cas9 protein comprises a combination of mutations that exhibit activity on a target sequence comprising a 5'-NAA-3' PAM sequence at its 3'-end. In some embodiments, the combination of mutations are present in any one of the clones listed in Table 1. In some embodiments, the combination of mutations are conservative mutations of the clones listed in Table 1. In some embodiments, the Cas9 protein comprises the combination of mutations of any one of the Cas9 clones listed in Table 1.

[0177] Table 1: NAA PAM Clones

Mutations from wild-type SpCas9 (e.g., SEQ ID NO: 11)
D177N, K218R, D614N, D1135N, P1137S, E1219V, A1320V, A1323D, R1333K
D177N, K218R, D614N, D1135N, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, G715C, D1135N, E1219V, Q1221H, H1264Y, A1320V, R1333K
A367T, K710E, R1114G, D1135N, P1137S, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, R753G, D861N, D1135N, K1188R, E1219V, Q1221H, H1264H, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, V743I, R753G, M1021T, D1135N, D1180G, K1211R, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, V743I, R753G, E762G, D1135N, D1180G, K1211R, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, R753G, D1135N, D1180G, K1211R, E1219V, Q1221H, H1264Y, S1274R, A1320V, R1333K
A10T, I322V, S409I, E427G, A589S, R753G, D1135N, E1219V, Q1221H, H1264H, A1320V, R1333K
A10T, I322V, S409I, E427G, R753G, E757K, G865G, D1135N, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, R753G, E757K, D1135N, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, K599R, M631A, R654L, K673E, V743I, R753G, N758H, E762G, D1135N, D1180G, E1219V, Q1221H, Q1256R, H1264Y, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, N869S, N1054D, R1114G, D1135N, D1180G, E1219V, Q1221H, H1264Y, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, R654L, L727I, V743I, R753G, E762G, R859S, N946D, F1134L, D1135N, D1180G, E1219V, Q1221H, H1264Y, N1317T, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, N803S, N869S, Y1016D, G1077D, R1114G, F1134L, D1135N, D1180G, E1219V, Q1221H, H1264Y, V1290G, L1318S, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, N803S, N869S, Y1016D, G1077D, R1114G, F1134L, D1135N, K1151E, D1180G, E1219V, Q1221H, H1264Y, V1290G, L1318S, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, N803S, N869S, Y1016D, G1077D, R1114G, F1134L, D1135N, D1180G, E1219V, Q1221H, H1264Y, V1290G, L1318S, A1320V, A1323D, R1333K

A10T, I322V, S409I, E427G, R654L, K673E, F693L, V743I, R753G, E762G, N803S, N869S, L921P, Y1016D, G1077D, F1080S, R1114G, D1135N, D1180G, E1219V, Q1221H, H1264Y, L1318S, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, E630K, R654L, K673E, V743I, R753G, E762G, Q768H, N803S, N869S, Y1016D, G1077D, R1114G, F1134L, D1135N, D1180G, E1219V, Q1221H, H1264Y, L1318S, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, F693L, V743I, R753G, E762G, Q768H, N803S, N869S, Y1016D, G1077D, R1114G, F1134L, D1135N, D1180G, E1219V, Q1221H, G1223S, H1264Y, L1318S, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, F693L, V743I, R753G, E762G, N803S, N869S, L921P, Y1016D, G1077D, F1801S, R1114G, D1135N, D1180G, E1219V, Q1221H, H1264Y, L1318S, A1320V, A1323D, R1333K
A10T, I322V, S409I, E427G, R654L, V743I, R753G, M1021T, D1135N, D1180G, K1211R, E1219V, Q1221H, H1264Y, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, M673I, N803S, N869S, G1077D, R1114G, D1135N, V1139A, D1180G, E1219V, Q1221H, A1320V, R1333K
A10T, I322V, S409I, E427G, R654L, K673E, V743I, R753G, E762G, N803S, N869S, R1114G, D1135N, E1219V, Q1221H, A1320V, R1333K

[0178] In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 80% identical to the amino acid sequence of a Cas9 protein as provided by any one of the variants of Table 1. In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a Cas9 protein as provided by any one of the variants of Table 1.

[0179] In some embodiments, the Cas9 protein exhibits an increased activity on a target sequence that does not comprise the canonical PAM (5'-NGG-3') at its 3' end as compared to *Streptococcus pyogenes* Cas9 as provided by SEQ ID NO: 11. In some embodiments, the Cas9 protein exhibits an activity on a target sequence having a 3' end that is not directly adjacent to the canonical PAM sequence (5'-NGG-3') that is at least 5-fold increased as compared to the activity of *Streptococcus pyogenes* Cas9 as provided by SEQ ID NO: 18 on the same target sequence. In some embodiments, the Cas9 protein exhibits an activity on a target sequence that is not directly adjacent to the canonical PAM sequence (5'-NGG-3') that is at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1,000-fold, at least 5,000-fold, at least 10,000-fold, at least 50,000-fold, at least 100,000-fold, at least 500,000-fold, or at least 1,000,000-fold increased as compared to the activity of *Streptococcus pyogenes* as provided by SEQ ID NO: 11 on the same target sequence. In some embodiments, the 3' end of the target sequence is directly adjacent to an AAA, GAA, CAA, or TAA sequence. In some embodiments, the Cas9 protein comprises a combination of mutations that exhibit activity on a target sequence comprising a 5'-NAC-3' PAM sequence

at its 3'-end. In some embodiments, the combination of mutations are present in any one of the clones listed in Table 2. In some embodiments, the combination of mutations are conservative mutations of the clones listed in Table 2. In some embodiments, the Cas9 protein comprises the combination of mutations of any one of the Cas9 clones listed in Table 2.

[0180] Table 2: NAC PAM Clones

MUTATIONS FROM WILD-TYPE SPCAS9 (E.G., SEQ ID NO: 11)
T472I, R753G, K890E, D1332N, R1335Q, T1337N
I1057S, D1135N, P1301S, R1335Q, T1337N
T472I, R753G, D1332N, R1335Q, T1337N
D1135N, E1219V, D1332N, R1335Q, T1337N
T472I, R753G, K890E, D1332N, R1335Q, T1337N
I1057S, D1135N, P1301S, R1335Q, T1337N
T472I, R753G, D1332N, R1335Q, T1337N
T472I, R753G, Q771H, D1332N, R1335Q, T1337N
E627K, T638P, K652T, R753G, N803S, K959N, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
E627K, T638P, K652T, R753G, N803S, K959N, R1114G, D1135N, K1156E, E1219V, D1332N, R1335Q, T1337N
E627K, T638P, V647I, R753G, N803S, K959N, G1030R, I1055E, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
E627K, E630G, T638P, V647A, G687R, N767D, N803S, K959N, R1114G, D1135N, E1219V, D1332G, R1335Q, T1337N
E627K, T638P, R753G, N803S, K959N, R1114G, D1135N, E1219V, N1266H, D1332N, R1335Q, T1337N
E627K, T638P, R753G, N803S, K959N, I1057T, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
E627K, T638P, R753G, N803S, K959N, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
E627K, M631I, T638P, R753G, N803S, K959N, Y1036H, R1114G, D1135N, E1219V, D1251G, D1332G, R1335Q, T1337N
E627K, T638P, R753G, N803S, V875I, K959N, Y1016C, R1114G, D1135N, E1219V, D1251G, D1332G, R1335Q, T1337N, I1348V
K608R, E627K, T638P, V647I, R654L, R753G, N803S, T804A, K848N, V922A, K959N, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
K608R, E627K, T638P, V647I, R753G, N803S, V922A, K959N, K1014N, V1015A, R1114G, D1135N, K1156N, E1219V, N1252D, D1332N, R1335Q, T1337N
K608R, E627K, R629G, T638P, V647I, A711T, R753G, K775R, K789E, N803S, K959N, V1015A, Y1036H, R1114G, D1135N, E1219V, N1286H, D1332N, R1335Q, T1337N
K608R, E627K, T638P, V647I, T740A, R753G, N803S, K948E, K959N, Y1016S, R1114G, D1135N, E1219V, N1286H, D1332N, R1335Q, T1337N
K608R, E627K, T638P, V647I, T740A, N803S, K948E, K959N, Y1016S, R1114G, D1135N, E1219V, N1286H, D1332N, R1335Q, T1337N
I670S, K608R, E627K, E630G, T638P, V647I, R653K, R753G, I795L, K797N, N803S, K866R, K890N, K959N, Y1016C, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N

K608R, E627K, T638P, V647I, T740A, G752R, R753G, K797N, N803S, K948E, K959N, V1015A, Y1016S, R1114G, D1135N, E1219V, N1266H, D1332N, R1335Q, T1337N
I570T, A589V, K608R, E627K, T638P, V647I, R654L, Q716R, R753G, N803S, K948E, K959N, Y1016S, R1114G, D1135N, E1207G, E1219V, N1234D, D1332N, R1335Q, T1337N
K608R, E627K, R629G, T638P, V647I, R654L, Q740R, R753G, N803S, K959N, N990S, T995S, V1015A, Y1036D, R1114G, D1135N, E1207G, E1219V, N1234D, N1266H, D1332N, R1335Q, T1337N
I562F, V565D, I570T, K608R, L625S, E627K, T638P, V647I, R654I, G752R, R753G, N803S, N808D, K959N, M1021L, R1114G, D1135N, N1177S, N1234D, D1332N, R1335Q, T1337N
I562F, I570T, K608R, E627K, T638P, V647I, R753G, E790A, N803S, K959N, V1015A, Y1036H, R1114G, D1135N, D1180E, A1184T, E1219V, D1332N, R1335Q, T1337N
I570T, K608R, E627K, T638P, V647I, R654H, R753G, E790A, N803S, K959N, V1015A, R1114G, D1127A, D1135N, E1219V, D1332N, R1335Q, T1337N
I570T, K608R, L625S, E627K, T638P, V647I, R654I, T703P, R753G, N803S, N808D, K959N, M1021L, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
I570S, K608R, E627K, E630G, T638P, V647I, R653K, R753G, I795L, N803S, K866R, K890N, K959N, Y1016C, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N
I570T, K608R, E627K, T638P, V647I, R654H, R753G, E790A, N803S, K959N, V1016A, R1114G, D1135N, E1219V, K1246E, D1332N, R1335Q, T1337N
K608R, E627K, T638P, V647I, R654L, K673E, R753G, E790A, N803S, K948E, K959N, R1114G, D1127G, D1135N, D1180E, E1219V, N1286H, D1332N, R1335Q, T1337N
K608R, L625S, E627K, T638P, V647I, R654I, I670T, R753G, N803S, N808D, K959N, M1021L, R1114G, D1135N, E1219V, N1286H, D1332N, R1335Q, T1337N
E627K, M631V, T638P, V647I, K710E, R753G, N803S, N808D, K948E, M1021L, R1114G, D1135N, E1219V, D1332N, R1335Q, T1337N, S1338T, H1349R

[0181] In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 80% identical to the amino acid sequence of a Cas9 protein as provided by any one of the variants of Table 2. In some embodiments, the Cas9 protein comprises an amino acid sequence that is at least 85%, at least 90%, at least 92%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to the amino acid sequence of a Cas9 protein as provided by any one of the variants of Table 2.

[0182] In some embodiments, the Cas9 protein exhibits an increased activity on a target sequence that does not comprise the canonical PAM (5'-NGG-3') at its 3' end as compared to *Streptococcus pyogenes* Cas9 as provided by SEQ ID NO: 11. In some embodiments, the Cas9 protein exhibits an activity on a target sequence having a 3' end that is not directly adjacent to the canonical PAM sequence (5'-NGG-3') that is at least 5-fold increased as compared to the activity of *Streptococcus pyogenes* Cas9 as provided by SEQ ID NO: 11 on the same target sequence. In some embodiments, the Cas9 protein exhibits an activity on a target sequence that is not directly adjacent to the canonical PAM sequence (5'-NGG-3') that is at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1,000-fold, at least 5,000-fold, at least 10,000-fold, at least 50,000-fold, at least 100,000-fold, at least 500,000-fold, or at least 1,000,000-fold increased as compared to the activity of

Streptococcus pyogenes as provided by SEQ ID NO: 11 on the same target sequence. In some embodiments, the 3' end of the target sequence is directly adjacent to an AAC, GAC, CAC, or TAC sequence.

[0183] In some embodiments, the Cas9 protein comprises a combination of mutations that exhibit activity on a target sequence comprising a 5'-NAT-3' PAM sequence at its 3'-end. In some embodiments, the combination of mutations are present in any one of the clones listed in Table 3. In some embodiments, the combination of mutations are conservative mutations of the clones listed in Table 3. In some embodiments, the Cas9 protein comprises the combination of mutations of any one of the Cas9 clones listed in Table 3.

[0184] Table 3: NAT PAM Clones

MUTATIONS FROM WILD-TYPE SPCAS9 (E.G., SEQ ID NO: 11)
K961E, H985Y, D1135N, K1191N, E1219V, Q1221H, A1320A, P1321S, R1335L
D1135N, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
V743I, R753G, E790A, D1135N, G1218S, E1219V, Q1221H, A1227V, P1249S, N1286K, A1293T, P1321S, D1322G, R1335L, T1339I
F575S, M631L, R654L, V748I, V743I, R753G, D853E, V922A, R1114G D1135N, G1218S, E1219V, Q1221H, A1227V, P1249S, N1286K, A1293T, P1321S, D1322G, R1335L, T1339I
F575S, M631L, R654L, R664K, R753G, D853E, V922A, R1114G D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, N1286K, P1321S, D1322G, R1335L
M631L, R654L, R753G, K797E, D853E, V922A, D1012A, R1114G D1135N, G1218S, E1219V, Q1221H, P1249S, N1317K, P1321S, D1322G, R1335L
F575S, M631L, R654L, R664K, R753G, D853E, V922A, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
F575S, M631L, R654L, R664K, R753G, D853E, V922A, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
F575S, D596Y, M631L, R654L, R664K, R753G, D853E, V922A, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, Q1256R, P1321S, D1322G, R1335L
F575S, M631L, R654L, R664K, K710E, V750A, R753G, D853E, V922A, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
F575S, M631L, K649R, R654L, R664K, R753G, D853E, V922A, R1114G, Y1131C, D1135N, K1156E, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
F575S, M631L, R654L, R664K, R753G, D853E, V922A, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1322G, R1335L
F575S, M631L, R654L, R664K, R753G, D853E, V922A, I1057G, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, N1308D, P1321S, D1322G, R1335L
M631L, R654L, R753G, D853E, V922A, R1114G, Y1131C, D1135N, E1150V, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1332G, R1335L
M631L, R654L, R664K, R753G, D853E, I1057V, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1332G, R1335L
M631L, R654L, R664K, R753G, I1057V, R1114G, Y1131C, D1135N, D1180G, G1218S, E1219V, Q1221H, P1249S, P1321S, D1332G, R1335L

[0185] The above description of various napDNABps which can be used in connection with the presently disclose genome editing system is not meant to be limiting in any way. The

genome editing system may comprise the canonical SpCas9, or any ortholog Cas9 protein, or any variant Cas9 protein—including any naturally occurring variant, mutant, or otherwise engineered version of Cas9—that is known or which can be made or evolved through a directed evolutionary or otherwise mutagenic process. In various embodiments, the Cas9 or Cas9 variants have a nickase activity, i.e., only cleave one strand of the target DNA sequence. In other embodiments, the Cas9 or Cas9 variants have inactive nucleases, i.e., are “dead” Cas9 proteins. Other variant Cas9 proteins that may be used are those having a smaller molecular weight than the canonical SpCas9 (e.g., for easier delivery) or having modified or rearranged primary amino acid structure (e.g., the circular permutant formats). The genome editing system described herein may also comprise Cas9 equivalents, including Cas12a/Cpf1 and Cas12b proteins which are the result of convergent evolution. The Cas9 proteins used herein (e.g., SpCas9, Cas9 variant, or Cas9 equivalents) may also contain various modifications that alter/enhance their PAM specificities. Lastly, the application contemplates any Cas9, Cas9 variant, or Cas9 equivalent which has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% sequence identity to a reference Cas9 sequence, such as a reference SpCas9 canonical sequence or a reference Cas9 equivalent (e.g., Cas12a/Cpf1).

[0186] In a particular embodiment, the Cas9 variant having expanded PAM capabilities is SpCas9 (H840A) VRQR (SEQ ID NO: 77), which has the following amino acid sequence (with the V, R, Q, R substitutions relative to the SpCas9 (H840A) of SEQ ID NO: 77 being shown in bold underline. In addition, the methionine residue in SpCas9 (H840) was removed for SpCas9 (H840A) VRQR):

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DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGET
AEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHE
RHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLLIYLALAHMIKFRGHFLIE
GDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLLENLIAQ
LPGEKKNGFLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLNLLAQIGD
QYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQ
QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDL
LRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPFLKDNREKIEKILTFRIPYYVGPLA
RGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHK
SLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE
DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLT
LFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTIL
DFLKSDGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIIKKGI
LQTVKVVDLVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIIEGIKELG
SQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFL
KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKKNYWRQLLNAKLITQRKFDNLT

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KAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVIT
LKSKLVSDFRKDFQFYKVRINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGD
YKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGET
GEIVWDKGRDFATVRKVLSPQVNVKKTEVQTGGFSKESILPKRNSDKLIARKKD
WDPKKYGGFVSPTVAYSVLVVAKEKGKSKKLKSVKELLGITIMERSSEKPNIDF
LEAKGYKEVKKDLIIKLPKYSLEFENGKRMLASARELQKGNELALPSKYVNFL
YLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQ
SITGLYETRIDLSQLGGD (SEQ ID NO: 77)

[0187] In another particular embodiment, the Cas9 variant having expanded PAM

capabilities is SpCas9 (H840A) VRER, which has the following amino acid sequence (with the V, R, E, R substitutions relative to the SpCas9 (H840A) of SEQ ID NO: 78 being shown in bold underline. In addition, the methionine residue in SpCas9 (H840) was removed for SpCas9 (H840A) VRER):

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGET
AEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKHE
RHPIFGNIVDEVAYHEKYPTIYHLRKKLVSDTDKADLRLLIYLALAHMIKFRGHFLIE
GDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQ
LPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLNLLAQIGD
QYADLFLAAKNLSAAILSDILRVNTEITKAPLSASMIKRYDEHHQDITLLKALVRQ
QLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNREDL
LRKQRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTRIPYYVGPLA
RGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHK
SLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE
DYFKKIECFDSVEISGVEDRFNASLGTYHDLKIIKDKDFLDNEENEDILEDIVLTLT
LFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTL
DFLKSDGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIIKKGI
LQTVKVVDLVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIIEGKELG
SQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVAIVPQSFL
KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLT
KAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVIT
LKSKLVSDFRKDFQFYKVRINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGD
YKVYDVRKMIKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGET
GEIVWDKGRDFATVRKVLSPQVNVKKTEVQTGGFSKESILPKRNSDKLIARKKD
WDPKKYGGFVSPTVAYSVLVVAKEKGKSKKLKSVKELLGITIMERSSEKPNIDF
LEAKGYKEVKKDLIIKLPKYSLEFENGKRMLASARELQKGNELALPSKYVNFL
YLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVLADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKEYRSTKEVLDATLIHQ
SITGLYETRIDLSQLGGD (SEQ ID NO: 78)

[0188] In some embodiments, the napDNAbp that functions with a non-canonical PAM

sequence is an Argonaute protein. One example of such a nucleic acid programmable DNA binding protein is an Argonaute protein from *Natronobacterium gregoryi* (NgAgo). NgAgo is a ssDNA-guided endonuclease. NgAgo binds 5' phosphorylated ssDNA of ~24 nucleotides (gDNA) to guide it to its target site and will make DNA double-strand breaks at the gDNA site. In contrast to Cas9, the NgAgo–gDNA system does not require a

protospacer-adjacent motif (PAM). Using a nuclease inactive NgAgo (dNgAgo) can greatly expand the bases that may be targeted. The characterization and use of NgAgo have been described in Gao *et al.*, *Nat Biotechnol.*, 2016 Jul;34(7):768-73. PubMed PMID: 27136078; Swarts *et al.*, *Nature*. 507(7491) (2014):258-61; and Swarts *et al.*, *Nucleic Acids Res.* 43(10) (2015):5120-9, each of which is incorporated herein by reference.

[0189] In some embodiments, the napDNAbp is a prokaryotic homolog of an Argonaute protein. Prokaryotic homologs of Argonaute proteins are known and have been described, for example, in Makarova K., et al., “Prokaryotic homologs of Argonaute proteins are predicted to function as key components of a novel system of defense against mobile genetic elements”, *Biol Direct*. 2009 Aug 25;4:29. doi: 10.1186/1745-6150-4-29, the entire contents of which is hereby incorporated by reference. In some embodiments, the napDNAbp is a *Marinitoga piezophila* Argonaute (MpAgo) protein. The CRISPR-associated *Marinitoga piezophila* Argonaute (MpAgo) protein cleaves single-stranded target sequences using 5'-phosphorylated guides. The 5' guides are used by all known Argonautes. The crystal structure of an MpAgo-RNA complex shows a guide strand binding site comprising residues that block 5' phosphate interactions. This data suggests the evolution of an Argonaute subclass with noncanonical specificity for a 5'-hydroxylated guide. See, e.g., Kaya et al., “A bacterial Argonaute with noncanonical guide RNA specificity”, *Proc Natl Acad Sci U S A*. 2016 Apr 12;113(15):4057-62, the entire contents of which are hereby incorporated by reference). It should be appreciated that other argonaute proteins may be used, and are within the scope of this disclosure.

[0190] Some aspects of the disclosure provide Cas9 domains that have different PAM specificities. Typically, Cas9 proteins, such as Cas9 from *S. pyogenes* (spCas9), require a canonical NGG PAM sequence to bind a particular nucleic acid region. This may limit the ability to edit desired bases within a genome. In some embodiments, the base editing fusion proteins provided herein may need to be placed at a precise location, for example where a target base is placed within a 4 base region (e.g., a “editing window”), which is approximately 15 bases upstream of the PAM. See Komor, A.C., et al., “Programmable editing of a target base in genomic DNA without double-stranded DNA cleavage” *Nature* 533, 420-424 (2016), the entire contents of which are hereby incorporated by reference. Accordingly, in some embodiments, any of the fusion proteins provided herein may contain a Cas9 domain that is capable of binding a nucleotide sequence that does not contain a canonical (e.g., NGG) PAM sequence. Cas9 domains that bind to non-canonical PAM sequences have been described in the art and would be apparent to the skilled artisan. For

example, Cas9 domains that bind non-canonical PAM sequences have been described in Kleinstiver, B. P., *et al.*, “Engineered CRISPR-Cas9 nucleases with altered PAM specificities” *Nature* 523, 481-485 (2015); and Kleinstiver, B. P., *et al.*, “Broadening the targeting range of *Staphylococcus aureus* CRISPR-Cas9 by modifying PAM recognition” *Nature Biotechnology* 33, 1293-1298 (2015); the entire contents of each are hereby incorporated by reference.

[0191] For example, a napDNAbp domain with altered PAM specificity, such as a domain with at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity with wild type *Francisella novicida* Cpf1 (D917, E1006, and D1255) (SEQ ID NO: 79), which has the following amino acid sequence:

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MSIYQEFVNKYSLSKTLRFELIPQGKTLENIKARGLILDDEKRAKDYKKAKQIIDKY
HQFFIEEILSSVCISEDLLQNYSDVYFKLKKSSDDNLQKDFKSAKDTIKKQISEYIKD
SEKFKNLFNQNLIDAKKGQESDLILWLKQSKDNGIELFKANSDITDIDEALEIISFK
GWTTFYFKGFHENRKNVYSSNDIPTSIYRIVDDNLPKFLENKAKYESLKDKAPEAIN
YEQIKKDLAEELTFDIDYKTSEVNQRVFSLDEVFEIANFNNYLNQSGITKFNTIIGGK
FVNGENTKRKGINEYINLYSQQINDKTLKKYKMSVLFKQILSDTESKSFVIDKLEDD
SDVVTTMQSFYEQIAAFKTVEEKSIKETLSLLFDDLKAQKLDLSKIYFKNDKSLTDL
SQQVFDDYSVIGTAVLEYITQQIAPKNLDNPSKKEQELIAKKTEKAKYLSLETIKLA
LEEFNKHRRDIDKQCRFEEILANFAAIPMIFDEIAQNKDNLAQISIKYQNQGKKDLLQ
ASAEDDVKAIKDLLDQTNLLHKLKIFHISQSEDKANILDKDEHFYLVFEECYFELA
NIVPLYNKIRNYITQKPYSDEKFKLNFENSTLANGWCKNKEPDNTAILFIKDDKYLL
GVMNKKNNKIFDDKAIKENKGEYKIVYKLLPGANKMLPKVFFSAKSIFYNPS
EDILRIRNHSTHTKNGSPQKGYEKFENIEDCRKFIDFYKQSISKHPEWKDFGFRFS
DTQRYNSIDEFYREVENQGYKLTFFENISESYIDSVVNQGLYLFQIYNKDFSAYSKG
RPNLHTLYWKALFDERNLQDVVYKLNGEAELFYRKQSIPKKITHPAKEAIANKNK
DNPKKESVFYEDLIKDKRFTEDKFFFHCPITINFKSSGANKFNDEINLLLKEKANDV
HILSIDRGERHLAYYTLVDGKGNIKQDTFNIIGNDRMKTNYHDKLAAIEKDRDSAR
KDWKKINNIKEMKEGYLSQVVHEIAKLVIEYNAIVVFEDLNFGFKRGRFKVEKQV
YQKLEKMLIEKLNLYLVFKDNEFDKTGGVLRAYQLTAPFETFKKMGKQTGIIYYVPA
GFTSKICPVTGFVNQLYPKYESVSKSQEFFSKFDKICYNLDKGYFEFSFDYKNFGDK
AAKGKWTIASFGSRLINFRNSDKNHNWDTREVYPTKELEKLLKDYSIEYGHGECIK
AAICGESDKKFFAKLTSVLNTILQMRNSKTGTLDYLISPVADVNGNFFDSRQAPKN
MPQDADANGAYHIGLKGLMLLGRIKNNQEGKKLNLVIKNEEYFEFVQNRNN (SEQ
ID NO: 79)
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[0192] An additional napDNAbp domain with altered PAM specificity, such as a domain having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity with wild type *Geobacillus thermodenitrificans* Cas9 (SEQ ID NO: 80), which has the following amino acid sequence:

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MKYKIGLDIGITSIGWAVINLDIPRIEDLGVRIFDRAENPKTGESLALPRRLARSARR
RLRRRKHRLERIRRLFVREGILTKEELNKLFEKKHEIDVWQLRVEALDRKLNDEL
ARILLHLAKRRGFRSNRKSERTNKENSTMLKHIEENQSILSSYRTVAEMVVKDPKFS
LHKRNKEDNYTNTVARDDLEREIKLIFAKQREYGNIVCTEAFEHEYISIWASQRPFA
SKDDIEKKVGFCFTFEPKEKRAPKATYTFQSFTVWEHINKLRLVSPGGIRALTDERR
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LIYKQAFHKKNKITFHDVRTLLNLPDDTRFKGLLYDRNTTLKENEKVRFLELGAYHK
IRKAIDSVYKGGAAKSFRPIDFDTFGYALTMFKDDTDIRSYLRNEYEQNGKRMENL
ADKVYDEELIEELLNLSFSKFGHLSLKALRNILPYMEQGEVYSTACERAGYTFTGP
KKKQKTVLLPNIPPIANPVVMRALTQARKVVNAIHKKYGSPVSIHIELARELSQSFD
ERRKMQKEQEGNRKKNETAIRQLVEYGLTLNPTGLDIVKFKLWSEQNGKCAYSLQ
PIEIERLLEPGYTEVDHVIPYSRSLDDSYTNKVLVLTKENREKGNRTPAEYLGLGSR
WQQFETFVLTKNQFSKKKRDRLRLHYDENEENEFEKNRNLDTRYISRFLANFIRE
HLKFADSDDKQKVYTVNGRITAHLSRWNFNKNREESNLHHAVDAAIVACTTPSDI
ARVTAFYQRREQNKELSKKTDPPQFPQWPHFADELQARLSKNPKESIKALNLGNY
DNEKLESQPVFVSRMPKRSITGAAHQETLRRYIGIDERSGKIQTVVKKKLSEIQLD
KTGHFPMYKESDPRTYEAIRQLLEHNNDPKKAFQEPLYKPKKNGELGPIIRTIKII
DTTNQVIPLNDGKTVAYNSNIVRVDVFEDGKYYCVPIYTIDMMKGILPNKAIEPN
KPYSEWKEMTEDYTFRFSLYPNDLIRIEFPREKTIKTAVGEEIKIKDLFAYYQTIDSSN
GGLSLVSHDNNFSLRSIGSRTLKRFEKYQVDVLGNIYKVRGEKRVGVASSSHSKAG
ETIRPL (SEQ ID NO: 80)

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[0193] In some embodiments, the nucleic acid programmable DNA binding protein (napDNAbp) is a nucleic acid programmable DNA binding protein that does not require a canonical (NGG) PAM sequence. In some embodiments, the napDNAbp is an argonaute protein. One example of such a nucleic acid programmable DNA binding protein is an Argonaute protein from *Natronobacterium gregoryi* (NgAgo). NgAgo is a ssDNA-guided endonuclease. NgAgo binds 5' phosphorylated ssDNA of ~24 nucleotides (gDNA) to guide it to its target site and will make DNA double-strand breaks at the gDNA site. In contrast to Cas9, the NgAgo–gDNA system does not require a protospacer-adjacent motif (PAM). Using a nuclease inactive NgAgo (dNgAgo) can greatly expand the bases that may be targeted. The characterization and use of NgAgo have been described in Gao *et al.*, *Nat Biotechnol.*, 34(7): 768-73 (2016), PubMed PMID: 27136078; Swarts *et al.*, *Nature*, 507(7491): 258-61 (2014); and Swarts *et al.*, *Nucleic Acids Res.* 43(10) (2015): 5120-9, each of which is incorporated herein by reference. The sequence of *Natronobacterium gregoryi* Argonaute is provided in SEQ ID NO: 81.

[0194] The disclosed fusion proteins may comprise a napDNAbp domain having at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity with wild type *Natronobacterium gregoryi* Argonaute (SEQ ID NO: 81), which has the following amino acid sequence:

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MTVIDLDSTTTADELTSGHTYDISVTLTGVDNTDEQHPRMSLAFEQDNGERRYIT
LWKNTTPKDVFTYDYATGSTYIFTNIDYEVKDGYNLTATYQTTVENATAQEVGTT
DEDETFAGGEPLDHHLLDDALNETPDDAETESDSGHVMTSFASRDQLPEWTLHTYT
LTATDGAKTDEYARRTLAYTVRQELYTDHDAAPVATDGLMLLTPEPLGETPLDLD
CGVRVEADETRTLDYTTAKDRLLARELVEEGLKRSLWDDYLVRGIDEVLSKEPVL
CDEFDLHERYDLSVEVGHSGRAYLHINFRHRFVPKLTLADIDDDNIYPGLRVKTTY
RPRRGHIVWGLRDECATDSLNTLGNQSVVAYHRNNQTPINTDLLDAIEAADRRVVE
TRRQGHGDDAVSFPQELLAVEPNTHQIKQFASDGFHQQARSKTRLSASRCSEKAQA

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FAERLDPVRLNGSTVEFSSEFFTGNNEQQLRLLYENGESVLTFRDGARGAHPDETFS
 KGIVNPPESFEVAVVLPEQQADTCKAQWDTMADLLNQAGAPPTRSETVQYDAFSS
 PESISLNVAGAI DPSEVDAAFVVLPPDQEGFADLASPTETYDELKKALANMGIYSQ
 MAYFDRFRDAKIFYTRNVALGLLAAAGGVAFTTEHAMPGDADMFIGIDVSRSTPE
 DGASGQINIAATATAVYKDGITLGHSSSTRPQLGEKLQSTDVVRDIMKNAILGYQQVT
 GESPTHIVIH RDGFMNEDLDPATEFLNEQGV EYDIVEIRKQPQTRLLAVSDVQYDTP
 VKSIAAINQNEPRATVATFGAPEY LATRDGGGLPRPIQIERVAGETDIETLTRQVYLL
 SQSHIQVHNSTARLPITTAYADQASTHATKGYLVQTGAFESNVGFL (SEQ ID NO:
 81)

[0195] In addition, any available methods may be utilized to obtain or construct a variant or mutant Cas9 protein. The term “mutation,” as used herein, refers to a substitution of a residue within a sequence, e.g., a nucleic acid or amino acid sequence, with another residue, or a deletion or insertion of one or more residues within a sequence. Mutations are typically described herein by identifying the original residue followed by the position of the residue within the sequence and by the identity of the newly substituted residue. Various methods for making the amino acid substitutions (mutations) provided herein are well known in the art, and are provided by, for example, Green and Sambrook, *Molecular Cloning: A Laboratory Manual* (4th ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (2012)). Mutations can include a variety of categories, such as single base polymorphisms, microduplication regions, indel, and inversions, and is not meant to be limiting in any way. Mutations can include “loss-of-function” mutations which is the normal result of a mutation that reduces or abolishes a protein activity. Most loss-of-function mutations are recessive, because in a heterozygote the second chromosome copy carries an unmutated version of the gene coding for a fully functional protein whose presence compensates for the effect of the mutation. Mutations also embrace “gain-of-function” mutations, which is one which confers an abnormal activity on a protein or cell that is otherwise not present in a normal condition. Many gain-of-function mutations are in regulatory sequences rather than in coding regions, and can therefore have a number of consequences. For example, a mutation might lead to one or more genes being expressed in the wrong tissues, these tissues gaining functions that they normally lack. Because of their nature, gain-of-function mutations are usually dominant.

[0196] Mutations can be introduced into a reference Cas9 protein using site-directed mutagenesis. Older methods of site-directed mutagenesis known in the art rely on sub-cloning of the sequence to be mutated into a vector, such as an M13 bacteriophage vector, that allows the isolation of single-stranded DNA template. In these methods, one anneals a mutagenic primer (i.e., a primer capable of annealing to the site to be mutated but bearing one or more mismatched nucleotides at the site to be mutated) to the single-stranded template and then polymerizes the complement of the template starting from the 3' end of the mutagenic

primer. The resulting duplexes are then transformed into host bacteria and plaques are screened for the desired mutation. More recently, site-directed mutagenesis has employed PCR methodologies, which have the advantage of not requiring a single-stranded template. In addition, methods have been developed that do not require sub-cloning. Several issues must be considered when PCR-based site-directed mutagenesis is performed. First, in these methods it is desirable to reduce the number of PCR cycles to prevent expansion of undesired mutations introduced by the polymerase. Second, a selection must be employed in order to reduce the number of non-mutated parental molecules persisting in the reaction. Third, an extended-length PCR method is preferred in order to allow the use of a single PCR primer set. And fourth, because of the non-template-dependent terminal extension activity of some thermostable polymerases it is often necessary to incorporate an end-polishing step into the procedure prior to blunt-end ligation of the PCR-generated mutant product.

[0197] Mutations may also be introduced by directed evolution processes, such as phage-assisted continuous evolution (PACE) or phage-assisted noncontinuous evolution (PANCE). The term “phage-assisted continuous evolution (PACE),” as used herein, refers to continuous evolution that employs phage as viral vectors. The general concept of PACE technology has been described, for example, in International PCT Application, PCT/US2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Application, U.S. Patent No. 9,023,594, issued May 5, 2015, International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015, and International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, the entire contents of each of which are incorporated herein by reference. Variant Cas9s may also be obtain by phage-assisted non-continuous evolution (PANCE),” which as used herein, refers to non-continuous evolution that employs phage as viral vectors. PANCE is a simplified technique for rapid in vivo directed evolution using serial flask transfers of evolving ‘selection phage’ (SP), which contain a gene of interest to be evolved, across fresh *E. coli* host cells, thereby allowing genes inside the host *E. coli* to be held constant while genes contained in the SP continuously evolve. Serial flask transfers have long served as a widely-accessible approach for laboratory evolution of microbes, and, more recently, analogous approaches have been developed for bacteriophage evolution. The PANCE system features lower stringency than the PACE system.

[0198] Any of the references noted above which relate to Cas9 or Cas9 equivalents are hereby incorporated by reference in their entireties, if not already stated so.

J. Divided napDNAbp domains for split genome editor delivery

[0199] In various embodiments, the genome editing system described herein may be delivered to cells as two or more fragments which become assembled inside the cell (either by passive assembly, or by active assembly, such as using split intein sequences) into a reconstituted genome editor. In some cases, the self assembly may be passive whereby the two or more genome editor fragments associate inside the cell covalently or non-covalently to reconstitute the genome editor. In other cases, the self-assembly may be catalyzed by dimerization domains installed on each of the fragments. Examples of dimerization domains are described herein. In still other cases, the self-assembly may be catalyzed by split intein sequences installed on each of the genome editor fragments.

[0200] Split PE delivery may be advantageous to address various size constraints of different delivery approaches. For example, delivery approaches may include virus-based delivery methods, messenger RNA-based delivery methods, or RNP-based delivery (ribonucleoprotein-based delivery). And, each of these methods of delivery may be more efficient and/or effective by dividing up the genome editor into smaller pieces. Once inside the cell, the smaller pieces can assemble into a functional genome editor. Depending on the means of splitting, the divided genome editor fragments can be reassembled in a non-covalent manner or a covalent manner to reform the genome editor. In one embodiment, the genome editor can be split at one or more split sites into two or more fragments. The fragments can be unmodified (other than being split). Once the fragments are delivered to the cell (e.g., by direct delivery of a ribonucleoprotein complex or by nucleic delivery – e.g., mRNA delivery or virus vector based delivery), the fragments can reassociate covalently or non-covalently to reconstitute the genome editor. In another embodiment, the genome editor can be split at one or more split sites into two or more fragments. Each of the fragments can be modified to comprise a dimerization domain, whereby each fragment that is formed is coupled to a dimerization domain. Once delivered or expressed within a cell, the dimerization domains of the different fragments associate and bind to one another, bringing the different genome editor fragments together to reform a functional genome editor. In yet another embodiment, the genome editor fragment may be modified to comprise a split intein. Once delivered or expressed within a cell, the split intein domains of the different fragments associate and bind to one another, and then undergo trans-splicing, which results in the excision of the split-

intein domains from each of the fragments, and a concomitant formation of a peptide bond between the fragments, thereby restoring the genome editor.

[0201] In one embodiment, the genome editor can be delivered using a split-intein approach.

[0202] The location of the split site can be positioned between any one or more pair of residues in the genome editor and in any domains therein, including within the napDNABp domain, the polymerase domain (e.g., RT domain), linker domain that joins the napDNABp domain and the polymerase domain.

[0203] In certain embodiments, the napDNABp is a canonical SpCas9 polypeptide of SEQ ID NO: 82, as follows:

SpCas9 <i>Streptococcus pyogenes</i> M1 SwissProt Accession No. Q99ZW2 Wild type 1368 AA	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGN TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRR KNRICYLQEIFSNEMAKVDDSFHRLEESFLVEEDKKH ERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADL RLIYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQ TYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQL PGEKKNGLFGNLIASLGLTPNFKSDFDLAEDAKLQLS KDTYDDDLNLLAQIGDQYADLFLAAKNLSDAILLSDI LRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEK MDGTEELLVKLNRDILLRKQRTFDNGSIPHQIHLGELH AILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGN SRFAWMTRKSEETITPWNFEEVVDKGASQSFIERMTN FDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGM RKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKI ECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEE NEDILEDIVLTTLTFEDREMIEERLKTYAHLFDDKVMK QLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDG FANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIA NLAGSPAIKKILQTVKVVDLVKVMGRHKPENIVIEEM ARENQTQKGQKNSRERMKRIEELGKSGILKEHPV ENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYD VDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEV VKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSEL DKAGFIKQRLVETRQITKHVAQILDSRMNTKYDENDK LIREVKVITLKSCLVSDFRKDFQFYKVREINNYHHAHD AYLNNAVGTALIKKYPKLESEFVYGDYKVYDVRKMIA KSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLI ETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEV QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT VAYSVLVAKVEKGKSKKLKSVKELLGITIMERSSSFEEK NPIDFLEAKGYKEVKKDLIIKLPKYSLELENGRKRML ASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDE NEQKQLFVEQHKHYLDEIEQISEFSKRVLADANLDKV LSAYNKHHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDT TIDRKRYTSTKEVLDTLHQSIITGLYETRIDLSQLGGD	SEQ ID NO: 82
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[0204] In certain embodiments, the SpCas9 is split into two fragments at a split site located between residues 1 and 2, or 2 and 3, or 3 and 4, or 4 and 5, or 5 and 6, or 6 and 7, or 7 and 8, or 8 and 9, or 9 and 10, or between any two pair of residues located anywhere between residues 1-10, 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, 1000-1100, 1100-1200, 1200-1300, or 1300-1368 of canonical SpCas9 of SEQ ID NO: 11.

[0205] In certain embodiments, a napDNAbp is split into two fragments at a split site that is located at a pair of residue that corresponds to any two pair of residues located anywhere between positions 1-10, 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, 1000-1100, 1100-1200, 1200-1300, or 1300-1368 of canonical SpCas9 of SEQ ID NO: 11.

[0206] In certain embodiments, the SpCas9 is split into two fragments at a split site located between residues 1 and 2, or 2 and 3, or 3 and 4, or 4 and 5, or 5 and 6, or 6 and 7, or 7 and 8, or 8 and 9, or 9 and 10, or between any two pair of residues located anywhere between residues 1-10, 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, 1000-1100, 1100-1200, 1200-1300, or 1300-1368 of canonical SpCas9 of SEQ ID NO: 11. In certain embodiments, the split site is located one or more polypeptide bond sites (i.e., a “split site or split-intein split site”), fused to a split intein, and then delivered to cells as separately-encoded fusion proteins. Once the split-intein fusion proteins (i.e., protein halves) are expressed within a cell, the proteins undergo trans-splicing to form a complete or whole PE with the concomitant removal of the joined split-intein sequences.

[0207] For example, the N-terminal extein can be fused to a first split-intein (e.g., N intein) and the C-terminal extein can be fused to a second split-intein (e.g., C intein). The N-terminal extein becomes fused to the C-terminal extein to reform a whole genome editor fusion protein comprising an napDNAbp domain and a polymerase domain (e.g., RT domain) upon the self-association of the N intein and the C intein inside the cell, followed by their self-excision, and the concomitant formation of a peptide bond between the N-terminal extein and C-terminal extein portions of a whole genome editor (GE).

[0208] To take advantage of a split-PE delivery strategy using split-inteins, the genome editor needs to be divided at one or more split sites to create at least two separate halves of a genome editor, each of which may be rejoined inside a cell if each half is fused to a split-intein sequence.

[0209] In certain embodiments, the genome editor is split at a single split site. In certain other embodiments, the genome editor is split at two split sites, or three split sites, or four split sites, or more.

[0210] In a preferred embodiment, the genome editor is split at a single split site to create two separate halves of a genome editor, each of which can be fused to a split intein sequence

[0211] An exemplary split intein is the *Ssp* DnaE intein, which comprises two subunits, namely, DnaE-N and DnaE-C. The two different subunits are encoded by separate genes, namely *dnaE-n* and *dnaE-c*, which encode the DnaE-N and DnaE-C subunits, respectively. DnaE is a naturally occurring split intein in *Synechocystis sp.* PCC6803 and is capable of directing trans-splicing of two separate proteins, each comprising a fusion with either DnaE-N or DnaE-C.

[0212] Additional naturally occurring or engineered split-intein sequences are known in the art or can be made from whole-intein sequences described herein or those available in the art. Examples of split-intein sequences can be found in Stevens et al., "A promiscuous split intein with expanded protein engineering applications," PNAS, 2017, Vol.114: 8538-8543; Iwai et al., "Highly efficient protein trans-splicing by a naturally split DnaE intein from *Nostoc punctiforme*, FEBS Lett, 580: 1853-1858, each of which are incorporated herein by reference. Additional split intein sequences can be found, for example, in WO 2013/045632, WO 2014/055782, WO 2016/069774, and EP2877490, the contents each of which are incorporated herein by reference.

[0213] In addition, protein splicing in trans has been described *in vivo* and *in vitro* (Shingledacker, et al., *Gene* 207:187 (1998), Southworth, et al., *EMBO J.* 17:918 (1998); Mills, et al., *Proc. Natl. Acad. Sci. USA*, 95:3543-3548 (1998); Lew, et al., *J. Biol. Chem.*, 273:15887-15890 (1998); Wu, et al., *Biochim. Biophys. Acta* 35732:1 (1998b), Yamazaki, et al., *J. Am. Chem. Soc.* 120:5591 (1998), Evans, et al., *J. Biol. Chem.* 275:9091 (2000); Otomo, et al., *Biochemistry* 38:16040-16044 (1999); Otomo, et al., *J. Biolmol. NMR* 14:105-114 (1999); Scott, et al., *Proc. Natl. Acad. Sci. USA* 96:13638-13643 (1999)) and provides the opportunity to express a protein as to two inactive fragments that subsequently undergo ligation to form a functional product.

[0214] In various embodiments described herein, the continuous evolution methods (e.g., PACE) may be used to evolve a first portion of a base editor. A first portion could include a single component or domain, e.g., a Cas9 domain, a deaminase domain, or a UGI domain. The separately evolved component or domain can be then fused to the remaining portions of the base editor within a cell by separately express both the evolved portion and the remaining

non-evolved portions with split-intein polypeptide domains. The first portion could more broadly include any first amino acid portion of a base editor that is desired to be evolved using a continuous evolution method described herein. The second portion would in this embodiment refer to the remaining amino acid portion of the base editor that is not evolved using the herein methods. The evolved first portion and the second portion of the base editor could each be expressed with split-intein polypeptide domains in a cell. The natural protein splicing mechanisms of the cell would reassemble the evolved first portion and the non-evolved second portion to form a single fusion protein evolved base editor. The evolved first portion may comprise either the N- or C-terminal part of the single fusion protein. In an analogous manner, use of a second orthogonal trans-splicing intein pair could allow the evolved first portion to comprise an internal part of the single fusion protein.

[0215] Thus, any of the evolved and non-evolved components of the base editors herein described may be expressed with split-intein tags in order to facilitate the formation of a complete base editor comprising the evolved and non-evolved component within a cell.

[0216] The mechanism of the protein splicing process has been studied in great detail (Chong, et al., J. Biol. Chem. 1996, 271, 22159-22168; Xu, M-Q & Perler, F. B. EMBO Journal, 1996, 15, 5146-5153) and conserved amino acids have been found at the intein and extein splicing points (Xu, et al., EMBO Journal, 1994, 13 5517-522). The constructs described herein contain an intein sequence fused to the 5'-terminus of the first gene (e.g., the evolved portion of the base editor). Suitable intein sequences can be selected from any of the proteins known to contain protein splicing elements. A database containing all known inteins can be found on the World Wide Web (Perler, F. B. Nucleic Acids Research, 1999, 27, 346-347). The intein sequence is fused at the 3' end to the 5' end of a second gene. For targeting of this gene to a certain organelle, a peptide signal can be fused to the coding sequence of the gene. After the second gene, the intein-gene sequence can be repeated as often as desired for expression of multiple proteins in the same cell. For multi-intein containing constructs, it may be useful to use intein elements from different sources. After the sequence of the last gene to be expressed, a transcription termination sequence must be inserted. In one embodiment, a modified intein splicing unit is designed so that it can both catalyze excision of the exteins from the inteins as well as prevent ligation of the exteins. Mutagenesis of the C-terminal extein junction in the *Pyrococcus* species GB-D DNA polymerase was found to produce an altered splicing element that induces cleavage of exteins and inteins but prevents subsequent ligation of the exteins (Xu, M-Q & Perler, F. B. EMBO Journal, 1996, 15, 5146-5153). Mutation of serine 538 to either an alanine or glycine induced cleavage but prevented

ligation. Mutation of equivalent residues in other intein splicing units should also prevent extein ligation due to the conservation of amino acids at the C-terminal extein junction to the intein. A preferred intein not containing an endonuclease domain is the *Mycobacterium xenopi* GyrA protein (Telenti, et al. J. Bacteriol. 1997, 179, 6378-6382). Others have been found in nature or have been created artificially by removing the endonuclease domains from endonuclease containing inteins (Chong, et al. J. Biol. Chem. 1997, 272, 15587-15590). In a preferred embodiment, the intein is selected so that it consists of the minimal number of amino acids needed to perform the splicing function, such as the intein from the *Mycobacterium xenopi* GyrA protein (Telenti, A., et al., J. Bacteriol. 1997, 179, 6378-6382). In an alternative embodiment, an intein without endonuclease activity is selected, such as the intein from the *Mycobacterium xenopi* GyrA protein or the *Saccharomyces cerevisiae* VMA intein that has been modified to remove endonuclease domains (Chong, 1997). Further modification of the intein splicing unit may allow the reaction rate of the cleavage reaction to be altered allowing protein dosage to be controlled by simply modifying the gene sequence of the splicing unit.

[0217] Inteins can also exist as two fragments encoded by two separately transcribed and translated genes. These so-called split inteins self-associate and catalyze protein- splicing activity in trans. Split inteins have been identified in diverse cyanobacteria and archaea (Caspi et al, Mol Microbiol. 50: 1569-1577 (2003); Choi J. et al, J Mol Biol. 556: 1093-1106 (2006.); Dassa B. et al, Biochemistry. 46:322-330 (2007.); Liu X. and Yang J., J Biol Chem. 275:26315-26318 (2003); Wu H. et al.

[0218] Proc Natl Acad Sci USA. 95:9226-9231 (1998.); and Zettler J. et al, FEBS Letters. 553:909-914 (2009)), but have not been found in eukaryotes thus far. Recently, a bioinformatic analysis of environmental metagenomic data revealed 26 different loci with a novel genomic arrangement. At each locus, a conserved enzyme coding region is interrupted by a split intein, with a freestanding endonuclease gene inserted between the sections coding for intein subdomains. Among them, five loci were completely assembled: DNA helicases (gp41-1, gp41-8); Inosine-5'-monophosphate dehydrogenase (IMPDH-1); and Ribonucleotide reductase catalytic subunits (NrdA-2 and NrdJ-1). This fractured gene organization appears to be present mainly in phages (Dassa et al, Nucleic Acids Research. 57:2560-2573 (2009)).

[0219] The split intein Npu DnaE was characterized as having the highest rate reported for the protein trans-splicing reaction. In addition, the Npu DnaE protein splicing reaction is considered robust and high-yielding with respect to different extein sequences, temperatures from 6 to 37°C, and the presence of up to 6M Urea (Zettler J. et al, FEBS Letters. 553:909-

914 (2009); Iwai I. et al, FEBS Letters 550: 1853-1858 (2006)). As expected, when the Cys1 Ala mutation at the N-domain of these inteins was introduced, the initial N to S- acyl shift and therefore protein splicing was blocked. Unfortunately, the C- terminal cleavage reaction was also almost completely inhibited. The dependence of the asparagine cyclization at the C-terminal splice junction on the acyl shift at the N-terminal scissile peptide bond seems to be a unique property common to the naturally split DnaE intein alleles (Zettler J. et al. FEBS Letters. 555:909-914 (2009)).

[0220] The mechanism of protein splicing typically has four steps [29-30]: 1) an N-S or N-O acyl shift at the intein N-terminus, which breaks the upstream peptide bond and forms an ester bond between the N- extein and the side chain of the intein's first amino acid (Cys or Ser); 2) a transesterification relocating the N-extein to the intein C-terminus, forming a new ester bond linking the N-extein to the side chain of the C-extein's first amino acid (Cys, Ser, or Thr); 3) Asn cyclization breaking the peptide bond between the intein and the C-extein; and 4) a S-N or O-N acyl shift that replaces the ester bond with a peptide bond between the N-extein and C-extein.

[0221] Protein trans-splicing, catalyzed by split inteins, provides an entirely enzymatic method for protein ligation. A split-intein is essentially a contiguous intein (e.g. a mini-intein) split into two pieces named N-intein and C-intein, respectively. The N-intein and C-intein of a split intein can associate non-covalently to form an active intein and catalyze the splicing reaction essentially in same way as a contiguous intein does. Split inteins have been found in nature and also engineered in laboratories. As used herein, the term "split intein" refers to any intein in which one or more peptide bond breaks exists between the N-terminal and C-terminal amino acid sequences such that the N-terminal and C-terminal sequences become separate molecules that can non-covalently reassociate, or reconstitute, into an intein that is functional for trans-splicing reactions. Any catalytically active intein, or fragment thereof, may be used to derive a split intein for use in the methods of the invention. For example, in one aspect the split intein may be derived from a eukaryotic intein. In another aspect, the split intein may be derived from a bacterial intein. In another aspect, the split intein may be derived from an archaeal intein. Preferably, the split intein so-derived will possess only the amino acid sequences essential for catalyzing trans-splicing reactions.

[0222] As used herein, the "N-terminal split intein (In)" refers to any intein sequence that comprises an N- terminal amino acid sequence that is functional for trans-splicing reactions. An In thus also comprises a sequence that is spliced out when trans-splicing occurs. An In can comprise a sequence that is a modification of the N-terminal portion of a naturally

occurring intein sequence. For example, an In can comprise additional amino acid residues and/or mutated residues so long as the inclusion of such additional and/or mutated residues does not render the In non-functional in trans-splicing. Preferably, the inclusion of the additional and/or mutated residues improves or enhances the trans-splicing activity of the In.

[0223] As used herein, the "C-terminal split intein (Ic)" refers to any intein sequence that comprises a C-terminal amino acid sequence that is functional for trans-splicing reactions. In one aspect, the Ic comprises 4 to 7 contiguous amino acid residues, at least 4 amino acids of which are from the last β -strand of the intein from which it was derived. An Ic thus also comprises a sequence that is spliced out when trans-splicing occurs. An Ic can comprise a sequence that is a modification of the C-terminal portion of a naturally occurring intein sequence. For example, an Ic can comprise additional amino acid residues and/or mutated residues so long as the inclusion of such additional and/or mutated residues does not render the In non-functional in trans-splicing. Preferably, the inclusion of the additional and/or mutated residues improves or enhances the trans-splicing activity of the Ic.

[0224] In some embodiments of the invention, a peptide linked to an Ic or an In can comprise an additional chemical moiety including, among others, fluorescence groups, biotin, polyethylene glycol (PEG), amino acid analogs, unnatural amino acids, phosphate groups, glycosyl groups, radioisotope labels, and pharmaceutical molecules. In other embodiments, a peptide linked to an Ic can comprise one or more chemically reactive groups including, among others, ketone, aldehyde, Cys residues and Lys residues. The N-intein and C-intein of a split intein can associate non-covalently to form an active intein and catalyze the splicing reaction when an "intein-splicing polypeptide (ISP)" is present. As used herein, "intein-splicing polypeptide (ISP)" refers to the portion of the amino acid sequence of a split intein that remains when the Ic, In, or both, are removed from the split intein. In certain embodiments, the In comprises the ISP. In another embodiment, the Ic comprises the ISP. In yet another embodiment, the ISP is a separate peptide that is not covalently linked to In nor to Ic.

[0225] Split inteins may be created from contiguous inteins by engineering one or more split sites in the unstructured loop or intervening amino acid sequence between the -12 conserved beta-strands found in the structure of mini-inteins. Some flexibility in the position of the split site within regions between the beta-strands may exist, provided that creation of the split will not disrupt the structure of the intein, the structured beta-strands in particular, to a sufficient degree that protein splicing activity is lost.

In protein trans-splicing, one precursor protein consists of an N-extein part followed by the N-intein, another precursor protein consists of the C-intein followed by a C-extein part, and a trans-splicing reaction (catalyzed by the N- and C-inteins together) excises the two intein sequences and links the two extein sequences with a peptide bond. Protein trans-splicing, being an enzymatic reaction, can work with very low (e.g. micromolar) concentrations of proteins and can be carried out under physiological conditions.

[2] Ribozymes

[0226] The genome editing system described here comprise one or more ribozymes. The ribozymes can be naturally occurring in some embodiments so long as the naturally occurring ribozymes are capable of using DNA as a substrate. In other embodiments, the ribozymes can be derived from naturally occurring ribozymes, e.g., by genetic engineering, mutagenesis, or installation of chemical modifications into a naturally occurring ribozyme. The ribozymes may also be fully synthetic. In preferred embodiments, the ribozymes should possess (a) the capability of annealing to a strand of the target edit site bound by a napDNAbp/guide RNA complex, (b) cleaving a phosphodiester bond at a ribozyme nick site on the annealed strand, (c) installing on the annealed strand one or more nucleotides at the ribozyme nick site, and then (d) ligating the installed one or more nucleotides to the annealed strand.

[0227] In one embodiment, the ribozyme can be the engineered ribozyme of FIG. 1A. FIG. 1A shows the sequence and secondary structure of (a) an exemplary engineered ribozyme based on the ribozyme of *Tetrahymena* group I intron with mutations identified in directed evolution that enable the ribozyme to bind and cleave ssDNA (blue and/or indicated with a “star”) and insertions and deletions that enable nucleotide (e.g., GTP) insertion (red boxes). For example, element (b) refers to the deletion of the terminal nucleotides (e.g., the terminal 4 nucleotides) of the ribozyme, which inactivates the self-insertion activity of the ribozyme for self-insertion into the DNA target or substrate with which the ribozyme is interacting. This is also shown in more details in FIG. 3B. Element (c) shows engineered changes in the active site which interacts with the substrate DNA, catalyzing the insertion of the nucleotide at the target site of the target DNA substrate. Element (d) refers to the location or site of insertion of an MS2 hairpin (AUCUU sequence is removed and replaced with the MS2 hairpin), which functions as a targeting moiety to localize the engineered ribozyme to a bound napDNAbp/guide RNA complex to a target DNA site, wherein the napDNAbp is modified to incorporate a cognate targeting moiety receptor. The nucleotide sequence of the ribozyme of FIG. 1A, as shown, is SEQ ID NO: 88.

[0228] The combination of FIG. 2A and 2D depict an embodiment of the ribozymes contemplated herein and how they function in relation to a napDNAbp/guide RNA complex at target site in DNA. FIG. 2A is a schematic showing the repair of a frameshift mutation via single-nucleotide insertion of a G into genomic DNA as carried about by a genomic editing system comprising a ribozyme (referred to as a “group I insertase”, which is one broad category of ribozymes known in the art) and a Cas9/guide RNA complex. In reference to FIG. 2A and also the detailed illustration of FIG. 2D, binding of the Cas9/guide RNA complex to genomic DNA forms a ssDNA R-loop opposite the strand occupied by the guide RNA’s spacer sequence. The engineered ribozyme (as provided in trans) then binds to its single strand DNA substrate, whereby a portion of the ribozyme anneals to the single strand DNA of the R loop over a short complementary (or partly complementary) sequence (e.g., at least a 3, at least a 4, at least a 5, at least a 6, at least a 7, at least a 8, at least a 9, at least a 10, at least an 11, at least a 12, at least a 13, at least a 14, or at least a 15 nucleotide stretch in the R loop region). Once hybridized to the R loop at the complementary region, the ribozyme installs a ribozyme nick in the R loop strand, leaving ...A-5’ and 3’-T... ends on either side of the nick. The ribozyme then catalyzes the formation of a phosphodiester bond between the ...A-5’ end and a G. There is then a shift in hybridization pairing by one base pair of the annealed strand which moves one base position towards the 5’ end of the ribozyme. Lastly, the ribozyme catalyzes a ligation between the inserted G and the pre-existing T to form a new phosphodiester bond, thereby ligating the previously-nicked strands together again, which now includes the inserted G as a +1 nucleotide. In subsequent rounds of replication and/or DNA repair, the inserted G leads to the introduction of a C base pair on the opposite strand, thereby permanently installing a G:C nucleobase pair, and thus, a frameshift change. The ribozyme is released and can participate in another such reaction.

[0229] FIG. 3B shows the structural and functional details of an embodiment of a ribozyme contemplated for use in the present genome editing system. The skilled person will appreciate that the various sequence regions defined in FIG. 3B can be varied so long as they maintain their function. For example, the region labeled as “(j)” may be adjusted based on the target sequence of the R loop induced to form by a given napDNAbp/guide RNA complex. Element (a) refers to the exemplary engineered ribozyme contemplated herein which is annealed at elements (h), (i), and (j) to a complementary or mostly complementary region in the R loop of a Cas9/guide RNA complex (complex not depicted). Element (b) represents the backbone portion of an exemplary engineered ribozyme, which can include the nucleotides in FIG. 1A identified with a “star” symbol, which enable the ribozyme to bind

and act on DNA, as opposed to a natural RNA substrate. Examples of such modifications can be found described in Joyce et al., “Selection *in vitro* of an RNA enzyme that specifically cleaves single-stranded DNA,” *Nature*, 1990, p. 467, which is incorporated herein by reference. Element (c) refers to the deletion of the terminal nucleotides (e.g., the terminal 4 nucleotides) of the ribozyme, which inactivates or removes the self-insertion activity of the ribozyme for self-insertion into the DNA target or substrate with which the ribozyme is interacting. Element (d) refers to a GTP (nucleotide) substrate, which is inserted by the ribozyme into the DNA at the insertion site between elements (h) and (i) to change the target edit DNA sequence from GATCTGGG-5’ to GAGTCTGGG-5’. Without being bound by theory, and in reference to the stepwise mechanism of FIG. 2D, insertion would result in the breakage of the phosphodiester bond between the A and T nucleotides in the DNA substrate, inserting of a G from the GTP at the insertion site through formation of a phosphiester bond between the inserted G and the existing A on the DNA strand. The downstream A-G- would then shift such that the G would hybridize to the unpaired C in the ribozyme (the C located at element (g)), causing at the same time the pairing of the inserted G with the U on the ribozyme in element (h). Lastly, the ribozyme would catalyze the ligation of the introduced G to the upstream T in element (i), thereby introducing a G into the target DNA sequence. Through subsequent DNA repair and/or replication processes, a complete G:C nucleobase pair will have been inserted/incorporated into the double strand DNA target site.

[0230] Element (d) can preferably be a GTP or an ATP. In some embodiments, element (d) can be a TTP or a CTP. Element (e) refers to G nucleotides which facilitate effective transcription of the ribozyme. Element (f) refers to an extension of the P0 region of the ribozyme, which improves the binding of the substrate DNA to the ribozyme (e.g., as described further in Tsang and Joyce, “Specialization of the DNA-cleaving activity of a group I ribozyme through *in vitro* evolution,” *J. Mol. Biol.*, 1996, 262(1):31-42, which is incorporated herein by reference). The length of this region can vary, e.g., can be from about 1-10 nucleobase pairs, or 2-12 nucleobase pairs, or 3-13 nucleobase pairs, or 4-14 nucleobase pairs, or from 5-20 nucleobase pairs, or the length can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30, or more nucleotides. Element (g) is an unpaired nucleotide, which results in fewer required purines of element (h) needed to shift the substrate sequences upon insertion of the new nucleotide (e.g., GTP). In the example shown, element (g) is an unpaired C, however this can be G, A, or T, in some embodiments.

[0231] Since regions (f), (h), (i), and (j) of the P0 region of the ribozyme of FIG. 3B will depend upon the sequence of the target strand, these nucleotide sequences can be varied, in various embodiments, in accordance with the following rules in order to interact with a desired target sequence:

[0232] Rule 1: Region (j) should form the complement of the target sequence over a multi-nucleotide stretch. In the embodiment shown, the stretch of nucleotides shown in (j) is 5 nucleotides; however, this region could range from 3 nucleotides, 4 nucleotides, 5 nucleotides, 6 nucleotides, 7 nucleotides, 8 nucleotides, 9 nucleotides, 10 nucleotides, 11 nucleotides, 12 nucleotides, 13 nucleotides, 14 nucleotides, 15 nucleotides, or more. The longer the region (j), the longer the region of complementarity is needed in the target sequence, which will be limited to the length of the single-stranded region of the R loop of the Cas9/guideRNA bubble. The exact sequence of the complementary target sequence will depend upon the R loop sequence, which is determined, in turn, by the sequence that is targeted by the Cas9/guide RNA complex.

[0233] Rule 2: Region (i) is the “wobble” position. Preferably, the wobble position is created by an imperfect Watson-Crick hydrogen bond pairing. Thus, if the target sequence is a T at position corresponding to (i), then position (i) in the ribozyme should be designed as G, C, or T, but not an A. If the target sequence is an A at position corresponding to (i), then position (i) in the ribozyme should be designed as G, C, or A, but not a T. If the target sequence is a G at position corresponding to (i), then position (i) in the ribozyme should be designed as T, A, or G, but not a C. If the target sequence is a C at position corresponding to (i), then position (i) in the ribozyme should be designed as T, A, or C, but not a G. These conditions should provide for imperfect Watson-Crick hydrogen bond pairing, or wobble pairing.

[0234] Rule 3: Preferably, element (h) of the ribozyme should be a string of uracils, and can include a string of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or more uracils at this position. Preferably, the element (h) is a string of two consecutive uracils.

[0235] Rule 4: Preferably, there is an extra C inserted at position (g) in the ribozyme, which will facilitate the shifting of the target sequence upward such that a hydrogen bond forms between the G in the target sequence corresponding to position (h) in the ribozyme, leaving room for insertion of a nucleotide (e.g., GTP) of element (d). This means that preferably the 3'-most nucleotide in the target sequence opposite element (h) of the ribozyme is a G, so that it may hydrogen bond with the extra C at position (g).

[0236] Rule 5: Element (f) can be designed as a complement to additional target sequence to enhance the binding of the ribozyme to the target sequence.

[0237] Element (h) is a series of pyrimidine-purine nucleobase pairs (e.g., can be 1, 2, 3, 4, or 5 or more U-G, U-A, or C-G nucleobase pairs) that sit adjacent to the “wobble” nucleobase pair of element (i). The nucleobases of element (h) function to enable shifting in the active site of the ribozyme (or shifting of the target DNA sequence) upon insertion of the nucleotide of element (d) (e.g., the GTP). The nucleobases of element (h) also enable the ligation step at the nick site formed subsequent or simultaneous to the GTP insertion (i.e., or another nucleotide of element (d)). Element (i) is a “wobble” nucleobase pair. In the example, the wobble nucleobase is a G-T pair, but other wobble pairs are acceptable. Element (j) represents the region of the active site which recognizes the DNA substrate (i.e., the target sequence, e.g., the R loop of a Cas9/guide RNA complex formed at a target DNA site). The region shown has the sequence 5'-GGACCC-3', which is exemplary. This sequence can be represented more broadly at 5'-SSSWST-3', wherein S is G or C and W is A or T.

[0238] The “active” site of the ribozyme for purposes of this disclosure can comprise elements (i) and (h). More broadly, the “active” site may refer to regions (g), (h), (i), and (j) since all four regions are involved in different aspects of the mechanism of insertion by the ribozyme. In general, element (j) binds and interacts with the target DNA substrate, element (i) is a “wobble” pair that helps define the location of the insertion point as between element (i) and (h), element (h) facilitates the upward (i.e., in the 5' to 3' direction, i.e., downstream shifting) shifting of the DNA substrate following the breakage or nicking of the phosphodiester bond between elements (h) and (i) on the DNA substrate. Element (g) also facilitates the downstream shift of the nicked portion of the DNA substrate (due to the interaction of the C on the ribozyme and the G on the DNA), making room for insertion of the G into the nicked site, and the subsequent ligation of that nucleotide to reform the DNA now-modified +1 nucleotide DNA substrate.

[0239] The herein disclosed genome editing system may comprise any known or obtainable ribozyme. The ribozymes can be naturally occurring in some embodiments so long as the naturally occurring ribozymes are capable of using DNA as a substrate. The ribozymes can also be derived from naturally occurring ribozymes, e.g., by genetic engineering, mutagenesis, or installation of chemical modifications into a naturally occurring ribozyme. The ribozymes may also be fully synthetic.

[0240] Naturally occurring ribozymes include, but are not limited to, RNase P, ribosomal RNA (rRNA), hammerhead ribozyme, hairpin ribozyme, twister ribozyme, twister sister ribozyme, hatchet ribozyme, pistol ribozyme, GIR1 branching ribozyme, *glmS* ribozyme, and splicing ribozymes (e.g., Group I self-splicing intron and Group II self-splicing intron). The

genome editing systems (e.g., complexes comprising napDNA_{bp}, guide RNA, and a ribozyme), pharmaceutical compositions, kits, and methods of editing may utilize naturally occurring ribozymes (modified to act on DNA), variants thereof, or artificial or engineered ribozymes, such as those described herein.

[0241] In various embodiments, the ribozymes are “engineered ribozymes” which refers to ribozymes which have been modified in one or more specific ways to modify one or more functions of the ribozyme. The ribozymes can be naturally occurring or genetically engineered. The ribozymes can also be modified to include one or more targeting moieties to facilitate localization of the ribozyme to a DNA-bound napDNA_{bp}/guide RNA complex, wherein the napDNA_{bp} (e.g., Cas9) has been modified to comprise a cognate targeting moiety receptor.

[0242] In some embodiments, the ribozyme is a modified group I intron from *Tetrahymena thermophila*, which has the following nucleotide sequence:

[0243] GUGGGACCCAAAAGUUAUCAGGCAUACACCUGGAGAAUAGCUAGUCUU
UAAACCAAUAGAUUGCAUCGGUUUAAAGGCUAGACCGUCAAAUUGCGGGAAU
AGGGUCAACAGCCGUUCAGUACCAAGUCUCAGGGGAAACUUUGAGAUGGCAU
UGUAAAGGGUAUGGUAAUAAACAUACGGACAUGGUCCCAACCACGCAACCAA
GUCCUAAGUCAACAGUCUCGUACACCAUCAGGGUACGUCUCAGACACCAUCAG
GGUCUGUCUGGUACAGCAUCAGCGUACCCUGUUGAUUAUGGAUGCAGUUCACA
GACUAAAUGUCGGUCGGGGAAGAUGUAUUCUUCUCAUAAGAUUAUAGUCGCGC
CUCUCCUUAUUGGGAGCUAGCGGAUGAAGUGAUGCAACACUGGAGCCGCUGG
GAACUAAUUUGUAUGCGAAAGUAUAUUGAUUAGUUUUGGAGUA [SEQ ID NO:
83], or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to the above sequence.

[0244] In other embodiments, the ribozyme is a modified group I intron ribozyme from *Tetrahymena thermophile* having the following nucleotide sequence:

[0245] GCAGGGAAAAGUUAUCAGGCAUACACCUGGAGAAUAGCUAGUCUUUAA
ACCAAUAGAUUGCAUCGGUUUAAAGGCUAGACCGUCAAAUUGCGGGAAUAGG
GUCAACAGCCGUUCAGUACCAAGUCUCAGGGGAAACUUUGAGAUGGCAUUGU
AAAGGGUAUGGUAAUAAACAUACGGACAUGGUCCCAACCACGCAACCAAGUCC
UAAGUCAACAGUCUCGUACACCAUCAGGGUACGUCUCAGACACCAUCAGGGUC
UGUCUGGUACAGCAUCAGCGUACCCUGUUGAUUAUGGAUGCAGUUCACAGACU
AAAUGUCGGUCGGGGAAGAUGUAUUCUUCUCAUAAGAUUAUAGUCGCGCCUCU

CCUUA AUGGGAGCUAGCGGAUGAAGUGAUGCAACACUGGAGCCGCUGGGAAC
UAAUUUGUAUGCGAAAGUAUAUUGAUUAGUUUUGGAGUA [SEQ ID NO: 84], or a
ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at
least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at
least 99%, or at least 99.5% identical to the above sequence.

[0246] In some embodiments, the ribozyme is a modified group I intron from *Tetrahymena thermophila* containing a guide RNA (guide:ribozyme fusion), having the following
nucleotide sequence:

[0247] GCAGCUGAGGGUCUCAUGGGCGUUUAGAGCUAGAAAUAGCAAGUUA
AAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACA
CGGACCCAAAAGUUAUCAGGCAUACACCUGGAGAAUAGCUAGUCUUUAAACCA
AUAGAUUGCAUCGGUUUAAAGGCUAGACCGUCAAAUUGCGGGAAUAGGGUCA
ACAGCCGUUCAGUACCAAGUCUCAGGGGAAACUUUGAGAUGGCAUUGUAAAG
GGUAUGGUAAUAAACAUACGGACAUGGUCCCAACCACGCAACCAAGUCCUAAG
UCAACAGAUCUUCUGUUGAU AUGGAUGCAGUUCACAGACUAAAUGUCGGUCG
GGGAAGAUGUAUUCUUCUCAUAAGAU AUAGUCGCGCCUCUCCUAA AUGGGAG
CUAGCGGAUGAAGUGAUGCAACACUGGAGCCGCUGGGAACUAAUUUGUAUGC
GAAAGUAUAUUGAUUAGUUUUGGAGUA [SEQ ID NO: 85], or a ribozyme

comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least
92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least
99%, or at least 99.5% identical to the above sequence. In such embodiments, the guide
RNA can facilitate the localization of ribozyme to the target site of DNA desired to be edited.

[0248] The ribozymes of the disclosed methods can be engineered. Ribozyme engineering
can be broadly broken down into three distinct areas: (1) the recognition site where the
ribozyme can be targeted to individual DNA sequences, (2) the 3' terminus of the ribozyme
where the active site is, and (3) the internal loop P6 (see the structure of FIG. 1A for
reference), where large sequences can be inserted without drastically affecting ribozyme
activity.

[0249] In some embodiments, the recognition site can be engineered to enable the ribozyme
to both insert a GTP nucleotide into DNA (or another nucleotide) and then allow the now-
nicked DNA substrate to shift within the active site, enabling the ribozyme to ligate the
resulting nick and generate a +1 nucleotide product. The 3' terminus of the enzyme can be
engineered to prevent undesired enzymatic activity.

[0250] In some embodiments, the ribozyme can be modified to contain one or more targeting moieties. For example, an MS2-binding RNA hairpin (or more precisely N numbers of RNA hairpins) can be inserted into loop 6 to enable binding of the ribozyme to the MS2-Cas9 fusion protein (i.e., a Cas9 protein, or more broadly, a napDNABp that has been modified to comprise a targeting moiety receptor).

[0251] Ribozymes can further be evolved to have improved activity, and those changes to the ribozyme likely will not be confined to these locations.

[0252] In certain embodiments, the ribozyme cannot be fused to Cas9. In certain other embodiments, the ribozyme is fused to the Cas9 via a linker. In still other embodiments, the ribozyme is recruited to and becomes coupled to the Cas9 via a recruitment means, e.g., an MS2 tagging system.

[0253] However, in other embodiments, the ribozyme could be fused to or co-transcribed with a guide RNA such that the ribozyme-guide RNA fusion localizes and binds to the target DNA site. In this embodiment, a napDNABp (e.g., Cas9) would then interact with the guide RNA to form the R-loop and the single-strand DNA portion of the Cas9 bubble, which is acted upon by the ribozyme (which requires a single-strand DNA as a substrate).

[0254] Additional background on ribozymes and various ribozyme modifications that may be implemented herein include the following references, which are incorporated herein by reference:

[0255] Sullenger and Cech. Ribozyme-mediated repair of defective mRNA by targeted trans-splicing. *Nature* 1994 619;

[0256] Johnson, Sinha, and Testa. Trans insertion-splicing: ribozyme-catalyzed insertion of targeted sequences into RNAs. *Biochemistry* 2005 10702;

[0257] Bell, Johnson, and Testa. Ribozyme-catalyzed excision of targeted sequences from within RNAs. *Biochemistry* 2002 15327;

[0258] Robertson and Joyce. Selection in vitro of an RNA enzyme that specifically cleaves single-stranded DNA. *Nature* 1990 467;

[0259] Tsang and Joyce. Specialization of the DNA-cleaving activity of a group I ribozyme through in vitro evolution. *J. Mol. Biol.* 1996 262;

[0260] Dolan and Müller. Trans-splicing with the group I intron ribozyme from *Azoarcus*. *RNA* 2014 202; and

[0261] Guo and Cech. Evolution of *Tetrahymena* ribozyme mutants with increased structural stability. *Nature Structural Biology* 2002 855.

[0262] In addition, the following patent publications disclose ribozymes, ribozyme modifications, and methods for making such modifications. All such teachings and disclosures can be implemented to provide / obtain appropriate or suitable ribozymes for this disclose methods and are incorporated herein by reference.

No.	Patent No.	Title	No. Seqs Disclosed
1	EP 0321201 B2	Ribozymes	27
2	US 5856463 A	Pskh-1 Ribozymes	14
3	US 7067650 B1	Ribozymes Targeting Bradeion Transcripts And Use Thereof	23
4	US 6015794 A	Trans-splicing Ribozymes	49
5	US 5849548 A	Cell Ablation Using Trans-splicing Ribozymes	56
6	US 2014/0283156 A1	Trans-splicing Ribozymes And Silent Recombinases	31
7	US 6355415 B1	Compositions And Methods For The Use Of Ribozymes To Determine Gene Function	27
8	US 2010/0305197 A1	Conditionally Active Ribozymes And Uses Thereof	49
9	US 6077705 A	Ribozyme-mediated Gene Replacement	25
10	US 6716973 B2	Use Of A Ribozyme To Join Nucleic Acids And Peptides	9

[0263] In addition, the following scientific publications disclose ribozymes, ribozyme modifications, and methods for making such modifications. All such teachings and disclosures can be implemented to provide / obtain appropriate or suitable ribozymes for this disclose methods and are incorporated herein by reference.

[0264] Bentin. A ribozyme transcribed by a ribozyme. Artif DNA PNA XNA. 2011 Apr;2(2):40-42.

[0265] De la Pena et al., The Hammerhead Ribozyme: A Long History for a Short RNA. Molecules. 2017 Jan 4;22(1). pii: E78. doi: 10.3390/molecules22010078.

[0266] Muller. Design and Experimental Evolution of trans-Splicing Group I Intron Ribozymes. Molecules. 2017 Jan 2;22(1). pii: E75. doi: 10.3390/molecules22010075.

[0267] Samanata et al., A reverse transcriptase ribozyme. Elife. 2017 Sep 26;6. pii: e31153. doi: 10.7554/eLife.31153.

[0268] The following are a series of ribozyme sequences which are further exemplary of the ribozymes that may be used in the instant genome editing system, including a (i) first ribozyme (a naturally occurring ribozyme from *Tetrahymena* group I intron reported in Joyce et al., "Selection *in vitro* of an RNA enzyme that specifically cleaves single-stranded DNA,"

Nature, 1990, p. 467, a (ii) second ribozyme (an evolved ribozyme reported in Joyce et al. to specifically cleave single-stranded DNA), a (iii) third ribozyme, which is a novel engineered variant of the second ribozyme comprising the indicated modified changes (and as shown in FIG. 1A), and a (iv) fourth ribozyme that is the third ribozyme but further modified to comprise an MS2 hairpin (i.e., MS2 aptamer) which facilitates the co-localization of the ribozyme to a napDNAbp/guide RNA complex wherein the napDNAbp is also modified to comprise the MPC protein of the MS2 tagging system.

[0269] These sequences are as follows:

[0270] Ribozyme (i) (wild type Joyce ribozyme)

[0271] 5'-

TAATACGACTCACTATAGGAGGGAAAAGTTATCAGGCATGCACCTGGTAGCTAG
TCTTTAAACCAATAGATTGCATCGGTTTAAAAGGCAAGACCGTCAAATTGCGGGA
AAGGGGTCAACAGCCGTTTCAGTACCAAGTCTCAGGGGAACTTTGAGATGGCCT
TGCAAAGGGTATGGTAATAAGCTGACGGACATGGTCCTAACCACGCAGCCAAGT
CCTAAGTCAACAGATCTTCTGTTGATATGGATGCAGTTCACAGACTAAATGTTCGG
TCGGGGAAGATGTATTCTTCTCATAAGATATAGTCGGACCTCTCCTTAATGGGAG
CTAGCGGATGAAGTGATGCAACACTGGAGCCGCTGGGAACTAATTTGTATGCGA
AAGTATATTGATTAGTTTTGGAGTACTCG-3' (SEQ ID NO: 86), or a ribozyme
comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least
92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least
99%, or at least 99.5% identical to SEQ ID NO: 86.

[0272] Ribozyme (ii) (evolved Joyce ribozyme)

[0273] 5'-

TAATACGACTCACTATAGGAGGGAAAAGTTATCAGGCATACACCTGGAGAATAG
CTAGTCTTTAAACCAATAGATTGCATCGGTTTAAAGGCTAGACCGTCAAATTGCG
GGAATAGGGTCAACAGCCGTTTCAGTACCAAGTCTCAGGGGAACTTTGAGATGG
CATTGTAAAGGGTATGGTAATAAACATACGGACATGGTCCCAACCACGCAACCA
AGTCCTAAGTCAACAGATCTTCTGTTGATATGGATGCAGTTCACAGACTAAATGT
CGGTCTGGGGAAGATGTATTCTTCTCATAAGATATAGTCGCGCCTCTCCTTAATGG
GAGCTAGCGGATGAAGTGATGCAACACTGGAGCCGCTGGGAACTAATTTGTATG
CGAAAGTATATTGATTAGTTTTGGAGTACTCG-3' (SEQ ID NO: 87), or a ribozyme
comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least
92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least
99%, or at least 99.5% identical to SEQ ID NO: 87.

[0274] Ribozyme (iii) (novel engineered ribozyme derived from evolved Joyce ribozyme and as shown in FIG. 1A)

[0275] 5'-

GCCCTTGGACCCAAAAGTTATCAGGCATGCACCTGGTAGCTAGTCTTTAAACCAA
TAGATTGCATCGGTTTAAAAGGCAAGACCGTCAAATTGCGGGAAAGGGGTCAAC
AGCCGTTTCAGTACCAAGTCTCAGGGGAAACTTTGAGATGGCCTTGCAAAGGGTA
TGGTAATAAGCTGACGGACATGGTCCTAACCACGCAGCCAAGTCCTAAGTCAAC
AGATCTTCTGTTGATATGGATGCAGTTCACAGACTAAATGTCGGTCGGGGAAGAT
GTATTCTTCTCATAAGATATAGTCGGACCTCTCCTTAATGGGAGCTAGCGGATGA
AGTGATGCAACACTGGAGCCGCTGGGAACTAATTTGTATGCGAAAGTATATTGAT
TAGTTTTGGAGTA*-3' (SEQ ID NO: 88), or a ribozyme comprising a nucleotide sequence
that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at
least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to
SEQ ID NO: 88.

[0276] P0 (underlined), engineered to bind the targeted site and affect nucleotide ligation.

This sequence region may be customized depending on the sequence of the target edit site.

[0277] * indicates deletion of 4 nt to prevent ribozyme insertion into DNA

[0278] Ribozyme (iv) (engineered ribozyme (iii) modified with MS2 aptamer)

[0279] CCGGACCCAAAAGTTATCAGGCATACACCTGGAGAATAGCTAGTCTTTAA
ACCAATAGATTGCATCGGTTTAAAGGCTAGACCGTCAAATTGCGGGAATAGGGT
CAACAGCCGTTTCAGTACCAAGTCTCAGGGGAAACTTTGAGATGGCATTGTAAAG
GGTATGGTAATAAACATACGGACATGGTCCCAACCACGCAACCAAGTCCTAAGT
CAACAGTTTTTCGTACACCATCAGGGTACGTTTTTCAGACACCATCAGGGTC
TGTTTTTGGTACAGCATCAGCGTACCTTTTTTCGTACAGGATCACCGTACGTT
TTTCAGACAGGATCACCGTCTGTTTTTCTGTTGATATGGATGCAGTTCACAGAC
TAAATGTCGGTCGGGGAAGATGTATTCTTCTCATAAGATATAGTCGCGCCTCTCC
TTAATGGGAGCTAGCGGATGAAGTGATGCAACACTGGAGCCGCTGGGAACTAAT
TTGTATGCGAAAGTATATTGATTAGTTTTGGAGTA* (SEQ ID NO: 89), or a ribozyme
comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least
92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least
99%, or at least 99.5% identical to SEQ ID NO: 89.

[0280] P0 (underlined), engineered to bind the targeted site and affect nucleotide ligation.

This sequence region may be customized depending on the sequence of the target edit site.

[0281] MS2 aptamer sequence (bold, underlined)

[0282] * indicates deletion of 4 nt to prevent ribozyme insertion into DNA

Predicted secondary structure of Ribozyme (iv):

```
CCGGACCCAAAAGTTATCAGGCATACACCTGGAGAATAGCTAGTCTTTAAACCAATA
.....<<<<<<<<<.....>>>>.....>>>>.<<<<<<<<<<.<<
GATTGCATCGGTTTAAAGGCTAGACCGTCAAATTGCGGGAATAGGGTCAACAGCCGT
.....>>.>>>>>>>>>>..(((.(....<<<<<<....<<<<<<....<<
TCAGTACCAAGTCTCAGGGGAACTTTGAGATGGCATTGTAAAGGGTATGGTAATAA
<<<<<<<<<.<<<<<<<<<.....>>>>>>>>>>..>>>>.....>>>>.....
ACATACGGACATGGTCCCAACACGCAACCAAGTCCCTAAGTCAACAGATCTTCTGTT
>>>>>>>>..>>>>>>>>..>>>>>>>>..>>>>>>>>>>.....>>>>
GATATGGATGCAGTTCACAGACTAAATGTCGGTTCGGGGAAGATGTATTCTTCTCATA
>>>..>>>>..>>>..<.<<<<<....).)))).<<<<<<<.....>>>>>>>>...
AGATATAGTCGCGCCTCTCCTTAATGGGAGCTAGCGGATGAAGTGTATGCAACACTGG
.....>>>>>>>>.....<<<<<.....>>>>>>>>>>>>>>>>>>>>>>..
AGCCGCTGGGAACCTAATTTGTATGCGAAAGTATATTGATTAGTTTGGAGTA (SEQ ID NO: 90)
..>>>>>>>>.<<<<<<<<.<<<<<<.....>>>>>>>>..>>>>>>>>.....
```

Key to structural symbols:

<> and () indicate basepairing, while [.] indicates an unpaired nucleotide. For example, an 8 nt hairpin would be written as follows:AGGGGGGGGAAAACCCCCCCCCA (SEQ ID NO: 91)

..<<<<<<<<.....>>>>>>>>..

Where nt 8 pairs with nt 13 and so on

() indicate base-pairing through space, called a pseudoknot. So an 8 nt hairpin with a 4 nt pseudoknot would be written as

GGGGGGGGGAAAACCCCCCCCCAAAAATTTT (SEQ ID NO: 92)

<<<<<<<<((((>>>>>>>>.....)))

Where nt 8 pairs with nt 13 and nt 9 pairs with nt 21

[0283] Given that the P0 region of the ribozyme will depend on the sequence of the target region in the R-loop of the target gene locus of the napDNAbp/guide RNA complex, the P0 region of the ribozyme can designed based on any given target DNA sequence. As such, the P0 sequence of ribozyme (iii) is represented with a string of Ns, representing any nucleotide sequence, as follows:

[0284] 5'-

NNNNNNNNNNNNAAAAGTTATCAGGCATGCACCTGGTAGCTAGTCTTTAAACCA
ATAGATTGCATCGGTTTAAAGGCAAGACCGTCAAATTGCGGGAAGGGGTCAA
CAGCCGTTTCAGTACCAAGTCTCAGGGGAACTTTGAGATGGCCTTGCAAAGGGT
ATGGTAATAAGCTGACGGACATGGTCCTAACCACGCAGCCAAGTCCTAAGTCAA
CAGATCTTCTGTTGATATGGATGCAGTTCACAGACTAAATGTCGGTTCGGGGAAGA
TGTATTCTTCTCATAAGATATAGTCGGACCTCTCCTTAATGGGAGCTAGCGGATG

AAGTGATGCAACACTGGAGCCGCTGGGAACTAATTTGTATGCGAAAGTATATTG
ATTAGTTTTGGAGTA*-3' (SEQ ID NO: 156), or a ribozyme comprising a nucleotide
sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least
94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5%
identical to the above sequence.

[0285] P0 (underlined), engineered to bind the targeted site and affect nucleotide ligation.
This sequence region may be customized depending on the sequence of the target edit site.

[0286] * indicates deletion of 4 nt to prevent ribozyme insertion into DNA

[0287] Given that the P0 region of the ribozyme will depend on the sequence of the target
region in the R-loop of the target gene locus of the napDNAbp/guide RNA complex, the P0
region of the ribozyme can be designed based on any given target DNA sequence. As such, the
P0 sequence of ribozyme (iv) is represented with a string of Ns, representing any nucleotide
sequence, as follows:

[0288] NNNNNNNNAAAAGTTATCAGGCATACACCTGGAGAATAGCTAGTCTTTAA
ACCAATAGATTGCATCGGTTTAAAGGCTAGACCGTCAAATTGCGGGAATAGGGT
CAACAGCCGTTTCAGTACCAAGTCTCAGGGGAACTTTGAGATGGCATTGTAAAG
GGTATGGTAATAAACATACGGACATGGTCCCAACCACGCAACCAAGTCCTAAGT
CAACAG**TTTTTCGTACACCATCAGGGTACGTTTTTCAGACACCATCAGGGTC**
TGTTTTTGGTACAGCATCAGCGTACCTTTTTTCGTACAGGATCACCGTACGTT
TTTCAGACAGGATCACCGTCTGTTTTTCTGTTGATATGGATGCAGTTCACAGAC
TAAATGTCGGTCGGGGAAGATGTATTCTTCTCATAAGATATAGTCGCGCCTCTCC
TTAATGGGAGCTAGCGGATGAAGTGATGCAACACTGGAGCCGCTGGGAACTAAT
TTGTATGCGAAAGTATATTGATTAGTTTTGGAGTA* (SEQ ID NO: 157), or a
ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at
least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at
least 99%, or at least 99.5% identical to the above sequence.

[0289] P0 (underlined), engineered to bind the targeted site and affect nucleotide ligation.
This sequence region may be customized depending on the sequence of the target edit site.

[0290] MS2 aptamer sequence (bold, underlined)

[0291] * indicates deletion of 4 nt to prevent ribozyme insertion into DNA.

[0292] Ribozyme activity can be optimized as described by Stinchcomb et al., supra. The
details will not be repeated here, but include altering the length of the ribozyme binding arms,
or chemically synthesizing ribozymes with modifications that prevent their degradation by
serum ribonucleases (see e.g., Eckstein et al., International Publication No. WO 92/07065;

Perrault et al., Nature 1990, 344:565; Pieken et al., Science 1991, 253:314; Usman and Cedergren, Trends in Biochem. Sci. 1992, 17:334; Usman et al., International Publication No. WO 93/15187; and Rossi et al., International Publication No. WO 91/03162, as well as Usman, N. et al. U.S. Patent Application Ser. No. 07/829,729, and Sproat, B. European Patent Application 92110298.4 which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules. All these publications are hereby incorporated by reference herein.

[3] Recruitment domains

[0293] In various embodiments, it will be advantageous to modify one or more components of the genome editing system described herein with targeting or recruitment domains, such as an RNA-protein recruitment system.

[0294] The genome editing system described herein may utilize RNA-protein recruitment systems to co-localize components of the editing system at a target DNA site (e.g., for achieving co-localization of napDNAbp/guide RNA complex with a ribozyme at a target DNA site).

[0295] Such recruitment systems generally combine an “RNA-protein interaction domain” coupled to a first interacting element (e.g., a ribozyme) with a cognate RNA-binding protein coupled to a second interacting element (e.g., a napDNAbp). The cognate RNA-binding protein binds to the RNA-protein interaction domain. In this way, one would be able to co-localize two separately expressed elements of the genome editing system, e.g., co-localization of ribozyme to a napDNAbp. These types of systems can be leveraged to recruit a variety of functionalities together within a cell, e.g., at a DNA editing target site.

[0296] An exemplary RNA-protein recruitment system is the MS2 tagging technique, which is based on the natural interaction of the MS2 bacteriophage coat protein (“MCP” or “MS2cp”) and the stem-loop or hairpin structure present in the genome of the phage, i.e., the “MS2 hairpin.” Thus, with MS2 tagging, as it could be applied in the instant disclosure, the napDNAbp could be modified as a fusion protein comprising MCP and the ribozyme could be modified with the MS2 hairpin (e.g., as a transcriptional fusion to the ribozyme sequence or engineered to occur within the ribozyme sequence). In operation, the napDNAbp-MCP fusion, once targeted to a DNA edit site by an appropriate guide RNA, would recruit the MS2-tagged ribozyme to the edit site.

[0297] A review of other RNA-protein recruitment systems are described in the art, for example, in Johansson et al., “RNA recognition by the MS2 phage coat protein,” *Sem Viro.*, 1997, Vol. 8(3): 176-185; Delebecque et al., “Organization of intracellular reactions with

rationally designed RNA assemblies,” *Science*, 2011, Vol. 333: 470-474; Mali et al., “Cas9 transcriptional activators for target specificity screening and paired nickases for cooperative genome engineering,” *Nat. Biotechnol.*, 2013, Vol.31: 833-838; and Zalatan et al., “Engineering complex synthetic transcriptional programs with CRISPR RNA scaffolds,” *Cell*, 2015, Vol.160: 339-350, each of which are incorporated herein by reference in their entireties. Other systems include the PP7 hairpin, which specifically recruits the PCP protein, and the “com” hairpin, which specifically recruits the Com protein. See Zalatan et al.

[0298] The nucleotide sequence of the MS2 hairpin (or equivalently referred to as the “MS2 aptamer”) is: GCCAACATGAGGATCACCCATGTCTGCAGGGCC (SEQ ID NO: 93).

This application is not intended to be limited in any way to any particular RNA-protein recruitment system and may include any available system and described in the art.

[0299] The amino acid sequence of the MCP or MS2cp is:

GSASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQ
NRKYTIKVEVPKVATQTVGGEELPVAGWRSYLNMEITPIFATNSDCELIVKAMQGL
LKDGNPIPSAIAANSIGY (SEQ ID NO: 94), or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO: 94.

[0300] In other embodiments, the napDNAbp may be modified with one or more targeting domains that function to enhance the targeting of the ribozyme to the genomic locus bound by the napDNAbp, thereby increasing the efficiency of the ribozyme’s enzymatic action at the desired target site. In addition, the ribozyme may also be engineered to comprise the corresponding structural feature that will interact with the one or more targeting domains.

[0301] Any suitable targeting domain may be incorporated into the napDNAbp as a fusion protein, and fused optionally via a linker. In addition, the targeting domain will either recognize a corresponding structural naturally occurring feature on the ribozyme or the ribozyme can be engineered to incorporate the corresponding structural feature which binds and/or interacts with the targeting domain.

[0302] In one embodiment, the napDNAbp may be fused to a bacteriophage coat protein. Without being bound by theory, the bacteriophage coat protein binds to an MS2 RNA hairpin sequence, which can be incorporated as a structure into the engineered ribozyme.

[0303] MS2 coat protein:

NP_040648.1

GSASNFTQFVLVDNNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQ
NRKYTIKVEVPKVATQTVGGEELPVAGWRSYLNMELTIPIFATNSDCELIVKAMQGL
LKDGNPIPSAIAANSIY [SEQ ID NO: 94], or an amino acid sequence having at least
85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least
96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ
ID NO: 94.

[0304] MS2 hairpin sequences:

UCUCGUACACCAUCAGGGUACGUCUCAGACACCAUCAGGGUCUGUCUGGUACA
GCAUCAGCGUACC [SEQ ID NO: 96], or a nucleotide sequence having at least 85%, at
least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at
least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO:
96.

UUUUUCGUACACCAUCAGGGUACGUUUUUCAGACACCAUCAGGGUCUGUUUU
UGGUACAGCAUCAGCGUACCUUUUUCGUACAGGAUACCGUACGUUUUUCAGA
CAGGAUACCGUCUGUUUUU [SEQ ID NO: 97], or a nucleotide sequence having at
least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at
least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with
SEQ ID NO: 97.

[0305] In addition, targeting moieties and cognate targeting moiety receptors could utilize
protein-RNA binding pairs, RNA – RNA binding proteins, and RNA aptamers. Examples of
such pairs include:

[0306] Hfq protein/RprA

Hfq:

MAKGQSLQDPFLNALRRERVPSIYLVNGILQGQIESFDQFVILLKNTVSQMVKHAI
STVVPSPVSHHSNNAGGGTSSNYHHGSSAQNTSAQQDSEETE [SEQ ID NO: 98]

RprA:

[0307] ACGGUUAUAA AUCAACAUAU UGAUUUAUAA GCAUGGAAAU
CCCCUGAGUG AAACAACGAAUUGCUGUGUG UAGUCUUUGC CCAUCUCCCA
CGAUGGGCUU UUUUU [SEQ ID NO: 99]

[0308] Reference: Zhang, Wassarman, Rosenow, Tjaden, Storz, Gottesman. Global analysis
of small RNA and mRNA targets of Hfq. *Molecular Microbiology* 2003.

[0309] Streptavidin aptamer/streptavidin

Streptavidin aptamer:

ACCGACCAGAAUCAUGCAAGUGCGUAAGAUAGUCGCGGGCCGGG [SEQ ID NO: 100]

Streptavidin:

MRKIVVAAIAVSLTTVSITASASADPSKDSKAQVSAAEAGITGTWYNQLGSTFIVTAG
ADGALTGTYESAVGNAESRYVLTGRYDSAPATDGS GTALGWTVAWKNNYRNAHS
ATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASIDAAK
KAGVNNGNPLDAVQQ [SEQ ID NO: 101].

[0310] Such targeting moieties and/or targeting moiety receptors, i.e., recruitment domains, may also include any nucleic acid sequence or amino acid sequences, as the case may be, having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of the above-mentioned sequences.

[4] Linkers and other domains

[0311] The genome editing system described herein may comprise various other domains besides the napDNAbp (e.g., Cas9 domain) and the ribozymes. For example, in the case where the napDNAbp is fused to another functional domain (e.g., NLS or a recruitment domain), the fusions may comprise one or more linkers that join the Cas9 domain with the additional domain.

Linkers

[0312] As defined above, the term “linker,” as used herein, refers to a chemical group or a molecule linking two molecules or moieties, e.g., a binding domain and a cleavage domain of a nuclease. In some embodiments, a linker joins a gRNA binding domain of an RNA-programmable nuclease and the catalytic domain of a polymerase (e.g., a reverse transcriptase). In some embodiments, a linker joins a dCas9 and reverse transcriptase. Typically, the linker is positioned between, or flanked by, two groups, molecules, or other moieties and connected to each one via a covalent bond, thus connecting the two. In some embodiments, the linker is an amino acid or a plurality of amino acids (e.g., a peptide or protein). In some embodiments, the linker is an organic molecule, group, polymer, or chemical moiety. In some embodiments, the linker is 5-100 amino acids in length, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 30-35, 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-150, or 150-200 amino acids in length. Longer or shorter linkers are also contemplated.

[0313] The linker may be as simple as a covalent bond, or it may be a polymeric linker many atoms in length. In certain embodiments, the linker is a polypeptide or based on amino acids.

In other embodiments, the linker is not peptide-like. In certain embodiments, the linker is a covalent bond (e.g., a carbon-carbon bond, disulfide bond, carbon-heteroatom bond, etc.). In certain embodiments, the linker is a carbon-nitrogen bond of an amide linkage. In certain embodiments, the linker is a cyclic or acyclic, substituted or unsubstituted, branched or unbranched aliphatic or heteroaliphatic linker. In certain embodiments, the linker is polymeric (e.g., polyethylene, polyethylene glycol, polyamide, polyester, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminoalkanoic acid. In certain embodiments, the linker comprises an aminoalkanoic acid (e.g., glycine, ethanoic acid, alanine, beta-alanine, 3-aminopropanoic acid, 4-aminobutanoic acid, 5-pentanoic acid, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminohexanoic acid (Ahx). In certain embodiments, the linker is based on a carbocyclic moiety (e.g., cyclopentane, cyclohexane). In other embodiments, the linker comprises a polyethylene glycol moiety (PEG). In other embodiments, the linker comprises amino acids. In certain embodiments, the linker comprises a peptide. In certain embodiments, the linker comprises an aryl or heteroaryl moiety. In certain embodiments, the linker is based on a phenyl ring. The linker may include functionalized moieties to facilitate attachment of a nucleophile (e.g., thiol, amino) from the peptide to the linker. Any electrophile may be used as part of the linker. Exemplary electrophiles include, but are not limited to, activated esters, activated amides, Michael acceptors, alkyl halides, aryl halides, acyl halides, and isothiocyanates.

[0314] In some other embodiments, the linker comprises the amino acid sequence (GGGGS)N (SEQ ID NO: 102), (G)N (SEQ ID NO: 103), (EAAAK)N (SEQ ID NO: 104), (GGS)N (SEQ ID NO: 105), (SGGS)N (SEQ ID NO: 106), (XP)N (SEQ ID NO: 107), or any combination thereof, wherein n is independently an integer between 1 and 30, and wherein X is any amino acid. In some embodiments, the linker comprises the amino acid sequence (GGS)N (SEQ ID NO: 108), wherein n is 1, 3, or 7. In some embodiments, the linker comprises the amino acid sequence SGSETPGTSESATPES (SEQ ID NO: 109). In some embodiments, the linker comprises the amino acid sequence SGGSSGGSSGSETPGTSESATPESGGSSGGGS (SEQ ID NO: 110). In some embodiments, the linker comprises the amino acid sequence SGGSGGSGGS (SEQ ID NO: 111). In some embodiments, the linker comprises the amino acid sequence SGGS (SEQ ID NO: 112). In other embodiments, the linker comprises the amino acid sequence SGGSSGGSSGSETPGTSESATPESAGSYDPYDVPDYAGSAAPAAKKKKLDGSGSGGS (SEQ ID NO: 113, 60AA).

[0315] In certain embodiments, linkers may be used to link any of the peptides or peptide domains or moieties of the invention (e.g., a napDNAbp linked or fused to a reverse transcriptase).

[0316] As defined above, the term “linker,” as used herein, refers to a chemical group or a molecule linking two molecules or moieties, e.g., a binding domain and a cleavage domain of a nuclease. In some embodiments, a linker joins a gRNA binding domain of an RNA-programmable nuclease and the catalytic domain of a recombinase. In some embodiments, a linker joins a dCas9 and reverse transcriptase. Typically, the linker is positioned between, or flanked by, two groups, molecules, or other moieties and connected to each one via a covalent bond, thus connecting the two. In some embodiments, the linker is an amino acid or a plurality of amino acids (e.g., a peptide or protein). In some embodiments, the linker is an organic molecule, group, polymer, or chemical moiety. In some embodiments, the linker is 5-100 amino acids in length, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 30-35, 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-150, or 150-200 amino acids in length. Longer or shorter linkers are also contemplated.

[0317] The linker may be as simple as a covalent bond, or it may be a polymeric linker many atoms in length. In certain embodiments, the linker is a polypeptide or based on amino acids. In other embodiments, the linker is not peptide-like. In certain embodiments, the linker is a covalent bond (e.g., a carbon-carbon bond, disulfide bond, carbon-heteroatom bond, etc.). In certain embodiments, the linker is a carbon-nitrogen bond of an amide linkage. In certain embodiments, the linker is a cyclic or acyclic, substituted or unsubstituted, branched or unbranched aliphatic or heteroaliphatic linker. In certain embodiments, the linker is polymeric (e.g., polyethylene, polyethylene glycol, polyamide, polyester, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminoalkanoic acid. In certain embodiments, the linker comprises an aminoalkanoic acid (e.g., glycine, ethanoic acid, alanine, beta-alanine, 3-aminopropanoic acid, 4-aminobutanoic acid, 5-pentanoic acid, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminoHEXAnoic acid (Ahx). In certain embodiments, the linker is based on a carbocyclic moiety (e.g., cyclopentane, cycloHEXAnoic acid). In other embodiments, the linker comprises a polyethylene glycol moiety (PEG). In other embodiments, the linker comprises amino acids. In certain embodiments, the linker comprises a peptide. In certain embodiments, the linker comprises an aryl or heteroaryl moiety. In certain embodiments, the linker is based on a phenyl ring. The linker may include functionalized moieties to facilitate attachment of a

nucleophile (e.g., thiol, amino) from the peptide to the linker. Any electrophile may be used as part of the linker. Exemplary electrophiles include, but are not limited to, activated esters, activated amides, Michael acceptors, alkyl halides, aryl halides, acyl halides, and isothiocyanates.

[0318] In some other embodiments, the linker comprises the amino acid sequence (GGGS)_n (SEQ ID NO: 102), (G)_n (SEQ ID NO: 103), (EAAAK)_n (SEQ ID NO: 104), (GGS)_n (SEQ ID NO: 105), (SGGS)_n (SEQ ID NO: 106), (XP)_n (SEQ ID NO: 107), or any combination thereof, wherein n is independently an integer between 1 and 30, and wherein X is any amino acid. In some embodiments, the linker comprises the amino acid sequence (GGS)_n (SEQ ID NO: 108), wherein n is 1, 3, or 7. In some embodiments, the linker comprises the amino acid sequence SGSETPGTSESATPES (SEQ ID NO: 109). In some embodiments, the linker comprises the amino acid sequence SGGSSGGSSGSETPGTSESATPESSGGSSGGSS (SEQ ID NO: 110). In some embodiments, the linker comprises the amino acid sequence SGGSGGSGGS (SEQ ID NO: 111). In some embodiments, the linker comprises the amino acid sequence SGGS (SEQ ID NO: 112).

[0319] In particular, the following linkers can be used in various embodiments to join genome editing components with one another:

GGS (SEQ ID NO: 114);

GGSGGS (SEQ ID NO: 115);

GGSGGSGGS (SEQ ID NO: 1156);

SGGSSGGSSGSETPGTSESATPESSGGSSGGSS (SEQ ID NO: 117);

SGSETPGTSESATPES (SEQ ID NO: 109);

SGGSSGGSSGSETPGTSESATPESAGSYPYDVPDYAGSAAPAAKKKKLDGSGSGGSS
GG S (SEQ ID NO: 113).

Nuclear localization sequence (NLS)

[0320] In various embodiments, the genome editing system may comprise one or more nuclear localization sequences (NLS), which help promote translocation of a protein into the cell nucleus. Such sequences are well-known in the art and can include the following examples:

NLS OF SV40 LARGE T-AG:PKKKRKV (SEQ ID NO: 9).

NLS: MKRTADGSEFESPKKKRKV (SEQ ID NO: 118).

NLS: MDSLLMNRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO: 10).

NLS OF NUCLEOPLASMIN: AVKRPAATKKAGQAKKKKLD (SEQ ID NO: 119).

NLS OF EGL-13: MSRRRKANPTKLS ENAKKLAKEVEN (SEQ ID NO: 120).

NLS OF C-MYC: PAAKRVKLD (SEQ ID NO: 121).

NLS OF TUS-PROTEIN: KLIKIRPVK (SEQ ID NO: 122).

NLS OF POLYOMA LARGE T-AG: VSRKRPRP (SEQ ID NO: 123).

NLS OF HEPATITIS D VIRUS ANTIGEN: EGAPPAKRAR (SEQ ID NO: 124).

NLS OF MURINE P53: PPQPKKKPLDGE (SEQ ID NO: 125).

NLS OF PE1 AND PE2: SGGSKRTADGSEFEPKKKRKV (SEQ ID NO: 126).

[0321] The NLS examples above are non-limiting. The genome editing system may comprise any known NLS sequence, including any of those described in Cokol et al., “Finding nuclear localization signals,” *EMBO Rep.*, 2000, 1(5): 411-415 and Freitas et al., “Mechanisms and Signals for the Nuclear Import of Proteins,” *Current Genomics*, 2009, 10(8): 550-7, each of which are incorporated herein by reference.

[0322] In various embodiments, the editors and constructs encoding the editors disclosed herein further comprise one or more, preferably, at least two nuclear localization signals. In certain embodiments, the genome editors comprise at least two NLSs. In embodiments with at least two NLSs, the NLSs can be the same NLSs or they can be different NLSs. In addition, the NLSs may be expressed as part of a fusion protein with the remaining portions of the genome editors. In some embodiments, one or more of the NLSs are bipartite NLSs (“bpNLS”). In certain embodiments, the disclosed fusion proteins comprise two bipartite NLSs. In some embodiments, the disclosed fusion proteins comprise more than two bipartite NLSs.

[0323] The location of the NLS fusion can be at the N-terminus, the C-terminus, or within a sequence of a genome editor (e.g., inserted between the encoded napDNAbp component (e.g., Cas9) and a polymerase domain (e.g., a reverse transcriptase domain).

[0324] The NLSs may be any known NLS sequence in the art. The NLSs may also be any future-discovered NLSs for nuclear localization. The NLSs also may be any naturally-occurring NLS, or any non-naturally occurring NLS (e.g., an NLS with one or more desired mutations).

[0325] The term “nuclear localization sequence” or “NLS” refers to an amino acid sequence that promotes import of a protein into the cell nucleus, for example, by nuclear transport. Nuclear localization sequences are known in the art and would be apparent to the skilled artisan. For example, NLS sequences are described in Plank et al., International PCT application PCT/EP2000/011690, filed November 23, 2000, published as WO/2001/038547 on May 31, 2001, the contents of which are incorporated herein by reference. In some

embodiments, an NLS comprises the amino acid sequence PKKKRKV (SEQ ID NO: 9), MDSLLMNRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO: 10), KRTADGSEFESPKKKRKV (SEQ ID NO: 127), or KRTADGSEFEPKKKKRKV (SEQ ID NO: 128). In other embodiments, NLS comprises the amino acid sequences NLSKRPAAIKKAGQAKKKK (SEQ ID NO: 129), PAAKRVKLD (SEQ ID NO: 121), RQRRNELKRSF (SEQ ID NO: 130), NQSSNFGPMKGGNFGRSSGPYGGGGQYFAKPRNQGGY (SEQ ID NO: 131).

[0326] In one aspect of the disclosure, a genome editing system may be modified with one or more nuclear localization signals (NLS), preferably at least two NLSs. In certain embodiments, the genome editing systems are modified with two or more NLSs. The disclosure contemplates the use of any nuclear localization signal known in the art at the time of the disclosure, or any nuclear localization signal that is identified or otherwise made available in the state of the art after the time of the instant filing. A representative nuclear localization signal is a peptide sequence that directs the protein to the nucleus of the cell in which the sequence is expressed. A nuclear localization signal is predominantly basic, can be positioned almost anywhere in a protein's amino acid sequence, generally comprises a short sequence of four amino acids (Autieri & Agrawal, (1998) J. Biol. Chem. 273: 14731-37, incorporated herein by reference) to eight amino acids, and is typically rich in lysine and arginine residues (Magin et al., (2000) Virology 274: 11-16, incorporated herein by reference). Nuclear localization signals often comprise proline residues. A variety of nuclear localization signals have been identified and have been used to effect transport of biological molecules from the cytoplasm to the nucleus of a cell. See, e.g., Tinland et al., (1992) Proc. Natl. Acad. Sci. U.S.A. 89:7442-46; Moede et al., (1999) FEBS Lett. 461:229-34, which is incorporated by reference. Translocation is currently thought to involve nuclear pore proteins.

[0327] Most NLSs can be classified in three general groups: (i) a monopartite NLS exemplified by the SV40 large T antigen NLS (PKKKRKV (SEQ ID NO: 9)); (ii) a bipartite motif consisting of two basic domains separated by a variable number of spacer amino acids and exemplified by the Xenopus nucleoplasmin NLS (KRXXXXXXXXXXXXKKKL (SEQ ID NO: 132)); and (iii) noncanonical sequences such as M9 of the hnRNP A1 protein, the influenza virus nucleoprotein NLS, and the yeast Gal4 protein NLS (Dingwall and Laskey 1991).

[0328] Nuclear localization signals appear at various points in the amino acid sequences of proteins. NLS's have been identified at the N-terminus, the C-terminus and in the central region of proteins. Thus, the disclosure provides genome editing systems that may be

modified with one or more NLSs at the C-terminus, the N-terminus, as well as at in internal region of the genome editing system. The residues of a longer sequence that do not function as component NLS residues should be selected so as not to interfere, for example tonically or sterically, with the nuclear localization signal itself. Therefore, although there are no strict limits on the composition of an NLS-comprising sequence, in practice, such a sequence can be functionally limited in length and composition.

[0329] The present disclosure contemplates any suitable means by which to modify a genome editing system to include one or more NLSs. In one aspect, the genome editing systems may be engineered to express a genome editing system protein that is translationally fused at its N-terminus or its C-terminus (or both) to one or more NLSs, i.e., to form a genome editing system-NLS fusion construct. In other embodiments, the genome editing system-encoding nucleotide sequence may be genetically modified to incorporate a reading frame that encodes one or more NLSs in an internal region of the encoded genome editing system. In addition, the NLSs may include various amino acid linkers or spacer regions encoded between the genome editing system and the N-terminally, C-terminally, or internally-attached NLS amino acid sequence, e.g., and in the central region of proteins. Thus, the present disclosure also provides for nucleotide constructs, vectors, and host cells for expressing fusion proteins that comprise a genome editing system and one or more NLSs.

[0330] The genome editing systems described herein may also comprise nuclear localization signals which are linked to a genome editing system through one or more linkers, e.g., and polymeric, amino acid, nucleic acid, polysaccharide, chemical, or nucleic acid linker element. The linkers within the contemplated scope of the disclosure are not intended to have any limitations and can be any suitable type of molecule (e.g., polymer, amino acid, polysaccharide, nucleic acid, lipid, or any synthetic chemical linker domain) and be joined to the genome editing system by any suitable strategy that effectuates forming a bond (e.g., covalent linkage, hydrogen bonding) between the genome editing system and the one or more NLSs.

Inteins and split-inteins

[0331] It will be understood that in some embodiments (e.g., delivery of a genome editing system in vivo using AAV particles), it may be advantageous to split a polypeptide (e.g., a napDNAbp) or a fusion protein (e.g., a napDNAbp-NLS fusion) into an N-terminal half and a C-terminal half, delivery them separately, and then allow their colocalization to reform the complete protein (or fusion protein as the case may be) within the cell. Separate halves of a

protein or a fusion protein may each comprise a split-intein tag to facilitate the reformation of the complete protein or fusion protein by the mechanism of protein trans splicing.

[0332] Protein trans-splicing, catalyzed by split inteins, provides an entirely enzymatic method for protein ligation. A split-intein is essentially a contiguous intein (e.g. a mini-intein) split into two pieces named N-intein and C-intein, respectively. The N-intein and C-intein of a split intein can associate non-covalently to form an active intein and catalyze the splicing reaction essentially in same way as a contiguous intein does. Split inteins have been found in nature and also engineered in laboratories. As used herein, the term "split intein" refers to any intein in which one or more peptide bond breaks exists between the N-terminal and C-terminal amino acid sequences such that the N-terminal and C-terminal sequences become separate molecules that can non-covalently reassociate, or reconstitute, into an intein that is functional for trans-splicing reactions. Any catalytically active intein, or fragment thereof, may be used to derive a split intein for use in the methods of the invention. For example, in one aspect the split intein may be derived from a eukaryotic intein. In another aspect, the split intein may be derived from a bacterial intein. In another aspect, the split intein may be derived from an archaeal intein. Preferably, the split intein so-derived will possess only the amino acid sequences essential for catalyzing trans-splicing reactions.

[0333] As used herein, the "N-terminal split intein (In)" refers to any intein sequence that comprises an N- terminal amino acid sequence that is functional for trans-splicing reactions. An In thus also comprises a sequence that is spliced out when trans-splicing occurs. An In can comprise a sequence that is a modification of the N-terminal portion of a naturally occurring intein sequence. For example, an In can comprise additional amino acid residues and/or mutated residues so long as the inclusion of such additional and/or mutated residues does not render the In non-functional in trans-splicing. Preferably, the inclusion of the additional and/or mutated residues improves or enhances the trans-splicing activity of the In.

[0334] As used herein, the "C-terminal split intein (Ic)" refers to any intein sequence that comprises a C- terminal amino acid sequence that is functional for trans-splicing reactions. In one aspect, the Ic comprises 4 to 7 contiguous amino acid residues, at least 4 amino acids of which are from the last β -strand of the intein from which it was derived. An Ic thus also comprises a sequence that is spliced out when trans-splicing occurs. An Ic can comprise a sequence that is a modification of the C-terminal portion of a naturally occurring intein sequence. For example, an Ic can comprise additional amino acid residues and/or mutated residues so long as the inclusion of such additional and/or mutated residues does not render

the In non-functional in trans-splicing. Preferably, the inclusion of the additional and/or mutated residues improves or enhances the trans-splicing activity of the Ic.

[0335] In some embodiments of the invention, a peptide linked to an Ic or an In can comprise an additional chemical moiety including, among others, fluorescence groups, biotin, polyethylene glycol (PEG), amino acid analogs, unnatural amino acids, phosphate groups, glycosyl groups, radioisotope labels, and pharmaceutical molecules. In other embodiments, a peptide linked to an Ic can comprise one or more chemically reactive groups including, among others, ketone, aldehyde, Cys residues and Lys residues. The N-intein and C-intein of a split intein can associate non-covalently to form an active intein and catalyze the splicing reaction when an "intein-splicing polypeptide (ISP)" is present. As used herein, "intein-splicing polypeptide (ISP)" refers to the portion of the amino acid sequence of a split intein that remains when the Ic, In, or both, are removed from the split intein. In certain embodiments, the In comprises the ISP. In another embodiment, the Ic comprises the ISP. In yet another embodiment, the ISP is a separate peptide that is not covalently linked to In nor to Ic.

[0336] Split inteins may be created from contiguous inteins by engineering one or more split sites in the unstructured loop or intervening amino acid sequence between the -12 conserved beta-strands found in the structure of mini-inteins. Some flexibility in the position of the split site within regions between the beta-strands may exist, provided that creation of the split will not disrupt the structure of the intein, the structured beta-strands in particular, to a sufficient degree that protein splicing activity is lost.

[0337] In protein trans-splicing, one precursor protein consists of an N-extein part followed by the N-intein, another precursor protein consists of the C-intein followed by a C-extein part, and a trans-splicing reaction (catalyzed by the N- and C-inteins together) excises the two intein sequences and links the two extein sequences with a peptide bond. Protein trans-splicing, being an enzymatic reaction, can work with very low (e.g. micromolar) concentrations of proteins and can be carried out under physiological conditions.

[0338] Exemplary sequences are as follows:

2-4 INTEIN:

CLAEGTRIFDPVTGTTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVS WFDQGTRDVI
GLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPILYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCV EGMVEIFDML

LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEELRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 1)

3-2 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA VAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPILYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKYTNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEELRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 2)

30R3-1 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGATVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPIPYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEGLRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 3)

30R3-2

INTEINCLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVSWFDQG
TRDVI GLRIAGGATVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LT
ADQMVSALLDAEPPILYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGF
VDLTLHDQAHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVEGMV
EIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDK
ITDTLIHLMAGLTLQQQHQRQAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLY
DLLLEMLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEELRYSVIREVLPTRRA
RTFDLEVEELHTLVAEGVVVHNC (SEQ ID NO: 4)

30R3-3 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGATVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPIPYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMKAGLTLQQQHQR LAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEELRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 5)

37R3-1 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGATVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPILYSEYNPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLERAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMKAGLTLQQQHQR LAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEGLRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC ((SEQ ID NO: 6)

37R3-2 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA AAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGAIVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPILYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL
HDQAHLLERAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMKAGLTLQQQHQR LAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEGLRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 7)

37R3-3 INTEIN

CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVA VAKDGTLLARPVVSWFDQGTRDVI
GLRIAGGATVWATPDHKVLTEYGWRAAGELRKGDRVAGPGGSGNSLALS LTADQM
VSALLDAEPPILYSEYDPTSPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTL

HDQAHLLEAWLEILMIGLVWRSMHPGKLLFAPNLLLDNRNQGKCVEGMVEIFDML
LATSSRFRMMNLQGEEFVCLKSILLNSGVYTFLSSTLKSLEEKDHIHRALDKITDTLI
HLMKAGLTLQQQHQLAQLLLILSHIRHMSNKGMEHLYSMKYKNVVPLYDLLLE
MLDAHRLHAGGSGASRVQAFADALDDKFLHDMLAEELRYSVIREVLPTRRARTFDL
EVEELHTLVAEGVVVHNC (SEQ ID NO: 8)

[0339] Although inteins are most frequently found as a contiguous domain, some exist in a naturally split form. In this case, the two fragments are expressed as separate polypeptides and must associate before splicing takes place, so-called protein trans-splicing.

[0340] An exemplary split intein is the Ssp DnaE intein, which comprises two subunits, namely, DnaE-N and DnaE-C. The two different subunits are encoded by separate genes, namely dnaE-n and dnaE-c, which encode the DnaE-N and DnaE-C subunits, respectively. DnaE is a naturally occurring split intein in *Synechocystis* sp. PCC6803 and is capable of directing trans-splicing of two separate proteins, each comprising a fusion with either DnaE-N or DnaE-C.

[0341] Additional naturally occurring or engineered split-intein sequences are known in the art or can be made from whole-intein sequences described herein or those available in the art. Examples of split-intein sequences can be found in Stevens et al., “A promiscuous split intein with expanded protein engineering applications,” PNAS, 2017, Vol.114: 8538-8543; Iwai et al., “Highly efficient protein trans-splicing by a naturally split DnaE intein from *Nostoc punctiforme*,” FEBS Lett, 580: 1853-1858, each of which are incorporated herein by reference. Additional split intein sequences can be found, for example, in WO 2013/045632, WO 2014/055782, WO 2016/069774, and EP2877490, the contents each of which are incorporated herein by reference.

[0342] In addition, protein splicing in trans has been described in vivo and in vitro (Shingledacker, et al., Gene 207:187 (1998), Southworth, et al., EMBO J. 17:918 (1998); Mills, et al., Proc. Natl. Acad. Sci. USA, 95:3543-3548 (1998); Lew, et al., J. Biol. Chem., 273:15887-15890 (1998); Wu, et al., Biochim. Biophys. Acta 35732:1 (1998b), Yamazaki, et al., J. Am. Chem. Soc. 120:5591 (1998), Evans, et al., J. Biol. Chem. 275:9091 (2000); Otomo, et al., Biochemistry 38:16040-16044 (1999); Otomo, et al., J. Biomol. NMR 14:105-114 (1999); Scott, et al., Proc. Natl. Acad. Sci. USA 96:13638-13643 (1999)) and provides the opportunity to express a protein as two inactive fragments that subsequently undergo ligation to form a functional product, e.g., as shown in FIGs. 66 and 67 with regard to the formation of a complete PE fusion protein from two separately-expressed halves.

[5] Methods of treatment

[0343] The instant disclosure provides methods for the treatment of a subject diagnosed with a disease associated with or caused by a point mutation or a frameshift mutation that can be corrected by the ribozyme-directed programmable editing system provided herein. For example, in some embodiments, a method is provided that comprises administering to a subject having such a disease, e.g., a cancer associated with a point mutation as described above, an effective amount of the ribozyme-directed programmable editing system described herein that corrects a frameshift mutation. In some embodiments, a method is provided that comprises administering to a subject having such a disease, e.g., a cancer associated with a point mutation as described above, an effective amount of the ribozyme-directed programmable editing system described herein that corrects a frameshift mutation in a disease-associated gene. In some embodiments, the disease is a proliferative disease. In some embodiments, the disease is a genetic disease. In some embodiments, the disease is a neoplastic disease. In some embodiments, the disease is a metabolic disease. In some embodiments, the disease is a lysosomal storage disease. Other diseases that can be treated by correcting a frameshift mutation (or other mutation involving a single nucleotide insertion or deletion) will be known to those of skill in the art, and the disclosure is not limited in this respect.

[0344] The instant disclosure provides methods for the treatment of additional diseases or disorders, e.g., diseases or disorders that are associated or caused by a point mutation that can be corrected by ribozyme-directed programmable editing. Some such diseases are described herein, and additional suitable diseases that can be treated with the strategies and fusion proteins provided herein will be apparent to those of skill in the art based on the instant disclosure. Exemplary suitable diseases and disorders are listed below. It will be understood that the numbering of the specific positions or residues in the respective sequences depends on the particular protein and numbering scheme used. Numbering might be different, e.g., in precursors of a mature protein and the mature protein itself, and differences in sequences from species to species may affect numbering. One of skill in the art will be able to identify the respective residue in any homologous protein and in the respective encoding nucleic acid by methods well known in the art, e.g., by sequence alignment and determination of homologous residues. Exemplary suitable diseases and disorders include, without limitation: 2-methyl-3-hydroxybutyric aciduria; 3 beta-Hydroxysteroid dehydrogenase deficiency; 3-Methylglutaconic aciduria; 3-Oxo-5 alpha-steroid delta 4-dehydrogenase deficiency; 46,XY sex reversal, type 1, 3, and 5; 5-Oxoprolinase deficiency; 6-pyruvoyl-tetrahydropterin synthase deficiency; Aarskog syndrome; Aase syndrome; Achondrogenesis type 2;

Achromatopsia 2 and 7; Acquired long QT syndrome; Acrocallosal syndrome, Schinzel type; Acrocapitofemoral dysplasia; Acrodysostosis 2, with or without hormone resistance; Acroerythrokeratoderma; Acromicric dysplasia; Acth-independent macronodular adrenal hyperplasia 2; Activated PI3K-delta syndrome; Acute intermittent porphyria; deficiency of Acyl-CoA dehydrogenase family, member 9; Adams-Oliver syndrome 5 and 6; Adenine phosphoribosyltransferase deficiency; Adenylate kinase deficiency; hemolytic anemia due to Adenylosuccinate lyase deficiency; Adolescent nephronophthisis; Renal-hepatic-pancreatic dysplasia; Meckel syndrome type 7; Adrenoleukodystrophy; Adult junctional epidermolysis bullosa; Epidermolysis bullosa, junctional, localisata variant; Adult neuronal ceroid lipofuscinosis; Adult neuronal ceroid lipofuscinosis; Adult onset ataxia with oculomotor apraxia; ADULT syndrome; Afibrinogenemia and congenital Afibrinogenemia; autosomal recessive Agammaglobulinemia 2; Age-related macular degeneration 3, 6, 11, and 12; Aicardi Goutieres syndromes 1, 4, and 5; Chilbain lupus 1; Alagille syndromes 1 and 2; Alexander disease; Alkaptonuria; Allan-Herndon-Dudley syndrome; Alopecia universalis congenital; Alpers encephalopathy; Alpha-1-antitrypsin deficiency; autosomal dominant, autosomal recessive, and X-linked recessive Alport syndromes; Alzheimer disease, familial, 3, with spastic paraparesis and apraxia; Alzheimer disease, types, 1, 3, and 4; hypocalcification type and hypomaturational type, IIA1 Amelogenesis imperfecta; Aminoacylase 1 deficiency; Amish infantile epilepsy syndrome; Amyloidogenic transthyretin amyloidosis; Amyloid Cardiomyopathy, Transthyretin-related; Cardiomyopathy; Amyotrophic lateral sclerosis types 1, 6, 15 (with or without frontotemporal dementia), 22 (with or without frontotemporal dementia), and 10; Frontotemporal dementia with TDP43 inclusions, TARDBP-related; Andermann syndrome; Andersen Tawil syndrome; Congenital long QT syndrome; Anemia, nonspherocytic hemolytic, due to G6PD deficiency; Angelman syndrome; Severe neonatal-onset encephalopathy with microcephaly; susceptibility to Autism, X-linked 3; Angiopathy, hereditary, with nephropathy, aneurysms, and muscle cramps; Angiotensin i-converting enzyme, benign serum increase; Aniridia, cerebellar ataxia, and mental retardation; Anonychia; Antithrombin III deficiency; Antley-Bixler syndrome with genital anomalies and disordered steroidogenesis; Aortic aneurysm, familial thoracic 4, 6, and 9; Thoracic aortic aneurysms and aortic dissections; Multisystemic smooth muscle dysfunction syndrome; Moyamoya disease 5; Aplastic anemia; Apparent mineralocorticoid excess; Arginase deficiency; Argininosuccinate lyase deficiency; Aromatase deficiency; Arrhythmogenic right ventricular cardiomyopathy types 5, 8, and 10; Primary familial hypertrophic cardiomyopathy; Arthrogyrosis multiplex congenita, distal, X-linked;

Arthrogryposis renal dysfunction cholestasis syndrome; Arthrogryposis, renal dysfunction, and cholestasis 2; Asparagine synthetase deficiency; Abnormality of neuronal migration; Ataxia with vitamin E deficiency; Ataxia, sensory, autosomal dominant; Ataxia-telangiectasia syndrome; Hereditary cancer-predisposing syndrome; Atransferrinemia; Atrial fibrillation, familial, 11, 12, 13, and 16; Atrial septal defects 2, 4, and 7 (with or without atrioventricular conduction defects); Atrial standstill 2; Atrioventricular septal defect 4; Atrophia bulborum hereditaria; ATR-X syndrome; Auriculocondylar syndrome 2; Autoimmune disease, multisystem, infantile-onset; Autoimmune lymphoproliferative syndrome, type 1a; Autosomal dominant hypohidrotic ectodermal dysplasia; Autosomal dominant progressive external ophthalmoplegia with mitochondrial DNA deletions 1 and 3; Autosomal dominant torsion dystonia 4; Autosomal recessive centronuclear myopathy; Autosomal recessive congenital ichthyosis 1, 2, 3, 4A, and 4B; Autosomal recessive cutis laxa type IA and 1B; Autosomal recessive hypohidrotic ectodermal dysplasia syndrome; Ectodermal dysplasia 11b; hypohidrotic/hair/tooth type, autosomal recessive; Autosomal recessive hypophosphatemic bone disease; Axenfeld-Rieger syndrome type 3; Bainbridge-Ropers syndrome; Bannayan-Riley-Ruvalcaba syndrome; PTEN hamartoma tumor syndrome; Baraitser-Winter syndromes 1 and 2; Barakat syndrome; Bardet-Biedl syndromes 1, 11, 16, and 19; Bare lymphocyte syndrome type 2, complementation group E; Bartter syndrome antenatal type 2; Bartter syndrome types 3, 3 with hypocalciuria, and 4; Basal ganglia calcification, idiopathic, 4; Beaded hair; Benign familial hematuria; Benign familial neonatal seizures 1 and 2; Seizures, benign familial neonatal, 1, and/or myokymia; Seizures, Early infantile epileptic encephalopathy 7; Benign familial neonatal-infantile seizures; Benign hereditary chorea; Benign scapuloperoneal muscular dystrophy with cardiomyopathy; Bernard-Soulier syndrome, types A1 and A2 (autosomal dominant); Bestrophinopathy, autosomal recessive; beta Thalassemia; Bethlem myopathy and Bethlem myopathy 2; Bietti crystalline corneoretinal dystrophy; Bile acid synthesis defect, congenital, 2; Biotinidase deficiency; Birk Barel mental retardation dysmorphism syndrome; Blepharophimosis, ptosis, and epicanthus inversus; Bloom syndrome; Borjeson-Forssman-Lehmann syndrome; Boucher Neuhauser syndrome; Brachydactyly types A1 and A2; Brachydactyly with hypertension; Brain small vessel disease with hemorrhage; Branched-chain ketoacid dehydrogenase kinase deficiency; Branchiootic syndromes 2 and 3; Breast cancer, early-onset; Breast-ovarian cancer, familial 1, 2, and 4; Brittle cornea syndrome 2; Brody myopathy; Bronchiectasis with or without elevated sweat chloride 3; Brown-Vialetto-Van laere syndrome and Brown-Vialetto-Van Laere syndrome 2; Brugada syndrome; Brugada syndrome 1; Ventricular

fibrillation; Paroxysmal familial ventricular fibrillation; Brugada syndrome and Brugada syndrome 4; Long QT syndrome; Sudden cardiac death; Bull eye macular dystrophy; Stargardt disease 4; Cone-rod dystrophy 12; Bullous ichthyosiform erythroderma; Burn-McKeown syndrome; Candidiasis, familial, 2, 5, 6, and 8; Carbohydrate-deficient glycoprotein syndrome type I and II; Carbonic anhydrase VA deficiency, hyperammonemia due to; Carcinoma of colon; Cardiac arrhythmia; Long QT syndrome, LQT1 subtype; Cardioencephalomyopathy, fatal infantile, due to cytochrome c oxidase deficiency; Cardiofaciocutaneous syndrome; Cardiomyopathy; Danon disease; Hypertrophic cardiomyopathy; Left ventricular noncompaction cardiomyopathy; Carnevale syndrome; Carney complex, type 1; Carnitine acylcarnitine translocase deficiency; Carnitine palmitoyltransferase I, II, II (late onset), and II (infantile) deficiency; Cataract 1, 4, autosomal dominant, autosomal dominant, multiple types, with microcornea, coppock-like, juvenile, with microcornea and glucosuria, and nuclear diffuse nonprogressive; Catecholaminergic polymorphic ventricular tachycardia; Caudal regression syndrome; Cd8 deficiency, familial; Central core disease; Centromeric instability of chromosomes 1,9 and 16 and immunodeficiency; Cerebellar ataxia infantile with progressive external ophthalmoplegia and Cerebellar ataxia, mental retardation, and dysequilibrium syndrome 2; Cerebral amyloid angiopathy, APP-related; Cerebral autosomal dominant and recessive arteriopathy with subcortical infarcts and leukoencephalopathy; Cerebral cavernous malformations 2; Cerebrooculofacioskeletal syndrome 2; Cerebro-oculo-facio-skeletal syndrome; Cerebroretinal microangiopathy with calcifications and cysts; Ceroid lipofuscinosis neuronal 2, 6, 7, and 10; Chediak-Higashi syndrome, Chediak-Higashi syndrome, adult type; Charcot-Marie-Tooth disease types 1B, 2B2, 2C, 2F, 2I, 2U (axonal), 1C (demyelinating), dominant intermediate C, recessive intermediate A, 2A2, 4C, 4D, 4H, IF, IVF, and X; Scapuloperoneal spinal muscular atrophy; Distal spinal muscular atrophy, congenital nonprogressive; Spinal muscular atrophy, distal, autosomal recessive, 5; CHARGE association; Childhood hypophosphatasia; Adult hypophosphatasia; Cholecystitis; Progressive familial intrahepatic cholestasis 3; Cholestasis, intrahepatic, of pregnancy 3; Cholesterol storage disease; Cholesterol monooxygenase (side-chain cleaving) deficiency; Chondrodysplasia Blomstrand type; Chondrodysplasia punctata 1, X-linked recessive and 2 X-linked dominant; CHOPS syndrome; Chronic granulomatous disease, autosomal recessive cytochrome b-positive, types 1 and 2; Chudley-McCullough syndrome; Ciliary dyskinesia, primary, 7, 11, 15, 20 and 22; Citrullinemia type I; Citrullinemia type I and II; Cleidocranial dysostosis; C-like syndrome; Cockayne syndrome type A, ; Coenzyme Q10 deficiency,

primary 1, 4, and 7; Coffin Siris/Intellectual Disability; Coffin-Lowry syndrome; Cohen syndrome, ; Cold-induced sweating syndrome 1; COLE-CARPENTER SYNDROME 2; Combined cellular and humoral immune defects with granulomas; Combined d-2- and l-2-hydroxyglutaric aciduria; Combined malonic and methylmalonic aciduria; Combined oxidative phosphorylation deficiencies 1, 3, 4, 12, 15, and 25; Combined partial and complete 17-alpha-hydroxylase/17,20-lyase deficiency; Common variable immunodeficiency 9; Complement component 4, partial deficiency of, due to dysfunctional c1 inhibitor; Complement factor B deficiency; Cone monochromatism; Cone-rod dystrophy 2 and 6; Cone-rod dystrophy amelogenesis imperfecta; Congenital adrenal hyperplasia and Congenital adrenal hypoplasia, X-linked; Congenital amegakaryocytic thrombocytopenia; Congenital aniridia; Congenital central hypoventilation; Hirschsprung disease 3; Congenital contractural arachnodactyly; Congenital contractures of the limbs and face, hypotonia, and developmental delay; Congenital disorder of glycosylation types 1B, 1D, 1G, 1H, 1J, 1K, 1N, 1P, 2C, 2J, 2K, IIIm; Congenital dyserythropoietic anemia, type I and II; Congenital ectodermal dysplasia of face; Congenital erythropoietic porphyria; Congenital generalized lipodystrophy type 2; Congenital heart disease, multiple types, 2; Congenital heart disease; Interrupted aortic arch; Congenital lipomatous overgrowth, vascular malformations, and epidermal nevi; Non-small cell lung cancer; Neoplasm of ovary; Cardiac conduction defect, nonspecific; Congenital microvillous atrophy; Congenital muscular dystrophy; Congenital muscular dystrophy due to partial LAMA2 deficiency; Congenital muscular dystrophy-dystroglycanopathy with brain and eye anomalies, types A2, A7, A8, A11, and A14; Congenital muscular dystrophy-dystroglycanopathy with mental retardation, types B2, B3, B5, and B15; Congenital muscular dystrophy-dystroglycanopathy without mental retardation, type B5; Congenital muscular hypertrophy-cerebral syndrome; Congenital myasthenic syndrome, acetazolamide-responsive; Congenital myopathy with fiber type disproportion; Congenital ocular coloboma; Congenital stationary night blindness, type 1A, 1B, 1C, 1E, 1F, and 2A; Coproporphyrria; Cornea plana 2; Corneal dystrophy, Fuchs endothelial, 4; Corneal endothelial dystrophy type 2; Corneal fragility keratoglobus, blue sclerae and joint hypermobility; Cornelia de Lange syndromes 1 and 5; Coronary artery disease, autosomal dominant 2; Coronary heart disease; Hyperalphalipoproteinemia 2; Cortical dysplasia, complex, with other brain malformations 5 and 6; Cortical malformations, occipital; Corticosteroid-binding globulin deficiency; Corticosterone methyloxidase type 2 deficiency; Costello syndrome; Cowden syndrome 1; Coxa plana; Craniodiaphyseal dysplasia, autosomal dominant; Craniosynostosis 1 and 4; Craniosynostosis and dental anomalies; Creatine deficiency, X-linked; Crouzon syndrome;

Cryptophthalmos syndrome; Cryptorchidism, unilateral or bilateral; Cushing symphalangism; Cutaneous malignant melanoma 1; Cutis laxa with osteodystrophy and with severe pulmonary, gastrointestinal, and urinary abnormalities; Cyanosis, transient neonatal and atypical nephropathic; Cystic fibrosis; Cystinuria; Cytochrome c oxidase i deficiency; Cytochrome-c oxidase deficiency ; D-2-hydroxyglutaric aciduria 2; Darier disease, segmental; Deafness with labyrinthine aplasia microtia and microdontia (LAMM); Deafness, autosomal dominant 3a, 4, 12, 13, 15, autosomal dominant nonsyndromic sensorineural 17, 20, and 65; Deafness, autosomal recessive 1A, 2, 3, 6, 8, 9, 12, 15, 16, 18b, 22, 28, 31, 44, 49, 63, 77, 86, and 89; Deafness, cochlear, with myopia and intellectual impairment, without vestibular involvement, autosomal dominant, X-linked 2; Deficiency of 2-methylbutyryl-CoA dehydrogenase; Deficiency of 3-hydroxyacyl-CoA dehydrogenase; Deficiency of alpha-mannosidase; Deficiency of aromatic-L-amino-acid decarboxylase; Deficiency of bisphosphoglycerate mutase; Deficiency of butyryl-CoA dehydrogenase; Deficiency of ferroxidase; Deficiency of galactokinase; Deficiency of guanidinoacetate methyltransferase; Deficiency of hyaluronoglucosaminidase; Deficiency of ribose-5-phosphate isomerase; Deficiency of steroid 11-beta-monooxygenase; Deficiency of UDPglucose-hexose-1-phosphate uridylyltransferase; Deficiency of xanthine oxidase; Dejerine-Sottas disease; Charcot-Marie-Tooth disease, types ID and IVF; Dejerine-Sottas syndrome, autosomal dominant; Dendritic cell, monocyte, B lymphocyte, and natural killer lymphocyte deficiency; Desbuquois dysplasia 2; Desbuquois syndrome; DFNA 2 Nonsyndromic Hearing Loss; Diabetes mellitus and insipidus with optic atrophy and deafness; Diabetes mellitus, type 2, and insulin-dependent, 20; Diamond-Blackfan anemia 1, 5, 8, and 10; Diarrhea 3 (secretory sodium, congenital, syndromic) and 5 (with tufting enteropathy, congenital); Dicarboxylic aminoaciduria; Diffuse palmoplantar keratoderma, Bothnian type; Digitorenocerebral syndrome; Dihydropteridine reductase deficiency; Dilated cardiomyopathy 1A, 1AA, 1C, 1G, 1BB, 1DD, 1FF, 1HH, 1I, 1KK, 1N, 1S, 1Y, and 3B; Left ventricular noncompaction 3; Disordered steroidogenesis due to cytochrome p450 oxidoreductase deficiency; Distal arthrogryposis type 2B; Distal hereditary motor neuropathy type 2B; Distal myopathy Markesbery-Griggs type; Distal spinal muscular atrophy, X-linked 3; Distichiasis-lymphedema syndrome; Dominant dystrophic epidermolysis bullosa with absence of skin; Dominant hereditary optic atrophy; Donnai Barrow syndrome; Dopamine beta hydroxylase deficiency; Dopamine receptor d2, reduced brain density of; Dowling-degos disease 4; Doyme honeycomb retinal dystrophy; Malattia leventinese; Duane syndrome type 2; Dubin-Johnson syndrome; Duchenne muscular dystrophy; Becker muscular dystrophy; Dysfibrinogenemia;

Dyskeratosis congenita autosomal dominant and autosomal dominant, 3; Dyskeratosis congenita, autosomal recessive, 1, 3, 4, and 5; Dyskeratosis congenita X-linked; Dyskinesia, familial, with facial myokymia; Dysplasminogenemia; Dystonia 2 (torsion, autosomal recessive), 3 (torsion, X-linked), 5 (Dopa-responsive type), 10, 12, 16, 25, 26 (Myoclonic); Seizures, benign familial infantile, 2; Early infantile epileptic encephalopathy 2, 4, 7, 9, 10, 11, 13, and 14; Atypical Rett syndrome; Early T cell progenitor acute lymphoblastic leukemia; Ectodermal dysplasia skin fragility syndrome; Ectodermal dysplasia-syndactyly syndrome 1; Ectopia lentis, isolated autosomal recessive and dominant; Ectrodactyly, ectodermal dysplasia, and cleft lip/palate syndrome 3; Ehlers-Danlos syndrome type 7 (autosomal recessive), classic type, type 2 (progeroid), hydroxylysine-deficient, type 4, type 4 variant, and due to tenascin-X deficiency; Eichsfeld type congenital muscular dystrophy; Endocrine-cerebroosteodysplasia; Enhanced s-cone syndrome; Enlarged vestibular aqueduct syndrome; Enterokinase deficiency; Epidermodysplasia verruciformis; Epidermolysa bullosa simplex and limb girdle muscular dystrophy, simplex with mottled pigmentation, simplex with pyloric atresia, simplex, autosomal recessive, and with pyloric atresia; Epidermolytic palmoplantar keratoderma; Familial febrile seizures 8; Epilepsy, childhood absence 2, 12 (idiopathic generalized, susceptibility to) 5 (nocturnal frontal lobe), nocturnal frontal lobe type 1, partial, with variable foci, progressive myoclonic 3, and X-linked, with variable learning disabilities and behavior disorders; Epileptic encephalopathy, childhood-onset, early infantile, 1, 19, 23, 25, 30, and 32; Epiphyseal dysplasia, multiple, with myopia and conductive deafness; Episodic ataxia type 2; Episodic pain syndrome, familial, 3; Epstein syndrome; Fechtner syndrome; Erythropoietic protoporphyria; Estrogen resistance; Exudative vitreoretinopathy 6; Fabry disease and Fabry disease, cardiac variant; Factor H, VII, X, v and factor viii, combined deficiency of 2, xiii, a subunit, deficiency; Familial adenomatous polyposis 1 and 3; Familial amyloid nephropathy with urticaria and deafness; Familial cold urticarial; Familial aplasia of the vermis; Familial benign pemphigus; Familial cancer of breast; Breast cancer, susceptibility to; Osteosarcoma; Pancreatic cancer 3; Familial cardiomyopathy; Familial cold autoinflammatory syndrome 2; Familial colorectal cancer; Familial exudative vitreoretinopathy, X-linked; Familial hemiplegic migraine types 1 and 2; Familial hypercholesterolemia; Familial hypertrophic cardiomyopathy 1, 2, 3, 4, 7, 10, 23 and 24; Familial hypokalemia-hypomagnesemia; Familial hypoplastic, glomerulocystic kidney; Familial infantile myasthenia; Familial juvenile gout; Familial Mediterranean fever and Familial mediterranean fever, autosomal dominant; Familial porencephaly; Familial porphyria cutanea tarda; Familial pulmonary capillary hemangiomatosis; Familial renal

glucosuria; Familial renal hypouricemia; Familial restrictive cardiomyopathy 1; Familial type 1 and 3 hyperlipoproteinemia; Fanconi anemia, complementation group E, I, N, and O; Fanconi-Bickel syndrome; Favism, susceptibility to; Febrile seizures, familial, 11; Feingold syndrome 1; Fetal hemoglobin quantitative trait locus 1; FG syndrome and FG syndrome 4; Fibrosis of extraocular muscles, congenital, 1, 2, 3a (with or without extraocular involvement), 3b; Fish-eye disease; Fleck corneal dystrophy; Floating-Harbor syndrome; Focal epilepsy with speech disorder with or without mental retardation; Focal segmental glomerulosclerosis 5; Forebrain defects; Frank Ter Haar syndrome; Borrone Di Rocco Crovato syndrome; Frasier syndrome; Wilms tumor 1; Freeman-Sheldon syndrome; Frontometaphyseal dysplasia 1 and 3; Frontotemporal dementia; Frontotemporal dementia and/or amyotrophic lateral sclerosis 3 and 4; Frontotemporal Dementia Chromosome 3-Linked and Frontotemporal dementia ubiquitin-positive; Fructose-biphosphatase deficiency; Fuhrmann syndrome; Gamma-aminobutyric acid transaminase deficiency; Gamstorp-Wohlfart syndrome; Gaucher disease type 1 and Subacute neuronopathic; Gaze palsy, familial horizontal, with progressive scoliosis; Generalized dominant dystrophic epidermolysis bullosa; Generalized epilepsy with febrile seizures plus 3, type 1, type 2; Epileptic encephalopathy Lennox-Gastaut type; Giant axonal neuropathy; Glanzmann thrombasthenia; Glaucoma 1, open angle, e, F, and G; Glaucoma 3, primary congenital, d; Glaucoma, congenital and Glaucoma, congenital, Coloboma; Glaucoma, primary open angle, juvenile-onset; Glioma susceptibility 1; Glucose transporter type 1 deficiency syndrome; Glucose-6-phosphate transport defect; GLUT1 deficiency syndrome 2; Epilepsy, idiopathic generalized, susceptibility to, 12; Glutamate formiminotransferase deficiency; Glutaric acidemia IIA and IIB; Glutaric aciduria, type 1; Gluthathione synthetase deficiency; Glycogen storage disease 0 (muscle), II (adult form), IXa2, IXc, type 1A; type II, type IV, IV (combined hepatic and myopathic), type V, and type VI; Goldmann-Favre syndrome; Gordon syndrome; Gorlin syndrome; Holoprosencephaly sequence; Holoprosencephaly 7; Granulomatous disease, chronic, X-linked, variant; Granulosa cell tumor of the ovary; Gray platelet syndrome; Griscelli syndrome type 3; Groenouw corneal dystrophy type I; Growth and mental retardation, mandibulofacial dysostosis, microcephaly, and cleft palate; Growth hormone deficiency with pituitary anomalies; Growth hormone insensitivity with immunodeficiency; GTP cyclohydrolase I deficiency; Hajdu-Cheney syndrome; Hand foot uterus syndrome; Hearing impairment; Hemangioma, capillary infantile; Hematologic neoplasm; Hemochromatosis type 1, 2B, and 3; Microvascular complications of diabetes 7; Transferrin serum level quantitative trait locus 2; Hemoglobin H disease, nondeletional;

Hemolytic anemia, nonspherocytic, due to glucose phosphate isomerase deficiency;
 Hemophagocytic lymphohistiocytosis, familial, 2; Hemophagocytic lymphohistiocytosis,
 familial, 3; Heparin cofactor II deficiency; Hereditary acrodermatitis enteropathica;
 Hereditary breast and ovarian cancer syndrome; Ataxia-telangiectasia-like disorder;
 Hereditary diffuse gastric cancer; Hereditary diffuse leukoencephalopathy with spheroids;
 Hereditary factors II, IX, VIII deficiency disease; Hereditary hemorrhagic telangiectasia type
 2; Hereditary insensitivity to pain with anhidrosis; Hereditary lymphedema type I; Hereditary
 motor and sensory neuropathy with optic atrophy; Hereditary myopathy with early
 respiratory failure; Hereditary neuralgic amyotrophy; Hereditary Nonpolyposis Colorectal
 Neoplasms; Lynch syndrome I and II; Hereditary pancreatitis; Pancreatitis, chronic,
 susceptibility to; Hereditary sensory and autonomic neuropathy type IIB and IIA; Hereditary
 sideroblastic anemia; Hermansky-Pudlak syndrome 1, 3, 4, and 6; Heterotaxy, visceral, 2, 4,
 and 6, autosomal; Heterotaxy, visceral, X-linked; Heterotopia; Histiocytic medullary
 reticulosis; Histiocytosis-lymphadenopathy plus syndrome; Holocarboxylase synthetase
 deficiency; Holoprosencephaly 2, 3, 7, and 9; Holt-Oram syndrome; Homocysteinemia due to
 MTHFR deficiency, CBS deficiency, and Homocystinuria, pyridoxine-responsive;
 Homocystinuria-Megaloblastic anemia due to defect in cobalamin metabolism, cblE
 complementation type; Howel-Evans syndrome; Hurler syndrome; Hutchinson-Gilford
 syndrome; Hydrocephalus; Hyperammonemia, type III; Hypercholesterolaemia and
 Hypercholesterolemia, autosomal recessive; Hyperekplexia 2 and Hyperekplexia hereditary;
 Hyperferritinemia cataract syndrome; Hyperglycinuria; Hyperimmunoglobulin D with
 periodic fever; Mevalonic aciduria; Hyperimmunoglobulin E syndrome; Hyperinsulinemic
 hypoglycemia familial 3, 4, and 5; Hyperinsulinism-hyperammonemia syndrome;
 Hyperlysinemia; Hypermanganesemia with dystonia, polycythemia and cirrhosis;
 Hyperornithinemia-hyperammonemia-homocitrullinuria syndrome; Hyperparathyroidism 1
 and 2; Hyperparathyroidism, neonatal severe; Hyperphenylalaninemia, bh4-deficient, a, due
 to partial pts deficiency, BH4-deficient, D, and non-pku; Hyperphosphatasia with mental
 retardation syndrome 2, 3, and 4; Hypertrichotic osteochondrodysplasia;
 Hypobetalipoproteinemia, familial, associated with apob32; Hypocalcemia, autosomal
 dominant 1; Hypocalciuric hypercalcemia, familial, types 1 and 3; Hypochondrogenesis;
 Hypochromic microcytic anemia with iron overload; Hypoglycemia with deficiency of
 glycogen synthetase in the liver; Hypogonadotropic hypogonadism 11 with or without
 anosmia; Hypohidrotic ectodermal dysplasia with immune deficiency; Hypohidrotic X-linked
 ectodermal dysplasia; Hypokalemic periodic paralysis 1 and 2; Hypomagnesemia 1,

intestinal; Hypomagnesemia, seizures, and mental retardation; Hypomyelinating leukodystrophy 7; Hypoplastic left heart syndrome; Atrioventricular septal defect and common atrioventricular junction; Hypospadias 1 and 2, X-linked; Hypothyroidism, congenital, nongoitrous, 1; Hypotrichosis 8 and 12; Hypotrichosis-lymphedema-telangiectasia syndrome; I blood group system; Ichthyosis bullosa of Siemens; Ichthyosis exfoliativa; Ichthyosis prematurity syndrome; Idiopathic basal ganglia calcification 5; Idiopathic fibrosing alveolitis, chronic form; Dyskeratosis congenita, autosomal dominant, 2 and 5; Idiopathic hypercalcemia of infancy; Immune dysfunction with T-cell inactivation due to calcium entry defect 2; Immunodeficiency 15, 16, 19, 30, 31C, 38, 40, 8, due to defect in cd3-zeta, with hyper IgM type 1 and 2, and X-Linked, with magnesium defect, Epstein-Barr virus infection, and neoplasia; Immunodeficiency-centromeric instability-facial anomalies syndrome 2; Inclusion body myopathy 2 and 3; Nonaka myopathy; Infantile convulsions and paroxysmal choreoathetosis, familial; Infantile cortical hyperostosis; Infantile GM1 gangliosidosis; Infantile hypophosphatasia; Infantile nephronophthisis; Infantile nystagmus, X-linked; Infantile Parkinsonism-dystonia; Infertility associated with multi-tailed spermatozoa and excessive DNA; Insulin resistance; Insulin-resistant diabetes mellitus and acanthosis nigricans; Insulin-dependent diabetes mellitus secretory diarrhea syndrome; Interstitial nephritis, karyomegalic; Intrauterine growth retardation, metaphyseal dysplasia, adrenal hypoplasia congenita, and genital anomalies; Iodotyrosyl coupling defect; IRAK4 deficiency; Iridogoniodysgenesis dominant type and type 1; Iron accumulation in brain; Ischiopatellar dysplasia; Islet cell hyperplasia; Isolated 17,20-lyase deficiency; Isolated lutropin deficiency; Isovaleryl-CoA dehydrogenase deficiency; Jankovic Rivera syndrome; Jervell and Lange-Nielsen syndrome 2; Joubert syndrome 1, 6, 7, 9/15 (digenic), 14, 16, and 17, and Orofaciodigital syndrome xiv; Junctional epidermolysis bullosa gravis of Herlitz; Juvenile GM>1< gangliosidosis; Juvenile polyposis syndrome; Juvenile polyposis/hereditary hemorrhagic telangiectasia syndrome; Juvenile retinoschisis; Kabuki make-up syndrome; Kallmann syndrome 1, 2, and 6; Delayed puberty; Kanzaki disease; Karak syndrome; Kartagener syndrome; Kenny-Caffey syndrome type 2; Keppen-Lubinsky syndrome; Keratoconus 1; Keratosis follicularis; Keratosis palmoplantaris striata 1; Kindler syndrome; L-2-hydroxyglutaric aciduria; Larsen syndrome, dominant type; Lattice corneal dystrophy Type III; Leber amaurosis; Zellweger syndrome; Peroxisome biogenesis disorders; Zellweger syndrome spectrum; Leber congenital amaurosis 11, 12, 13, 16, 4, 7, and 9; Leber optic atrophy; Aminoglycoside-induced deafness; Deafness, nonsyndromic sensorineural, mitochondrial; Left ventricular noncompaction 5; Left-right axis malformations; Leigh

disease; Mitochondrial short-chain Enoyl-CoA Hydratase 1 deficiency; Leigh syndrome due to mitochondrial complex I deficiency; Leiner disease; Leri Weill dyschondrosteosis; Lethal congenital contracture syndrome 6; Leukocyte adhesion deficiency type I and III; Leukodystrophy, Hypomyelinating, 11 and 6; Leukoencephalopathy with ataxia, with Brainstem and Spinal Cord Involvement and Lactate Elevation, with vanishing white matter, and progressive, with ovarian failure; Leukonychia totalis; Lewy body dementia; Lichtenstein-Knorr Syndrome; Li-Fraumeni syndrome 1; Lig4 syndrome; Limb-girdle muscular dystrophy, type 1B, 2A, 2B, 2D, C1, C5, C9, C14; Congenital muscular dystrophy-dystroglycanopathy with brain and eye anomalies, type A14 and B14; Lipase deficiency combined; Lipid proteinosis; Lipodystrophy, familial partial, type 2 and 3; Lissencephaly 1, 2 (X-linked), 3, 6 (with microcephaly), X-linked; Subcortical laminar heterotopia, X-linked; Liver failure acute infantile; Loeys-Dietz syndrome 1, 2, 3; Long QT syndrome 1, 2, 2/9, 2/5, (digenic), 3, 5 and 5, acquired, susceptibility to; Lung cancer; Lymphedema, hereditary, id; Lymphedema, primary, with myelodysplasia; Lymphoproliferative syndrome 1, 1 (X-linked), and 2; Lysosomal acid lipase deficiency; Macrocephaly, macrosomia, facial dysmorphism syndrome; Macular dystrophy, vitelliform, adult-onset; Malignant hyperthermia susceptibility type 1; Malignant lymphoma, non-Hodgkin; Malignant melanoma; Malignant tumor of prostate; Mandibuloacral dysostosis; Mandibuloacral dysplasia with type A or B lipodystrophy, atypical; Mandibulofacial dysostosis, Treacher Collins type, autosomal recessive; Mannose-binding protein deficiency; Maple syrup urine disease type 1A and type 3; Marden Walker like syndrome; Marfan syndrome; Marinesco-Sjogren syndrome; Martsolf syndrome; Maturity-onset diabetes of the young, type 1, type 2, type 11, type 3, and type 9; May-Hegglin anomaly; MYH9 related disorders; Sebastian syndrome; McCune-Albright syndrome; Somatotroph adenoma; Sex cord-stromal tumor; Cushing syndrome; McKusick Kaufman syndrome; McLeod neuroacanthocytosis syndrome; Meckel-Gruber syndrome; Medium-chain acyl-coenzyme A dehydrogenase deficiency; Medulloblastoma; Megalencephalic leukoencephalopathy with subcortical cysts 1 and 2a; Megalencephaly cutis marmorata telangiectatica congenital; PIK3CA Related Overgrowth Spectrum; Megalencephaly-polymicrogyria-polydactyly-hydrocephalus syndrome 2; Megaloblastic anemia, thiamine-responsive, with diabetes mellitus and sensorineural deafness; Meier-Gorlin syndromes 1 and 4; Melnick-Needles syndrome; Meningioma; Mental retardation, X-linked, 3, 21, 30, and 72; Mental retardation and microcephaly with pontine and cerebellar hypoplasia; Mental retardation X-linked syndromic 5; Mental retardation, anterior maxillary protrusion, and strabismus; Mental retardation, autosomal dominant 12, 13, 15, 24, 3, 30, 4,

5, 6, and 9; Mental retardation, autosomal recessive 15, 44, 46, and 5; Mental retardation, stereotypic movements, epilepsy, and/or cerebral malformations; Mental retardation, syndromic, Claes-Jensen type, X-linked; Mental retardation, X-linked, nonspecific, syndromic, Hedera type, and syndromic, wu type; Merosin deficient congenital muscular dystrophy; Metachromatic leukodystrophy juvenile, late infantile, and adult types; Metachromatic leukodystrophy; Metatrophic dysplasia; Methemoglobinemia types I and 2; Methionine adenosyltransferase deficiency, autosomal dominant; Methylmalonic acidemia with homocystinuria, ; Methylmalonic aciduria cblB type, ; Methylmalonic aciduria due to methylmalonyl-CoA mutase deficiency; METHYLMALONIC ACIDURIA, mut(0) TYPE; Microcephalic osteodysplastic primordial dwarfism type 2; Microcephaly with or without chorioretinopathy, lymphedema, or mental retardation; Microcephaly, hiatal hernia and nephrotic syndrome; Microcephaly; Hypoplasia of the corpus callosum; Spastic paraplegia 50, autosomal recessive; Global developmental delay; CNS hypomyelination; Brain atrophy; Microcephaly, normal intelligence and immunodeficiency; Microcephaly-capillary malformation syndrome; Microcytic anemia; Microphthalmia syndromic 5, 7, and 9; Microphthalmia, isolated 3, 5, 6, 8, and with coloboma 6; Microspherophakia; Migraine, familial basilar; Miller syndrome; Minicore myopathy with external ophthalmoplegia; Myopathy, congenital with cores; Mitchell-Riley syndrome; mitochondrial 3-hydroxy-3-methylglutaryl-CoA synthase deficiency; Mitochondrial complex I, II, III, III (nuclear type 2, 4, or 8) deficiency; Mitochondrial DNA depletion syndrome 11, 12 (cardiomyopathic type), 2, 4B (MNGIE type), 8B (MNGIE type); Mitochondrial DNA-depletion syndrome 3 and 7, hepatocerebral types, and 13 (encephalomyopathic type); Mitochondrial phosphate carrier and pyruvate carrier deficiency; Mitochondrial trifunctional protein deficiency; Long-chain 3-hydroxyacyl-CoA dehydrogenase deficiency; Miyoshi muscular dystrophy 1; Myopathy, distal, with anterior tibial onset; Mohr-Tranebjaerg syndrome; Molybdenum cofactor deficiency, complementation group A; Mowat-Wilson syndrome; Mucopolipidosis III Gamma; Mucopolysaccharidosis type VI, type VI (severe), and type VII; Mucopolysaccharidosis, MPS-I-H/S, MPS-II, MPS-III-A, MPS-III-B, MPS-III-C, MPS-IV-A, MPS-IV-B; Retinitis Pigmentosa 73; Gangliosidosis GM1 type1 (with cardiac involvement) 3; Multicentric osteolysis nephropathy; Multicentric osteolysis, nodulosis and arthropathy; Multiple congenital anomalies; Atrial septal defect 2; Multiple congenital anomalies-hypotonia-seizures syndrome 3; Multiple Cutaneous and Mucosal Venous Malformations; Multiple endocrine neoplasia, types 1 and 4; Multiple epiphyseal dysplasia 5 or Dominant; Multiple gastrointestinal atresias; Multiple pterygium syndrome Escobar type; Multiple sulfatase

deficiency; Multiple synostoses syndrome 3; Muscle AMP guanine oxidase deficiency; Muscle eye brain disease; Muscular dystrophy, congenital, megaconial type; Myasthenia, familial infantile, 1; Myasthenic Syndrome, Congenital, 11, associated with acetylcholine receptor deficiency; Myasthenic Syndrome, Congenital, 17, 2A (slow-channel), 4B (fast-channel), and without tubular aggregates; Myeloperoxidase deficiency; MYH-associated polyposis; Endometrial carcinoma; Myocardial infarction 1; Myoclonic dystonia; Myoclonic-Atonic Epilepsy; Myoclonus with epilepsy with ragged red fibers; Myofibrillar myopathy 1 and ZASP-related; Myoglobinuria, acute recurrent, autosomal recessive; Myoneural gastrointestinal encephalopathy syndrome; Cerebellar ataxia infantile with progressive external ophthalmoplegia; Mitochondrial DNA depletion syndrome 4B, MNGIE type; Myopathy, centronuclear, 1, congenital, with excess of muscle spindles, distal, 1, lactic acidosis, and sideroblastic anemia 1, mitochondrial progressive with congenital cataract, hearing loss, and developmental delay, and tubular aggregate, 2; Myopia 6; Myosclerosis, autosomal recessive; Myotonia congenital; Congenital myotonia, autosomal dominant and recessive forms; Nail-patella syndrome; Nance-Horan syndrome; Nanophthalmos 2; Navajo neurohepatopathy; Nemaline myopathy 3 and 9; Neonatal hypotonia; Intellectual disability; Seizures; Delayed speech and language development; Mental retardation, autosomal dominant 31; Neonatal intrahepatic cholestasis caused by citrin deficiency; Nephrogenic diabetes insipidus, Nephrogenic diabetes insipidus, X-linked; Nephrolithiasis/osteoporosis, hypophosphatemic, 2; Nephronophthisis 13, 15 and 4; Infertility; Cerebello-oculo-renal syndrome (nephronophthisis, oculomotor apraxia and cerebellar abnormalities); Nephrotic syndrome, type 3, type 5, with or without ocular abnormalities, type 7, and type 9; Nestor-Guillermo progeria syndrome; Neu-Laxova syndrome 1; Neurodegeneration with brain iron accumulation 4 and 6; Neuroferritinopathy; Neurofibromatosis, type 1 and type 2; Neurofibrosarcoma; Neurohypophyseal diabetes insipidus; Neuropathy, Hereditary Sensory, Type IC; Neutral 1 amino acid transport defect; Neutral lipid storage disease with myopathy; Neutrophil immunodeficiency syndrome; Nicolaides-Baraitser syndrome; Niemann-Pick disease type C1, C2, type A, and type C1, adult form; Non-ketotic hyperglycinemia; Noonan syndrome 1 and 4, LEOPARD syndrome 1; Noonan syndrome-like disorder with or without juvenile myelomonocytic leukemia; Normokalemic periodic paralysis, potassium-sensitive; Norum disease; Epilepsy, Hearing Loss, And Mental Retardation Syndrome; Mental Retardation, X-Linked 102 and syndromic 13; Obesity; Ocular albinism, type I; Oculocutaneous albinism type 1B, type 3, and type 4; Oculodentodigital dysplasia; Odontohypophosphatasia; Odontotrichomelic syndrome; Oguchi disease; Oligodontia-

colorectal cancer syndrome; Opitz G/BBB syndrome; Optic atrophy 9; Oral-facial-digital syndrome; Ornithine aminotransferase deficiency; Orofacial cleft 11 and 7, Cleft lip/palate-ectodermal dysplasia syndrome; Orstavik Lindemann Solberg syndrome; Osteoarthritis with mild chondrodysplasia; Osteochondritis dissecans; Osteogenesis imperfecta type 12, type 5, type 7, type 8, type I, type III, with normal sclerae, dominant form, recessive perinatal lethal; Osteopathia striata with cranial sclerosis; Osteopetrosis autosomal dominant type 1 and 2, recessive 4, recessive 1, recessive 6; Osteoporosis with pseudoglioma; Oto-palato-digital syndrome, types I and II; Ovarian dysgenesis 1; Ovarioleukodystrophy; Pachyonychia congenita 4 and type 2; Paget disease of bone, familial; Pallister-Hall syndrome; Palmoplantar keratoderma, nonepidermolytic, focal or diffuse; Pancreatic agenesis and congenital heart disease; Papillon-Lefevre syndrome; Paragangliomas 3; Paramyotonia congenita of von Eulenburg; Parathyroid carcinoma; Parkinson disease 14, 15, 19 (juvenile-onset), 2, 20 (early-onset), 6, (autosomal recessive early-onset, and 9; Partial albinism; Partial hypoxanthine-guanine phosphoribosyltransferase deficiency; Patterned dystrophy of retinal pigment epithelium; PC-K6a; Pelizaeus-Merzbacher disease; Pendred syndrome; Peripheral demyelinating neuropathy, central dysmyelination; Hirschsprung disease; Permanent neonatal diabetes mellitus; Diabetes mellitus, permanent neonatal, with neurologic features; Neonatal insulin-dependent diabetes mellitus; Maturity-onset diabetes of the young, type 2; Peroxisome biogenesis disorder 14B, 2A, 4A, 5B, 6A, 7A, and 7B; Perrault syndrome 4; Perry syndrome; Persistent hyperinsulinemic hypoglycemia of infancy; familial hyperinsulinism; Phenotypes; Phenylketonuria; Pheochromocytoma; Hereditary Paraganglioma-Pheochromocytoma Syndromes; Paragangliomas 1; Carcinoid tumor of intestine; Cowden syndrome 3; Phosphoglycerate dehydrogenase deficiency; Phosphoglycerate kinase 1 deficiency; Photosensitive trichothiodystrophy; Phytanic acid storage disease; Pick disease; Pierson syndrome; Pigmentary retinal dystrophy; Pigmented nodular adrenocortical disease, primary, 1; Pilomatrixoma; Pitt-Hopkins syndrome; Pituitary dependent hypercortisolism; Pituitary hormone deficiency, combined 1, 2, 3, and 4; Plasminogen activator inhibitor type 1 deficiency; Plasminogen deficiency, type I; Platelet-type bleeding disorder 15 and 8; Poikiloderma, hereditary fibrosing, with tendon contractures, myopathy, and pulmonary fibrosis; Polycystic kidney disease 2, adult type, and infantile type; Polycystic lipomembranous osteodysplasia with sclerosing leukoencephalopathy; Polyglucosan body myopathy 1 with or without immunodeficiency; Polymicrogyria, asymmetric, bilateral frontoparietal; Polyneuropathy, hearing loss, ataxia, retinitis pigmentosa, and cataract; Pontocerebellar hypoplasia type 4; Popliteal pterygium syndrome;

Porencephaly 2; Porokeratosis 8, disseminated superficial actinic type; Porphobilinogen synthase deficiency; Porphyria cutanea tarda; Posterior column ataxia with retinitis pigmentosa; Posterior polar cataract type 2; Prader-Willi-like syndrome; Premature ovarian failure 4, 5, 7, and 9; Primary autosomal recessive microcephaly 10, 2, 3, and 5; Primary ciliary dyskinesia 24; Primary dilated cardiomyopathy; Left ventricular noncompaction 6; 4, Left ventricular noncompaction 10; Paroxysmal atrial fibrillation; Primary hyperoxaluria, type I, type, and type III; Primary hypertrophic osteoarthropathy, autosomal recessive 2; Primary hypomagnesemia; Primary open angle glaucoma juvenile onset 1; Primary pulmonary hypertension; Primrose syndrome; Progressive familial heart block type 1B; Progressive familial intrahepatic cholestasis 2 and 3; Progressive intrahepatic cholestasis; Progressive myoclonus epilepsy with ataxia; Progressive pseudorheumatoid dysplasia; Progressive sclerosing poliodystrophy; Prolidase deficiency; Proline dehydrogenase deficiency; Schizophrenia 4; Properdin deficiency, X-linked; Propionic academia; Proprotein convertase 1/3 deficiency; Prostate cancer, hereditary, 2; Protan defect; Proteinuria; Finnish congenital nephrotic syndrome; Proteus syndrome; Breast adenocarcinoma; Pseudoachondroplastic spondyloepiphyseal dysplasia syndrome; Pseudohypoaldosteronism type 1 autosomal dominant and recessive and type 2; Pseudohypoparathyroidism type 1A, Pseudopseudohypoparathyroidism; Pseudoneonatal adrenoleukodystrophy; Pseudoprimary hyperaldosteronism; Pseudoxanthoma elasticum; Generalized arterial calcification of infancy 2; Pseudoxanthoma elasticum-like disorder with multiple coagulation factor deficiency; Psoriasis susceptibility 2; PTEN hamartoma tumor syndrome; Pulmonary arterial hypertension related to hereditary hemorrhagic telangiectasia; Pulmonary Fibrosis And/Or Bone Marrow Failure, Telomere-Related, 1 and 3; Pulmonary hypertension, primary, 1, with hereditary hemorrhagic telangiectasia; Purine-nucleoside phosphorylase deficiency; Pyruvate carboxylase deficiency; Pyruvate dehydrogenase E1-alpha deficiency; Pyruvate kinase deficiency of red cells; Raine syndrome; Rasopathy; Recessive dystrophic epidermolysis bullosa; Nail disorder, nonsyndromic congenital, 8; Reifenshtein syndrome; Renal adysplasia; Renal carnitine transport defect; Renal coloboma syndrome; Renal dysplasia; Renal dysplasia, retinal pigmentary dystrophy, cerebellar ataxia and skeletal dysplasia; Renal tubular acidosis, distal, autosomal recessive, with late-onset sensorineural hearing loss, or with hemolytic anemia; Renal tubular acidosis, proximal, with ocular abnormalities and mental retardation; Retinal cone dystrophy 3B; Retinitis pigmentosa; Retinitis pigmentosa 10, 11, 12, 14, 15, 17, and 19; Retinitis pigmentosa 2, 20, 25, 35, 36, 38, 39, 4, 40, 43, 45, 48, 66, 7, 70, 72; Retinoblastoma; Rett disorder; Rhabdoid tumor predisposition syndrome 2;

Rhegmatogenous retinal detachment, autosomal dominant; Rhizomelic chondrodysplasia punctata type 2 and type 3; Roberts-SC phocomelia syndrome; Robinow Sorauf syndrome; Robinow syndrome, autosomal recessive, autosomal recessive, with brachy-syn-polydactyly; Rothmund-Thomson syndrome; Rapadilino syndrome; RRM2B-related mitochondrial disease; Rubinstein-Taybi syndrome; Salla disease; Sandhoff disease, adult and infantile types; Sarcoidosis, early-onset; Blau syndrome; Schindler disease, type 1; Schizencephaly; Schizophrenia 15; Schneckenbecken dysplasia; Schwannomatosis 2; Schwartz Jampel syndrome type 1; Sclerocornea, autosomal recessive; Sclerosteosis; Secondary hypothyroidism; Segawa syndrome, autosomal recessive; Senior-Loken syndrome 4 and 5, ; Sensory ataxic neuropathy, dysarthria, and ophthalmoparesis; Sepiapterin reductase deficiency; SeSAME syndrome; Severe combined immunodeficiency due to ADA deficiency, with microcephaly, growth retardation, and sensitivity to ionizing radiation, atypical, autosomal recessive, T cell-negative, B cell-positive, NK cell-negative of NK-positive; Severe congenital neutropenia; Severe congenital neutropenia 3, autosomal recessive or dominant; Severe congenital neutropenia and 6, autosomal recessive; Severe myoclonic epilepsy in infancy; Generalized epilepsy with febrile seizures plus, types 1 and 2; Severe X-linked myotubular myopathy; Short QT syndrome 3; Short stature with nonspecific skeletal abnormalities; Short stature, auditory canal atresia, mandibular hypoplasia, skeletal abnormalities; Short stature, onychodysplasia, facial dysmorphism, and hypotrichosis; Primordial dwarfism; Short-rib thoracic dysplasia 11 or 3 with or without polydactyly; Sialidosis type I and II; Silver spastic paraplegia syndrome; Slowed nerve conduction velocity, autosomal dominant; Smith-Lemli-Opitz syndrome; Snyder Robinson syndrome; Somatotroph adenoma; Prolactinoma; familial, Pituitary adenoma predisposition; Sotos syndrome 1 or 2; Spastic ataxia 5, autosomal recessive, Charlevoix-Saguenay type, 1,10, or 11, autosomal recessive; Amyotrophic lateral sclerosis type 5; Spastic paraplegia 15, 2, 3, 35, 39, 4, autosomal dominant, 55, autosomal recessive, and 5A; Bile acid synthesis defect, congenital, 3; Spermatogenic failure 11, 3, and 8; Spherocytosis types 4 and 5; Spheroid body myopathy; Spinal muscular atrophy, lower extremity predominant 2, autosomal dominant; Spinal muscular atrophy, type II; Spinocerebellar ataxia 14, 21, 35, 40, and 6; Spinocerebellar ataxia autosomal recessive 1 and 16; Splenic hypoplasia; Spondylocarpotarsal synostosis syndrome; Spondylocheirodysplasia, Ehlers-Danlos syndrome-like, with immune dysregulation, Aggreca type, with congenital joint dislocations, short limb-hand type, Sedaghatian type, with cone-rod dystrophy, and Kozlowski type; Parastremmatic dwarfism; Stargardt disease 1; Cone-rod dystrophy 3; Stickler syndrome type 1; Kniest dysplasia;

Stickler syndrome, types 1(nonsyndromic ocular) and 4; Sting-associated vasculopathy, infantile-onset; Stormorken syndrome; Sturge-Weber syndrome, Capillary malformations, congenital, 1; Succinyl-CoA acetoacetate transferase deficiency; Sucrase-isomaltase deficiency; Sudden infant death syndrome; Sulfite oxidase deficiency, isolated; Supravalvar aortic stenosis; Surfactant metabolism dysfunction, pulmonary, 2 and 3; Symphalangism, proximal, 1b; Syndactyly Cenani Lenz type; Syndactyly type 3; Syndromic X-linked mental retardation 16; Talipes equinovarus; Tangier disease; TARP syndrome; Tay-Sachs disease, B1 variant, Gm2-gangliosidosis (adult), Gm2-gangliosidosis (adult-onset); Temtamy syndrome; Tenorio Syndrome; Terminal osseous dysplasia; Testosterone 17-beta-dehydrogenase deficiency; Tetraamelia, autosomal recessive; Tetralogy of Fallot; Hypoplastic left heart syndrome 2; Truncus arteriosus; Malformation of the heart and great vessels; Ventricular septal defect 1; Thiel-Behnke corneal dystrophy; Thoracic aortic aneurysms and aortic dissections; Marfanoid habitus; Three M syndrome 2; Thrombocytopenia, platelet dysfunction, hemolysis, and imbalanced globin synthesis; Thrombocytopenia, X-linked; Thrombophilia, hereditary, due to protein C deficiency, autosomal dominant and recessive; Thyroid agenesis; Thyroid cancer, follicular; Thyroid hormone metabolism, abnormal; Thyroid hormone resistance, generalized, autosomal dominant; Thyrotoxic periodic paralysis and Thyrotoxic periodic paralysis 2; Thyrotropin-releasing hormone resistance, generalized; Timothy syndrome; TNF receptor-associated periodic fever syndrome (TRAPS); Tooth agenesis, selective, 3 and 4; Torsades de pointes; Townes-Brocks-branchiootorenal-like syndrome; Transient bullous dermolysis of the newborn; Treacher collins syndrome 1; Trichomegaly with mental retardation, dwarfism and pigmentary degeneration of retina; Trichorhinophalangeal dysplasia type I; Trichorhinophalangeal syndrome type 3; Trimethylaminuria; Tuberous sclerosis syndrome; Lymphangiomyomatosis; Tuberous sclerosis 1 and 2; Tyrosinase-negative oculocutaneous albinism; Tyrosinase-positive oculocutaneous albinism; Tyrosinemia type I; UDPglucose-4-epimerase deficiency; Ullrich congenital muscular dystrophy; Ulna and fibula absence of with severe limb deficiency; Upshaw-Schulman syndrome; Urocanate hydratase deficiency; Usher syndrome, types 1, 1B, 1D, 1G, 2A, 2C, and 2D; Retinitis pigmentosa 39; UV-sensitive syndrome; Van der Woude syndrome; Van Maldergem syndrome 2; Hennekam lymphangiectasia-lymphedema syndrome 2; Variegate porphyria; Ventriculomegaly with cystic kidney disease; Verheij syndrome; Very long chain acyl-CoA dehydrogenase deficiency; Vesicoureteral reflux 8; Visceral heterotaxy 5, autosomal; Visceral myopathy; Vitamin D-dependent rickets, types 1 and 2; Vitelliform dystrophy ; von Willebrand disease

type 2M and type 3; Waardenburg syndrome type 1, 4C, and 2E (with neurologic involvement); Klein-Waardenberg syndrome; Walker-Warburg congenital muscular dystrophy; Warburg micro syndrome 2 and 4; Warts, hypogammaglobulinemia, infections, and myelokathexis; Weaver syndrome; Weill-Marchesani syndrome 1 and 3; Weill-Marchesani-like syndrome; Weissenbacher-Zweymuller syndrome; Werdnig-Hoffmann disease; Charcot-Marie-Tooth disease; Werner syndrome; WFS1-Related Disorders; Wiedemann-Steiner syndrome; Wilson disease; Wolfram-like syndrome, autosomal dominant; Worth disease; Van Buchem disease type 2; Xeroderma pigmentosum, complementation group b, group D, group E, and group G; X-linked agammaglobulinemia; X-linked hereditary motor and sensory neuropathy; X-linked ichthyosis with steryl-sulfatase deficiency; X-linked periventricular heterotopia; Oto-palato-digital syndrome, type I; X-linked severe combined immunodeficiency; Zimmermann-Laband syndrome and Zimmermann-Laband syndrome 2; and Zonular pulverulent cataract 3.

[6] Pharmaceutical compositions

[0345] Other aspects of the present disclosure relate to pharmaceutical compositions comprising any of the various components of the ribozyme-directed programmable editing system described herein (e.g., including, but not limited to, the napDNAbps, engineered ribozymes, fusion proteins (e.g., comprising napDNAbps and/or target domain and/or engineered ribozymes), guide RNAs, and complexes comprising fusion proteins and guide RNAs, as well as accessory elements.

[0346] The term “pharmaceutical composition”, as used herein, refers to a composition formulated for pharmaceutical use. In some embodiments, the pharmaceutical composition further comprises a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical composition comprises additional agents (e.g. for specific delivery, increasing half-life, or other therapeutic compounds).

[0347] As used here, the term “pharmaceutically-acceptable carrier” means a pharmaceutically-acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (e.g., lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the compound from one site (e.g., the delivery site) of the body, to another site (e.g., organ, tissue or portion of the body). A pharmaceutically acceptable carrier is “acceptable” in the sense of being compatible with the other ingredients of the formulation and not injurious to the tissue of the subject (e.g., physiologically compatible, sterile, physiologic pH, etc.). Some examples of materials which can serve as pharmaceutically-acceptable carriers include:

(1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, methylcellulose, ethyl cellulose, microcrystalline cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) lubricating agents, such as magnesium stearate, sodium lauryl sulfate and talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol (PEG); (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; (22) bulking agents, such as polypeptides and amino acids (23) serum component, such as serum albumin, HDL and LDL; (22) C2-C12 alcohols, such as ethanol; and (23) other non-toxic compatible substances employed in pharmaceutical formulations. Wetting agents, coloring agents, release agents, coating agents, sweetening agents, flavoring agents, perfuming agents, preservative and antioxidants can also be present in the formulation. The terms such as “excipient”, “carrier”, “pharmaceutically acceptable carrier” or the like are used interchangeably herein.

[0348] In some embodiments, the pharmaceutical composition is formulated for delivery to a subject, e.g., for gene editing. Suitable routes of administering the pharmaceutical composition described herein include, without limitation: topical, subcutaneous, transdermal, intradermal, intralesional, intraarticular, intraperitoneal, intravesical, transmucosal, gingival, intradental, intracochlear, transtympanic, intraorgan, epidural, intrathecal, intramuscular, intravenous, intravascular, intraosseous, periocular, intratumoral, intracerebral, and intracerebroventricular administration.

[0349] In some embodiments, the pharmaceutical composition described herein is administered locally to a diseased site (e.g., tumor site). In some embodiments, the pharmaceutical composition described herein is administered to a subject by injection, by means of a catheter, by means of a suppository, or by means of an implant, the implant being of a porous, non-porous, or gelatinous material, including a membrane, such as a sialastic membrane, or a fiber.

[0350] In other embodiments, the pharmaceutical composition described herein is delivered in a controlled release system. In one embodiment, a pump may be used (see, e.g., Langer, 1990, Science 249:1527-1533; Sefton, 1989, CRC Crit. Ref. Biomed. Eng. 14:201; Buchwald

et al., 1980, *Surgery* 88:507; Saudek et al., 1989, *N. Engl. J. Med.* 321:574). In another embodiment, polymeric materials can be used. (See, e.g., *Medical Applications of Controlled Release* (Langer and Wise eds., CRC Press, Boca Raton, Fla., 1974); *Controlled Drug Bioavailability, Drug Product Design and Performance* (Smolen and Ball eds., Wiley, New York, 1984); Ranger and Peppas, 1983, *Macromol. Sci. Rev. Macromol. Chem.* 23:61. See also Levy et al., 1985, *Science* 228:190; During et al., 1989, *Ann. Neurol.* 25:351; Howard et al., 1989, *J. Neurosurg.* 71:105.) Other controlled release systems are discussed, for example, in Langer, *supra*.

[0351] In some embodiments, the pharmaceutical composition is formulated in accordance with routine procedures as a composition adapted for intravenous or subcutaneous administration to a subject, e.g., a human. In some embodiments, pharmaceutical composition for administration by injection are solutions in sterile isotonic aqueous buffer. Where necessary, the pharmaceutical can also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the pharmaceutical is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the pharmaceutical composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients can be mixed prior to administration.

[0352] A pharmaceutical composition for systemic administration may be a liquid, e.g., sterile saline, lactated Ringer's or Hank's solution. In addition, the pharmaceutical composition can be in solid forms and re-dissolved or suspended immediately prior to use. Lyophilized forms are also contemplated.

[0353] The pharmaceutical composition can be contained within a lipid particle or vesicle, such as a liposome or microcrystal, which is also suitable for parenteral administration. The particles can be of any suitable structure, such as unilamellar or plurilamellar, so long as compositions are contained therein. Compounds can be entrapped in "stabilized plasmid-lipid particles" (SPLP) containing the fusogenic lipid dioleoylphosphatidylethanolamine (DOPE), low levels (5-10 mol%) of cationic lipid, and stabilized by a polyethyleneglycol (PEG) coating (Zhang Y. P. et al., *Gene Ther.* 1999, 6:1438-47). Positively charged lipids such as N-[1-(2,3-dioleoyloxy)propyl]-N,N,N-trimethyl-amoniummethylsulfate, or "DOTAP," are particularly preferred for such particles and vesicles. The preparation of such

lipid particles is well known. See, e.g., U.S. Patent Nos. 4,880,635; 4,906,477; 4,911,928; 4,917,951; 4,920,016; and 4,921,757; each of which is incorporated herein by reference.

[0354] The pharmaceutical composition described herein may be administered or packaged as a unit dose, for example. The term “unit dose” when used in reference to a pharmaceutical composition of the present disclosure refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent; i.e., carrier, or vehicle.

[0355] Further, the pharmaceutical composition can be provided as a pharmaceutical kit comprising (a) a container containing a compound of the invention in lyophilized form and (b) a second container containing a pharmaceutically acceptable diluent (e.g., sterile water) for injection. The pharmaceutically acceptable diluent can be used for reconstitution or dilution of the lyophilized compound of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

[0356] In another aspect, an article of manufacture containing materials useful for the treatment of the diseases described above is included. In some embodiments, the article of manufacture comprises a container and a label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers may be formed from a variety of materials such as glass or plastic. In some embodiments, the container holds a composition that is effective for treating a disease described herein and may have a sterile access port. For example, the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle. The active agent in the composition is a compound of the invention. In some embodiments, the label on or associated with the container indicates that the composition is used for treating the disease of choice. The article of manufacture may further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution, or dextrose solution. It may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

[7] Delivery methods

[0357] In some aspects, the invention provides methods comprising delivering one or more polynucleotides, such as or one or more vectors as described herein encoding one or more

components of the ribozyme-directed programmable editing system described herein, one or more transcripts thereof, and/or one or proteins transcribed therefrom, to a host cell. In some aspects, the invention further provides cells produced by such methods, and organisms (such as animals, plants, or fungi) comprising or produced from such cells. In some embodiments, a base editor as described herein in combination with (and optionally complexed with) a guide sequence is delivered to a cell. Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids in mammalian cells or target tissues. Such methods can be used to administer nucleic acids encoding components of a base editor to cells in culture, or in a host organism. Non-viral vector delivery systems include DNA plasmids, RNA (e.g. a transcript of a vector described herein), naked nucleic acid, and nucleic acid complexed with a delivery vehicle, such as a liposome. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see Anderson, *Science* 256:808-813 (1992); Nabel & Felgner, *TIBTECH* 11:211-217 (1993); Mitani & Caskey, *TIBTECH* 11:162-166 (1993); Dillon, *TIBTECH* 11:167-175 (1993); Miller, *Nature* 357:455-460 (1992); Van Brunt, *Biotechnology* 6(10):1149-1154 (1988); Vigne, *Restorative Neurology and Neuroscience* 8:35-36 (1995); Kremer & Perricaudet, *British Medical Bulletin* 51(1):31-44 (1995); Haddada et al., in *Current Topics in Microbiology and Immunology* Doerfler and Bihm (eds) (1995); and Yu et al., *Gene Therapy* 1:13-26 (1994).

[0358] Methods of non-viral delivery of nucleic acids include lipofection, nucleofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Feigner, WO 91/17424; WO 91/16024. Delivery can be to cells (e.g. in vitro or ex vivo administration) or target tissues (e.g. in vivo administration).

[0359] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, *Science* 270:404-410 (1995); Blaese et al., *Cancer Gene Ther.* 2:291-297 (1995); Behr et al., *Bioconjugate Chem.* 5:382-389 (1994); Remy et al., *Bioconjugate Chem.* 5:647-654 (1994); Gao et al., *Gene Therapy* 2:710-722 (1995); Ahmad et al., *Cancer Res.* 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

[0360] The use of RNA or DNA viral based systems for the delivery of nucleic acids take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (in vivo) or they can be used to treat cells in vitro, and the modified cells may optionally be administered to patients (ex vivo). Conventional viral based systems could include retroviral, lentivirus, adenoviral, adeno-associated and herpes simplex virus vectors for gene transfer. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues.

[0361] The tropism of a viruses can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system would therefore depend on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., J. Virol. 66:2731-2739 (1992); Johann et al., J. Virol. 66:1635-1640 (1992); Sommnerfelt et al., Virol. 176:58-59 (1990); Wilson et al., J. Virol. 63:2374-2378 (1989); Miller et al., J. Virol. 65:2220-2224 (1991); PCT/US94/05700). In applications where transient expression is preferred, adenoviral based systems may be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and levels of expression have been obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors may also be used to transduce cells with target nucleic acids, e.g., in the in vitro production of nucleic acids and peptides, and for in vivo and ex vivo gene therapy procedures (see, e.g., West et al., Virology 160:38-47 (1987); U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, Human Gene Therapy 5:793-801 (1994); Muzyczka, J. Clin. Invest. 94:1351 (1994). Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin et al., Mol. Cell. Biol. 5:3251-3260 (1985); Tratschin, et al., Mol. Cell. Biol. 4:2072-2081 (1984);

Hermonat & Muzyczka, PNAS 81:6466-6470 (1984); and Samulski et al., J. Virol. 63:03822-3828 (1989).

[0362] Packaging cells are typically used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and ψ 2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by producing a cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host, other viral sequences being replaced by an expression cassette for the polynucleotide(s) to be expressed. The missing viral functions are typically supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess ITR sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences. The cell line may also be infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV. Additional methods for the delivery of nucleic acids to cells are known to those skilled in the art. See, for example, US20030087817, incorporated herein by reference.

[0363] Sullivan, et al., *supra*, describes the general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. The RNA/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Alternative routes of delivery include, but are not limited to, intramuscular injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Sullivan, et al., *supra* and Draper, et al., *supra* which have been incorporated by reference herein.

[0364]

[0365] Another means of accumulating high concentrations of a ribozyme(s) within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of

the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pot I), RNA polymerase II (pot II), or RNA polymerase III (pot III). Transcripts from pot I or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, etc.) present nearby. Prokaryotic RNA polymerase promoters are also used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells (Elroy-Stein and Moss, 1990 Proc. Natl. Acad. Sci. U S A, 87, 6743-7; Gao, and Huang, 1993 Nucleic Acids Res., 21, 2867-72; Lieber et al., 1993 Methods Enzymol., 217, 47-66; Zhou et al., 1990 Mol. Cell. Biol., 10, 4529-37). Several investigators have demonstrated that ribozymes expressed from such promoters can function in mammalian cells (e.g. Kashani-Sabet, et al., 1992 Antisense Res. Dev. 2, 3-15; Ojwang et al., 1992 Proc. Natl. Acad. Sci. U S A 89, 10802-6; Chen et al., 1992 Nucleic Acids Res., 20, 4581-9; Yu et al., 1993 Proc. Natl. Acad. Sci. U S A 90, 6340-4; L'Huillier, et al., 1992 EMBO J. 11, 4411-8; Lisiewicz et al., 1993 Proc. Natl. Acad. Sci. U. S. A. 90, 8000-4). The above ribozyme transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral vectors).

[8] Kits, cells, vectors, and delivery

Kits

[0366] The compositions of the present disclosure may be assembled into kits. In some embodiments, the kit comprises nucleic acid vectors for the expression of the genome editors described herein. In other embodiments, the kit further comprises appropriate guide nucleotide sequences (*e.g.*, guide RNAs) or nucleic acid vectors for the expression of such guide nucleotide sequences, to target the genome editors to the desired target sequence.

[0367] The kit described herein may include one or more containers housing components for performing the methods described herein and optionally instructions for use. Any of the kit described herein may further comprise components needed for performing the assay methods. Each component of the kits, where applicable, may be provided in liquid form (*e.g.*, in solution) or in solid form, (*e.g.*, a dry powder). In certain cases, some of the components may be reconstitutable or otherwise processible (*e.g.*, to an active form), for example, by the addition of a suitable solvent or other species (for example, water), which may or may not be provided with the kit.

[0368] In some embodiments, the kits may optionally include instructions and/or promotion for use of the components provided. As used herein, “instructions” can define a component of

instruction and/or promotion, and typically involve written instructions on or associated with packaging of the disclosure. Instructions also can include any oral or electronic instructions provided in any manner such that a user will clearly recognize that the instructions are to be associated with the kit, for example, audiovisual (e.g., videotape, DVD, directions to access online resources, etc.), Internet, and/or web-based communications, etc. The written instructions may be in a form prescribed by a governmental agency regulating the manufacture, use, or sale of pharmaceuticals or biological products, which can also reflect approval by the agency of manufacture, use or sale for animal administration. As used herein, “promoted” includes all methods of doing business including methods of education, hospital and other clinical instruction, scientific inquiry, drug discovery or development, academic research, pharmaceutical industry activity including pharmaceutical sales, and any advertising or other promotional activity including written, oral and electronic communication of any form, associated with the disclosure. Additionally, the kits may include other components depending on the specific application, as described herein.

[0369] The kits may contain any one or more of the components described herein in one or more containers. The components may be prepared sterilely, packaged in a syringe and shipped refrigerated. Alternatively it may be housed in a vial or other container for storage. A second container may have other components prepared sterilely. Alternatively the kits may include the active agents premixed and shipped in a vial, tube, or other container.

[0370] The kits may have a variety of forms, such as a blister pouch, a shrink wrapped pouch, a vacuum sealable pouch, a sealable thermoformed tray, or a similar pouch or tray form, with the accessories loosely packed within the pouch, one or more tubes, containers, a box or a bag. The kits may be sterilized after the accessories are added, thereby allowing the individual accessories in the container to be otherwise unwrapped. The kits can be sterilized using any appropriate sterilization techniques, such as radiation sterilization, heat sterilization, or other sterilization methods known in the art. The kits may also include other components, depending on the specific application, for example, containers, cell media, salts, buffers, reagents, syringes, needles, a fabric, such as gauze, for applying or removing a disinfecting agent, disposable gloves, a support for the agents prior to administration, etc. Some aspects of this disclosure provide kits comprising a nucleic acid construct comprising a nucleotide sequence encoding the various components of the genome editing system described herein (e.g., including, but not limited to, the napDNAbps, reverse transcriptases, polymerases, fusion proteins (e.g., comprising napDNAbps and reverse transcriptases (or more broadly, polymerases), extended guide RNAs, and complexes comprising fusion

proteins and extended guide RNAs, as well as accessory elements, such as second strand nicking components (e.g., second strand nicking gRNA) and 5' endogenous DNA flap removal endonucleases for helping to drive the genome editing process towards the edited product formation). In some embodiments, the nucleotide sequence(s) comprises a heterologous promoter (or more than a single promoter) that drives expression of the genome editing system components.

[0371] Other aspects of this disclosure provide kits comprising one or more nucleic acid constructs encoding the various components of the genome editing system described herein, e.g., the comprising a nucleotide sequence encoding the components of the genome editing system capable of modifying a target DNA sequence. In some embodiments, the nucleotide sequence comprises a heterologous promoter that drives expression of the genome editing system components.

[0372] Some aspects of this disclosure provides kits comprising a nucleic acid construct, comprising (a) a nucleotide sequence encoding a napDNAbp (e.g., a Cas9 domain) fused to a reverse transcriptase and (b) a heterologous promoter that drives expression of the sequence of (a).

Cells

[0373] Cells that may contain any of the compositions described herein include prokaryotic cells and eukaryotic cells. The methods described herein are used to deliver a napDNAbp or a genome editing system into a eukaryotic cell (e.g., a mammalian cell, such as a human cell). In some embodiments, the cell is in vitro (e.g., cultured cell. In some embodiments, the cell is in vivo (e.g., in a subject such as a human subject). In some embodiments, the cell is ex vivo (e.g., isolated from a subject and may be administered back to the same or a different subject).

[0374] Mammalian cells of the present disclosure include human cells, primate cells (e.g., vero cells), rat cells (e.g., GH3 cells, OC23 cells) or mouse cells (e.g., MC3T3 cells). There are a variety of human cell lines, including, without limitation, human embryonic kidney (HEK) cells, HeLa cells, cancer cells from the National Cancer Institute's 60 cancer cell lines (NCI60), DU145 (prostate cancer) cells, Lncap (prostate cancer) cells, MCF-7 (breast cancer) cells, MDA-MB-438 (breast cancer) cells, PC3 (prostate cancer) cells, T47D (breast cancer) cells, THP-1 (acute myeloid leukemia) cells, U87 (glioblastoma) cells, SHSY5Y human neuroblastoma cells (cloned from a myeloma) and Saos-2 (bone cancer) cells. In some embodiments, rAAV vectors are delivered into human embryonic kidney (HEK) cells (e.g., HEK 293 or HEK 293T cells). In some embodiments, rAAV vectors are delivered into stem

cells (e.g., human stem cells) such as, for example, pluripotent stem cells (e.g., human pluripotent stem cells including human induced pluripotent stem cells (hiPSCs)). A stem cell refers to a cell with the ability to divide for indefinite periods in culture and to give rise to specialized cells. A pluripotent stem cell refers to a type of stem cell that is capable of differentiating into all tissues of an organism, but not alone capable of sustaining full organismal development. A human induced pluripotent stem cell refers to a somatic (e.g., mature or adult) cell that has been reprogrammed to an embryonic stem cell-like state by being forced to express genes and factors important for maintaining the defining properties of embryonic stem cells (see, e.g., Takahashi and Yamanaka, *Cell* 126 (4): 663–76, 2006, incorporated by reference herein). Human induced pluripotent stem cell cells express stem cell markers and are capable of generating cells characteristic of all three germ layers (ectoderm, endoderm, mesoderm).

[0375] Additional non-limiting examples of cell lines that may be used in accordance with the present disclosure include 293-T, 293-T, 3T3, 4T1, 721, 9L, A-549, A172, A20, A253, A2780, A2780ADR, A2780cis, A431, ALC, B16, B35, BCP-1, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C2C12, C3H-10T1/2, C6, C6/36, Cal-27, CGR8, CHO, CML T1, CMT, COR-L23, COR-L23/5010, COR-L23/CPR, COR-L23/R23, COS-7, COV-434, CT26, D17, DH82, DU145, DuCaP, E14Tg2a, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, Hepa1c1c7, High Five cells, HL-60, HMEC, HT-29, HUVEC, J558L cells, Jurkat, JY cells, K562 cells, KCL22, KG1, Ku812, KYO1, LNCap, Ma-Mel 1, 2, 3....48, MC-38, MCF-10A, MCF-7, MDA-MB-231, MDA-MB-435, MDA-MB-468, MDCK II, MG63, MONO-MAC 6, MOR/0.2R, MRC5, MTD-1A, MyEnd, NALM-1, NCI-H69/CPR, NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NW-145, OPCN/OPCT Peer, PNT-1A/PNT 2, PTK2, Raji, RBL cells, RenCa, RIN-5F, RMA/RMAS, S2, Saos-2 cells, Sf21, Sf9, SiHa, SKBR3, SKOV-3, T-47D, T2, T84, THP1, U373, U87, U937, VCaP, WM39, WT-49, X63, YAC-1 and YAR cells.

[0376] Some aspects of this disclosure provide cells comprising any of the constructs disclosed herein. In some embodiments, a host cell is transiently or non-transiently transfected with one or more vectors described herein. In some embodiments, a cell is transfected as it naturally occurs in a subject. In some embodiments, a cell that is transfected is taken from a subject. In some embodiments, the cell is derived from cells taken from a subject, such as a cell line. A wide variety of cell lines for tissue culture are known in the art. Examples of cell lines include, but are not limited to, C8161, CCRF-CEM, MOLT, mIMCD-3, NHDF, HeLa-S3, Huh1, Huh4, Huh7, HUVEC, HASMC, HEKn, HEKa, MiaPaCell,

Panc1, PC-3, TF1, CTLL-2, C1R, Rat6, CV1, RPTE, A10, T24, J82, A375, ARH-77, Calu1, SW480, SW620, SKOV3, SK-UT, CaCo2, P388D1, SEM-K2, WEHI-231, HB56, TIB55, Jurkat, J45.01, LRMB, Bcl-1, BC-3, IC21, DLD2, Raw264.7, NRK, NRK-52E, MRC5, MEF, Hep G2, HeLa B, HeLa T4, COS, COS-1, COS-6, COS-M6A, BS-C-1 monkey kidney epithelial, BALB/3T3 mouse embryo fibroblast, 3T3 Swiss, 3T3-L1, 132-d5 human fetal fibroblasts; 10.1 mouse fibroblasts, 293-T, 3T3, 721, 9L, A2780, A2780ADR, A2780cis, A172, A20, A253, A431, A-549, ALC, B16, B35, BCP-1 cells, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C3H-10T1/2, C6/36, Cal-27, CHO, CHO-7, CHO-IR, CHO-K1, CHO-K2, CHO-T, CHO Dhfr $-/-$, COR-L23, COR-L23/CPR, COR-L23/5010, COR-L23/R23, COS-7, COV-434, CML T1, CMT, CT26, D17, DH82, DU145, DuCaP, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, HEK-293, HeLa, Hepa1c1c7, HL-60, HMEC, HT-29, Jurkat, JY cells, K562 cells, Ku812, KCL22, KG1, KYO1, LNCap, Ma-Mel 1-48, MC-38, MCF-7, MCF-10A, MDA-MB-231, MDA-MB-468, MDA-MB-435, MDCK II, MDCK 11, MOR/0.2R, MONO-MAC 6, MTD-1A, MyEnd, NCI-H69/CPR, NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NALM-1, NW-145, OPCN/OPCT cell lines, Peer, PNT-1A/PNT 2, RenCa, RIN-5F, RMA/RMAS, Saos-2 cells, Sf-9, SkBr3, T2, T-47D, T84, THP1 cell line, U373, U87, U937, VCaP, Vero cells, WM39, WT-49, X63, YAC-1, YAR, and transgenic varieties thereof.

[0377] Cell lines are available from a variety of sources known to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassus, Va.)). In some embodiments, a cell transfected with one or more vectors described herein is used to establish a new cell line comprising one or more vector-derived sequences. In some embodiments, a cell transiently transfected with the components of a CRISPR system as described herein (such as by transient transfection of one or more vectors, or transfection with RNA), and modified through the activity of a CRISPR complex, is used to establish a new cell line comprising cells containing the modification but lacking any other exogenous sequence. In some embodiments, cells transiently or non-transiently transfected with one or more vectors described herein, or cell lines derived from such cells are used in assessing one or more test compounds.

Vectors

[0378] Some aspects of the present disclosure relate to using recombinant virus vectors (e.g., adeno-associated virus vectors, adenovirus vectors, or herpes simplex virus vectors) for the delivery of the genome editor systems or components thereof described herein, e.g., a napDNAbp or a split napDNAbp, into a cell. In the case of delivering one or more protein

components of the genome editing system using a split-molecule approach, the N-terminal portion of a genome editor protein and the C-terminal portion of a genome editor protein are delivered by separate recombinant virus vectors (e.g., adeno-associated virus vectors, adenovirus vectors, or herpes simplex virus vectors) into the same cell, since the full-length napDNAbps (e.g., Cas9) often exceed the packaging limit of various virus vectors, e.g., rAAV (~4.9 kb).

[0379] Thus, in one embodiment, the disclosure contemplates vectors capable of delivering split genome editor proteins, or split components thereof. In some embodiments, a composition for delivering the split Cas9 protein or split genome editor into a cell (e.g., a mammalian cell, a human cell) is provided. In some embodiments, the composition of the present disclosure comprises: (i) a first recombinant adeno-associated virus (rAAV) particle comprising a first nucleotide sequence encoding a N-terminal portion of a Cas9 protein or prime editor fused at its C-terminus to an intein-N; and (ii) a second recombinant adeno-associated virus (rAAV) particle comprising a second nucleotide sequence encoding an intein-C fused to the N-terminus of a C-terminal portion of the Cas9 protein or genome editor. The rAAV particles of the present disclosure comprise a rAAV vector (i.e., a recombinant genome of the rAAV) encapsidated in the viral capsid proteins.

[0380] In some embodiments, the rAAV vector comprises: (1) a heterologous nucleic acid region comprising the first or second nucleotide sequence encoding the N-terminal portion or C-terminal portion of a split Cas9 protein or a split genome editor in any form as described herein, (2) one or more nucleotide sequences comprising a sequence that facilitates expression of the heterologous nucleic acid region (e.g., a promoter), and (3) one or more nucleic acid regions comprising a sequence that facilitate integration of the heterologous nucleic acid region (optionally with the one or more nucleic acid regions comprising a sequence that facilitates expression) into the genome of a cell. In some embodiments, viral sequences that facilitate integration comprise Inverted Terminal Repeat (ITR) sequences. In some embodiments, the first or second nucleotide sequence encoding the N-terminal portion or C-terminal portion of a split Cas9 protein or a split genome editor is flanked on each side by an ITR sequence. In some embodiments, the nucleic acid vector further comprises a region encoding an AAV Rep protein as described herein, either contained within the region flanked by ITRs or outside the region. The ITR sequences can be derived from any AAV serotype (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10) or can be derived from more than one serotype. In some embodiments, the ITR sequences are derived from AAV2 or AAV6.

[0381] Thus, in some embodiments, the rAAV particles disclosed herein comprise at least one rAAV2 particle, rAAV6 particle, rAAV8 particle, rPHP.B particle, rPHP.eB particle, or rAAV9 particle, or a variant thereof. In particular embodiments, the disclosed rAAV particles are rPHP.B particles, rPHP.eB particles, rAAV9 particles.

[0382] ITR sequences and plasmids containing ITR sequences are known in the art and commercially available (see, e.g., products and services available from Vector Biolabs, Philadelphia, PA; Cellbiolabs, San Diego, CA; Agilent Technologies, Santa Clara, Ca; and Addgene, Cambridge, MA; and Gene delivery to skeletal muscle results in sustained expression and systemic delivery of a therapeutic protein. Kessler PD, Podsakoff GM, Chen X, McQuiston SA, Colosi PC, Matelis LA, Kurtzman GJ, Byrne BJ. Proc Natl Acad Sci USA. 1996 Nov 26;93(24):14082-7; and Curtis A. Machida. Methods in Molecular Medicine™. Viral Vectors for Gene Therapy Methods and Protocols. 10.1385/1-59259-304-6:201 © Humana Press Inc. 2003. Chapter 10. Targeted Integration by Adeno-Associated Virus. Matthew D. Weitzman, Samuel M. Young Jr., Toni Cathomen and Richard Jude Samulski; U.S. Pat. Nos. 5,139,941 and 5,962,313, all of which are incorporated herein by reference).

[0383] In some embodiments, the rAAV vector of the present disclosure comprises one or more regulatory elements to control the expression of the heterologous nucleic acid region (e.g., promoters, transcriptional terminators, and/or other regulatory elements). In some embodiments, the first and/or second nucleotide sequence is operably linked to one or more (e.g., 1, 2, 3, 4, 5, or more) transcriptional terminators. Non-limiting examples of transcriptional terminators that may be used in accordance with the present disclosure include transcription terminators of the bovine growth hormone gene (bGH), human growth hormone gene (hGH), SV40, CW3, ϕ , or combinations thereof. The efficiencies of several transcriptional terminators have been tested to determine their respective effects in the expression level of the split Cas9 protein or the split genome editor. In some embodiments, the transcriptional terminator used in the present disclosure is a bGH transcriptional terminator. In some embodiments, the rAAV vector further comprises a Woodchuck Hepatitis Virus Posttranscriptional Regulatory Element (WPRE). In certain embodiments, the WPRE is a truncated WPRE sequence, such as “W3.” In some embodiments, the WPRE is inserted 5′ of the transcriptional terminator. Such sequences, when transcribed, create a tertiary structure which enhances expression, in particular, from viral vectors.

[0384] In some embodiments, the vectors used herein may encode the genome editors, or any of the components thereof (e.g., napDNAbp, linkers, or other functional domains). In

addition, the vectors used herein may encode the guide RNAs. The vectors may be capable of driving expression of one or more coding sequences in a cell. In some embodiments, the cell may be a prokaryotic cell, such as, e.g., a bacterial cell. In some embodiments, the cell may be a eukaryotic cell, such as, e.g., a yeast, plant, insect, or mammalian cell. In some embodiments, the eukaryotic cell may be a mammalian cell. In some embodiments, the eukaryotic cell may be a rodent cell. In some embodiments, the eukaryotic cell may be a human cell. Suitable promoters to drive expression in different types of cells are known in the art. In some embodiments, the promoter may be wild-type. In other embodiments, the promoter may be modified for more efficient or efficacious expression. In yet other embodiments, the promoter may be truncated yet retain its function. For example, the promoter may have a normal size or a reduced size that is suitable for proper packaging of the vector into a virus.

[0385] In some embodiments, the promoters that may be used in the genome editor vectors may be constitutive, inducible, or tissue-specific. In some embodiments, the promoters may be a constitutive promoters. Non-limiting exemplary constitutive promoters include cytomegalovirus immediate early promoter (CMV), simian virus (SV40) promoter, adenovirus major late (MLP) promoter, Rous sarcoma virus (RSV) promoter, mouse mammary tumor virus (MMTV) promoter, phosphoglycerate kinase (PGK) promoter, elongation factor- α (EF α) promoter, ubiquitin promoters, actin promoters, tubulin promoters, immunoglobulin promoters, a functional fragment thereof, or a combination of any of the foregoing. In some embodiments, the promoter may be a CMV promoter. In some embodiments, the promoter may be a truncated CMV promoter. In other embodiments, the promoter may be an EF α promoter. In some embodiments, the promoter may be an inducible promoter. Non-limiting exemplary inducible promoters include those inducible by heat shock, light, chemicals, peptides, metals, steroids, antibiotics, or alcohol. In some embodiments, the inducible promoter may be one that has a low basal (non-induced) expression level, such as, e.g., the Tet-On[®] promoter (Clontech). In some embodiments, the promoter may be a tissue-specific promoter. In some embodiments, the tissue-specific promoter is exclusively or predominantly expressed in liver tissue. Non-limiting exemplary tissue-specific promoters include B29 promoter, CD14 promoter, CD43 promoter, CD45 promoter, CD68 promoter, desmin promoter, elastase-1 promoter, endoglin promoter, fibronectin promoter, Flt-1 promoter, GFAP promoter, GPIIb promoter, ICAM-2 promoter, INF- β promoter, Mb promoter, Nphs1 promoter, OG-2 promoter, SP-B promoter, SYN1 promoter, and WASP promoter.

[0386] In some embodiments, the genome editor vectors (e.g., including any vectors encoding any genome editor fusion protein and/or the guide RNAs) may comprise inducible promoters to start expression only after it is delivered to a target cell. Non-limiting exemplary inducible promoters include those inducible by heat shock, light, chemicals, peptides, metals, steroids, antibiotics, or alcohol. In some embodiments, the inducible promoter may be one that has a low basal (non-induced) expression level, such as, e.g., the Tet-On® promoter (Clontech).

[0387] In additional embodiments, the genome editor vectors (e.g., including any vectors encoding the genome editor fusion proteins and/or the guide RNAs) may comprise tissue-specific promoters to start expression only after it is delivered into a specific tissue. Non-limiting exemplary tissue-specific promoters include B29 promoter, CD14 promoter, CD43 promoter, CD45 promoter, CD68 promoter, desmin promoter, elastase- 1 promoter, endoglin promoter, fibronectin promoter, Flt-1 promoter, GFAP promoter, GPIIb promoter, ICAM- 2 promoter, INF- β promoter, Mb promoter, Nphs1 promoter, OG-2 promoter, SP-B promoter, SYN1 promoter, and WASP promoter.

[0388] In some embodiments, the nucleotide sequence encoding the guide RNAs may be operably linked to at least one transcriptional or translational control sequence. In some embodiments, the nucleotide sequence encoding the guide RNAs may be operably linked to at least one promoter. In some embodiments, the promoter may be recognized by RNA polymerase III (Pol III). Non-limiting examples of Pol III promoters include U6, HI and tRNA promoters. In some embodiments, the nucleotide sequence encoding the guide RNA may be operably linked to a mouse or human U6 promoter. In other embodiments, the nucleotide sequence encoding the guide RNA may be operably linked to a mouse or human HI promoter. In some embodiments, the nucleotide sequence encoding the guide RNA may be operably linked to a mouse or human tRNA promoter. In embodiments with more than one guide RNA, the promoters used to drive expression may be the same or different. In some embodiments, the nucleotide encoding the crRNA of the guide RNA and the nucleotide encoding the tracr RNA of the guide RNA may be provided on the same vector. In some embodiments, the nucleotide encoding the crRNA and the nucleotide encoding the tracr RNA may be driven by the same promoter. In some embodiments, the crRNA and tracr RNA may be transcribed into a single transcript. For example, the crRNA and tracr RNA may be processed from the single transcript to form a double-molecule guide RNA. Alternatively, the crRNA and tracr RNA may be transcribed into a single-molecule guide RNA.

[0389] In some embodiments, the nucleotide sequence encoding the guide RNA may be located on the same vector comprising the nucleotide sequence encoding the PE fusion protein. In some embodiments, expression of the guide RNA and of the PE fusion protein may be driven by their corresponding promoters. In some embodiments, expression of the guide RNA may be driven by the same promoter that drives expression of a genome editor fusion protein. In some embodiments, the guide RNA and a genome editor fusion protein transcript may be contained within a single transcript. For example, the guide RNA may be within an untranslated region (UTR) of the Cas9 protein transcript. In some embodiments, the guide RNA may be within the 5' UTR of a genome editor fusion protein transcript. In other embodiments, the guide RNA may be within the 3' UTR of a genome editor fusion protein transcript. In some embodiments, the intracellular half-life of a genome editor fusion protein transcript may be reduced by containing the guide RNA within its 3' UTR and thereby shortening the length of its 3' UTR. In additional embodiments, the guide RNA may be within an intron of a genome editor fusion protein transcript. In some embodiments, suitable splice sites may be added at the intron within which the guide RNA is located such that the guide RNA is properly spliced out of the transcript. In some embodiments, expression of the Cas9 protein and the guide RNA in close proximity on the same vector may facilitate more efficient formation of the CRISPR complex.

[0390] The vectors used to deliver and express the genome editing system may comprise one vector, or two vectors, or three vectors, or four vectors, or five vector, or more. In some embodiments, the vector system may comprise one single vector, which encodes both the napDNAbp domain, the guide RNA, and the ribozyme component. In other embodiments, the vector system may comprise two vectors, wherein one vector encodes the napDNAbp component and the other encodes RNA components (i.e., the guide RNA and the ribozyme component). In additional embodiments, the vector system may comprise three vectors, wherein each vector encodes a component of the genome editing system, i.e., one vector to express the napDNAbp component, one vector to express the guide RNA component, and another vector to express the ribozyme component.

[0391] In some embodiments, the composition comprising the rAAV particle (in any form contemplated herein) further comprises a pharmaceutically acceptable carrier. In some embodiments, the composition is formulated in appropriate pharmaceutical vehicles for administration to human or animal subjects.

[0392] Some examples of materials which can serve as pharmaceutically-acceptable carriers include: (1) sugars, such as lactose, glucose and sucrose; (2) starches, such as corn starch and

potato starch; (3) cellulose, and its derivatives, such as sodium carboxymethyl cellulose, methylcellulose, ethyl cellulose, microcrystalline cellulose and cellulose acetate; (4) powdered tragacanth; (5) malt; (6) gelatin; (7) lubricating agents, such as magnesium stearate, sodium lauryl sulfate and talc; (8) excipients, such as cocoa butter and suppository waxes; (9) oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; (10) glycols, such as propylene glycol; (11) polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol (PEG); (12) esters, such as ethyl oleate and ethyl laurate; (13) agar; (14) buffering agents, such as magnesium hydroxide and aluminum hydroxide; (15) alginic acid; (16) pyrogen-free water; (17) isotonic saline; (18) Ringer's solution; (19) ethyl alcohol; (20) pH buffered solutions; (21) polyesters, polycarbonates and/or polyanhydrides; (22) bulking agents, such as polypeptides and amino acids (23) serum component, such as serum albumin, HDL and LDL; (22) C2-C12 alcohols, such as ethanol; and (23) other non-toxic compatible substances employed in pharmaceutical formulations. Wetting agents, coloring agents, release agents, coating agents, sweetening agents, flavoring agents, perfuming agents, preservative and antioxidants can also be present in the formulation. The terms such as "excipient", "carrier", "pharmaceutically acceptable carrier" or the like are used interchangeably herein.

Delivery methods

[0393] In some aspects, the invention provides methods comprising delivering one or more polynucleotides, such as or one or more vectors as described herein, one or more transcripts thereof, and/or one or proteins transcribed therefrom, to a host cell. In some aspects, the invention further provides cells produced by such methods, and organisms (such as animals, plants, or fungi) comprising or produced from such cells. In some embodiments, a genome editor as described herein in combination with (and optionally complexed with) a guide sequence is delivered to a cell.

[0394] Exemplary delivery strategies for delivering and expressing a genome editing system within a cell are described herein elsewhere, which include vector-based strategies, ribonucleoprotein complex delivery, and delivery of a genome editing system by mRNA methods.

[0395] In some embodiments, the method of delivery provided comprises nucleofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA.

[0396] Exemplary methods of delivery of nucleic acids include lipofection, nucleofection, electroporation, stable genome integration (e.g., piggybac), microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™, Lipofectin™ and SF Cell Line 4D-Nucleofector X Kit™ (Lonza)). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Feigner, WO 91/17424; WO 91/16024. Delivery may be to cells (e.g. in vitro or ex vivo administration) or target tissues (e.g. in vivo administration). Delivery may be achieved through the use of RNP complexes.

[0397] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science 270:404-410 (1995); Blaese et al., Cancer Gene Ther. 2:291-297 (1995); Behr et al., Bioconjugate Chem. 5:382-389 (1994); Remy et al., Bioconjugate Chem. 5:647-654 (1994); Gao et al., Gene Therapy 2:710-722 (1995); Ahmad et al., Cancer Res. 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

[0398] In other embodiments, the method of delivery and vector provided herein is an RNP complex. RNP delivery of fusion proteins markedly increases the DNA specificity of genome editing. RNP delivery of fusion proteins leads to decoupling of on- and off-target DNA editing. RNP delivery ablates off-target editing at non-repetitive sites while maintaining on-target editing comparable to plasmid delivery, and greatly reduces off-target DNA editing even at the highly repetitive VEGFA site 2. See Rees, H.A. et al., Improving the DNA specificity and applicability of base editing through protein engineering and protein delivery, Nat. Commun. 8, 15790 (2017), U.S. Patent No. 9,526,784, issued December 27, 2016, and U.S. Patent No. 9,737,604, issued August 22, 2017, each of which is incorporated by reference herein. Since the herein disclosed genome editing system involves not only a guide RNA, but also a ribozyme, delivery of the genome editing systems described herein may have improved efficiency by way of RNP delivery since the negative charge of both the guide RNA and the ribozyme combined with the napDNAbp component may facilitate entry into the cell better than RNP comprising the napDNAbp/guide RNA complex alone. The additional negative charge of the ribozyme component facilitates entry of the RNP complex.

[0399] Additional methods for the delivery of nucleic acids to cells are known to those skilled in the art. See, for example, US 2003/0087817, incorporated herein by reference.

[0400] Other aspects of the present disclosure provide methods of delivering the prime editor constructs into a cell to form a complete and functional prime editor within a cell. For example, in some embodiments, a cell is contacted with a composition described herein (e.g., compositions comprising nucleotide sequences encoding the split Cas9 or the split genome editor components or AAV particles containing nucleic acid vectors comprising such nucleotide sequences). In some embodiments, the contacting results in the delivery of such nucleotide sequences into a cell, wherein the N-terminal portion of the Cas9 protein or the genome editor and the C-terminal portion of the Cas9 protein or the genome editor are expressed in the cell and are joined to form a complete Cas9 protein or a complete genome editor.

[0401] It should be appreciated that any rAAV particle, nucleic acid molecule or composition provided herein may be introduced into the cell in any suitable way, either stably or transiently. In some embodiments, the disclosed proteins may be transfected into the cell. In some embodiments, the cell may be transduced or transfected with a nucleic acid molecule. For example, a cell may be transduced (e.g., with a virus encoding a split protein), or transfected (e.g., with a plasmid encoding a split protein) with a nucleic acid molecule that encodes a split protein, or an rAAV particle containing a viral genome encoding one or more nucleic acid molecules. Such transduction may be a stable or transient transduction. In some embodiments, cells expressing a split protein or containing a split protein may be transduced or transfected with one or more guide RNA sequences, for example in delivery of a split Cas9 (e.g., nCas9) protein. In some embodiments, a plasmid expressing a split protein may be introduced into cells through electroporation, transient (e.g., lipofection) and stable genome integration (e.g., piggybac) and viral transduction or other methods known to those of skill in the art.

[0402] In certain embodiments, the compositions provided herein comprise a lipid and/or polymer. In certain embodiments, the lipid and/or polymer is cationic. The preparation of such lipid particles is well known. See, e.g. U.S. Patent Nos. 4,880,635; 4,906,477; 4,911,928; 4,917,951; 4,920,016; 4,921,757; and 9,737,604, each of which is incorporated herein by reference.

[0403] The guide RNA sequence may be 15-100 nucleotides in length and comprise a sequence of at least 10, at least 15, or at least 20 contiguous nucleotides that is complementary to a target nucleotide sequence. The guide RNA may comprise a sequence of 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 contiguous nucleotides that is complementary to a target nucleotide sequence. The

guide RNA may be 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides in length.

[0404] In some embodiments, the target nucleotide sequence is a DNA sequence in a genome, e.g. a eukaryotic genome. In certain embodiments, the target nucleotide sequence is in a mammalian (e.g. a human) genome.

[0405] The compositions of this disclosure may be administered or packaged as a unit dose, for example. The term “unit dose” when used in reference to a pharmaceutical composition of the present disclosure refers to physically discrete units suitable as unitary dosage for the subject, each unit containing a predetermined quantity of active material calculated to produce the desired therapeutic effect in association with the required diluent, i.e., a carrier or vehicle.

[0406] Treatment of a disease or disorder includes delaying the development or progression of the disease, or reducing disease severity. Treating the disease does not necessarily require curative results.

[0407] As used therein, “delaying” the development of a disease means to defer, hinder, slow, retard, stabilize, and/or postpone progression of the disease. This delay can be of varying lengths of time, depending on the history of the disease and/or individuals being treated. A method that “delays” or alleviates the development of a disease, or delays the onset of the disease, is a method that reduces probability of developing one or more symptoms of the disease in a given time frame and/or reduces extent of the symptoms in a given time frame, when compared to not using the method. Such comparisons are typically based on clinical studies, using a number of subjects sufficient to give a statistically significant result.

[0408] “Development” or “progression” of a disease means initial manifestations and/or ensuing progression of the disease. Development of the disease can be detectable and assessed using standard clinical techniques as well known in the art. However, development also refers to progression that may be undetectable. For purpose of this disclosure, development or progression refers to the biological course of the symptoms. “Development” includes occurrence, recurrence, and onset.

[0409] As used herein “onset” or “occurrence” of a disease includes initial onset and/or recurrence. Conventional methods, known to those of ordinary skill in the art of medicine, can be used to administer the isolated polypeptide or pharmaceutical composition to the subject, depending upon the type of disease to be treated or the site of the disease.

[0410] Without further elaboration, it is believed that one skilled in the art can, based on the above description, utilize the present disclosure to its fullest extent. The following specific

embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. All publications cited herein are incorporated by reference for the purposes or subject matter referenced herein.

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EXAMPLES

Example 1. Modification of double-stranded DNA by way of ribozyme-mediated Cas9-based genome editing

[0468] The ability to site-specifically insert a nucleotide into DNA or RNA could enable the targeted repair of frameshift mutations in an analogous manner to the repair of point mutations by base-editing technologies. An RNA enzyme, or ribozyme, could readily serve as a means to site-specifically incorporate a nucleotide into DNA or RNA. The use of self-splicing group I introns as *in vitro* RNA editing agents has been well-precedented. Additionally, a ribozyme-based genome editing agent has a number of other advantages when compared to protein-based enzymes. First, the ribozyme is almost certain to be significantly smaller in size than a protein enzyme, making it likely less immunogenic and easier to deliver within size-limited viral vectors. Second, a ribozyme could be tailored to a specific genetic site, conferring added specificity and preventing the insertion of multiple nucleotides.

[0469] The goal of this work was to develop an RNA-based insertase capable of site-specifically inserting a single nucleotide into DNA, thus enabling the repair of frameshift mutations and potentially leading to the ability to correct a wide variety of mutations that underlie genetic diseases such as CDD. Additionally, the use of a ribozyme to perform genome editing is unprecedented and this work could pioneer a new subfield of genome editing, enabling the potential correction and treatment of other types of genetic diseases.

[0470] It was hypothesized that the *Tetrahymena* group I intron (**Fig. 1A**) would serve as a promising scaffold for the design of a ribozyme insertase. The group I intron splices itself out of mRNA via a two-step mechanism. First, it binds GTP and inserts it into the 5' splice site, resulting in the cleavage of the transcript. Next, it undergoes a conformational change that brings the 5' and 3' splice sites in close proximity, followed by catalyzing the nucleophilic attack of the free 2'-hydroxyl at the 5' splice site into the 3' splice site (**Fig. 1B**). Importantly, previous efforts by Joyce and coworkers in the 1990s resulted in an evolved *Tetrahymena* group I ribozyme that could bind and cleave single-stranded DNA, as well as RNA (see section 2 of this document). By further modifying this scaffold a ribozyme could be generated that could site-specifically insert GTP into DNA.

[0471] The insertion of a nucleotide into DNA results in a nicked intermediate. If not repaired, that nick will result in the removal of the inserted nucleotide by the intrinsic DNA repair machinery of the cell. As such, it is critical that the DNA be re-ligated shortly after insertion. It was hypothesized that it would be possible for the *Tetrahymena* ribozyme to not

only insert a nucleotide into DNA but also ligate that nucleotide into place (**Fig. 2A**). Despite being formed of different biopolymers, the active site of the *Tetrahymena* ribozyme and *E. coli* DNA polymerase are strikingly similar (**Fig. 2B**). The major difference is the positioning of substrate nucleotide within the binding pocket; in the *Tetrahymena* ribozyme, the nucleotide is positioned such that it is removed from the substrate following splicing, while in the ligase, it is positioned such that a pyrophosphate leaving group is removed and the nucleotide attached to the growing DNA strand. By allowing the DNA substrate to shift position within the binding site following the insertion of GTP through judicious engineering of the ribozyme-substrate pairing element (P0; **Fig. 2C and D**), the enzyme could ligate the resulting nick.

[0472] To determine if the modified ribozyme was capable of inserting a single nucleotide into DNA, a 5'-radiolabeled DNA substrate was added and monitored the reaction via polyacrylamide gel electrophoresis (PAGE). The appearance of a band equivalent in size to an authentic product was observed, suggesting that the modified ribozyme was indeed effective (**Fig. 3A**). High-throughput sequencing (HTS) indicated that a single G nucleotide had been incorporated at the desired side. *In vitro* yields approached 75%, with greater than 99% purity (**Fig. 3A**), demonstrating that the modified ribozyme is a good starting point for the design and evolution of an insertase.

[0473] A significant challenge associated with the shifting strategy employed is that it could potentially limit the number of DNA sequences that are targetable with this approach. For this strategy to be effective, the target DNA substrate must be able to base pair to the ribozyme both before and after the addition of a G nucleotide (**Fig. 2D**). To overcome this barrier, ribozyme was further modified by adding an extra, initially unpaired nucleotide within the substrate pairing element and increasing its overall length, thus reducing the number of nucleotides that need to shift during the reaction from 6 to 3 (**Fig. 3B**), potentially improving the number of targetable sequences by 64-fold. Robust insertion of a G nucleotide was observed with these modified ribozymes by PAGE (**Fig. 3C**). It may also be possible to engineer and/or evolve the ribozyme to accept an extra nucleotide closer to the active site, further dramatically improving substrate specificity.

[0474] The next goal was to design a system whereby the ribozyme could insert a nucleotide into double-stranded DNA (dsDNA) *in vitro*. Unsurprisingly, the modified ribozyme, like virtually all natural and evolved ribozymes, was not be able to act on a dsDNA substrate (data not shown). However, by targeting the ribozyme to a stretch of DNA rendered single-stranded upon being bound by a Cas9:sgRNA complex, it was reasoned it might be possible

to overcome this challenge. It was hypothesized that there are two key considerations that would govern the ability of the ribozyme to recognize its target. First, the ssDNA target must be long enough to enable binding, which we estimate to require roughly 10-20 nucleotides. This is potentially longer than that unveiled by a single Cas9 binding event. Therefore, we decided to target Cas9 to either side of the ribozyme binding site, theoretically increasing the amount of ssDNA unveiled (**Fig. 4**). Second, binding of the ribozyme to the target will occur via the formation of an RNA-DNA duplex, which will in turn induce local supercoiling of the ssDNA on either side of the duplex. This supercoiling will be highly entropically and enthalpically unstable. In biology, supercoiling in plasmids is released when topoisomerase nicks the plasmid, allowing the two strands to unwind. It was hypothesized that using a nicking Cas9 (nCas9) which cuts only one of the DNA strands could have a similar effect. In addition, nicking of the non-targeted strand will likely be necessary for effective genome editing in cells. To mimic the effect of a nCas9 and simplify initial assays, synthetic dsDNA substrates were used that contain nicks at the precise location where Cas9 would cut once bound. Upon incorporating these effects, robust insertion of a single G nucleotide was observed at several synthetic dsDNA substrates where the distances between the Cas9 binding sites and ribozyme target site was varied, with yields approached 50% and product purity greater than 95% (**Fig. 5**).

[0475] Following these experiments, it was next sought to determine whether the ribozyme:Cas9 system would be active in human cells (via the scheme shown in **Fig. 6A**). Upon transfecting plasmids that encode the components of this system to HEK293T cells, however, no editing activity was observed at sites targeted by the sgRNA and ribozyme (**Fig. 6B**). It was speculated that this might be due to an inability of the ribozyme to recognize the site without being recruited to it. Accordingly, we designed a system for the tethering of the ribozyme to Cas9 via an MS2 protein/aptamer linkage (**Fig. 7A-7D**). In this system, an MS2 coat protein is appended to the Cas9 protein, and one or more hairpins recognized by the MS2 coat protein (hereafter these hairpins are called the MS2 aptamer) installed in the variable loop 6 of the ribozyme (**Fig. 7A-7D**). Upon doing so, significant increase in the number of insertions and deletions (indels) was observed at the targeted site relative to nicking Cas9 alone, indicative of a double-strand break. This suggests that the ribozyme is inserting GTP into the R-loop, generating a break in that strand, but unable to ligate the resulting nick, resulting in a double-strand break and indel formation.

Example 2. Method for *in vitro* evolution of ribozymes to act on DNA

[0476] Previously, Joyce and coworkers (Robertson & Joyce, *Nature*, 1990; Beaudry & Joyce, *Science*, 1992; Tsang & Joyce, *Biochemistry*, 1994; Tsang & Joyce, *J. Mol. Biol.*, 1996; Raillard & Joyce, *Biochemistry*, 1996) demonstrated a system for the *in vitro* evolution of group I introns that cleave DNA. In this system (**FIG. 8** below), the ribozyme is incubated with a piece of single-stranded DNA. Ribozymes that are able to cleave the DNA (performing the E.S->EP reaction below) then have a constant region of DNA appended to the 3' end of the molecule. Reverse transcription with a complementary primer and subsequent PCR leads to the amplification of sequences that encode these ribozymes that pass the selection. Transcription of these DNA molecules then results in formation of ribozymes that can reenter the cycle. Repeated cycles result in ribozymes with improved DNA binding ability. However, excessive cycles can result in ribozymes that do not perform nucleotide insertion, as we have observed in our hands. This is due to the ribozymes becoming optimized at performing a specific chemical reaction which is subtly different from those required for nucleotide insertion. Sequences of group I introns that could theoretically be used as starting points for this evolution can be found here in the database described in Zhou, Y, Lu C, Wu QJ, Wang Y, Sun ZT, Deng JC, Zhang Y. *Nucl. Acids. Res.* 2008.

Example 3. Evidence for ribozyme-mediated nucleotide insertion in bacteria

[0477] It was hypothesized that, although nucleotide insertion and ligation didn't work in HEK cells, it might work in bacteria. Mg^{2+} is required for both GTP insertion and ligation, but more is required for ligation, and the Mg^{2+} concentration required is higher in bacteria than in mammalian cells. A bacterial-active ribozyme insertase could serve as a starting point for evolution of a ribozyme that can function in mammalian cells.

A series of three plasmids (see FIG. 9) to test if the ribozyme could be active in bacteria. These plasmids would express (i) the ribozyme or (ii) the nicking Cas9 and sgRNA that would target the complex to a site on a third plasmid (iii) which would contain a frame-shifted antibiotic cassette that could be rescued by the insertion of a single nucleotide. Upon expression all components of the system and selecting for bacteria that could grow on the selection antibiotic, roughly $1:10^6$ of inoculated bacteria could survive, and that these all contained the desired edit at the specified site. Bacteria treated with an inactive ribozyme were unable to survive treatment.

EQUIVALENTS AND SCOPE

[0478] In the claims articles such as “a,” “an,” and “the” may mean one or more than one unless indicated to the contrary or otherwise evident from the context. Claims or descriptions that include “or” between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The disclosure includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The disclosure includes embodiments in which more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process.

[0479] Furthermore, the disclosure encompasses all variations, combinations, and permutations in which one or more limitations, elements, clauses, and descriptive terms from one or more of the listed claims is introduced into another claim. For example, any claim that is dependent on another claim can be modified to include one or more limitations found in any other claim that is dependent on the same base claim. Where elements are presented as lists, e.g., in Markush group format, each subgroup of the elements is also disclosed, and any element(s) can be removed from the group. It should be understood that, in general, where the disclosure, or embodiments of the disclosure, is/are referred to as comprising particular elements and/or features, certain embodiments of the disclosure or embodiments of the disclosure consist, or consist essentially of, such elements and/or features. For purposes of simplicity, those embodiments have not been specifically set forth in haec verba herein. It is also noted that the terms “comprising” and “containing” are intended to be open and permits the inclusion of additional elements or steps. Where ranges are given, endpoints are included. Furthermore, unless otherwise indicated or otherwise evident from the context and understanding of one of ordinary skill in the art, values that are expressed as ranges can assume any specific value or sub-range within the stated ranges in different embodiments of the disclosure, to the tenth of the unit of the lower limit of the range, unless the context clearly dictates otherwise.

[0480] This application refers to various issued patents, published patent applications, journal articles, and other publications, all of which are incorporated herein by reference. If there is a conflict between any of the incorporated references and the present disclosure, the specification shall control. In addition, any particular embodiment of the present disclosure that falls within the prior art may be explicitly excluded from any one or more of the claims. Because such embodiments are deemed to be known to one of ordinary skill in the art, they may be excluded even if the exclusion is not set forth explicitly herein. Any particular

embodiment of the disclosure can be excluded from any claim, for any reason, whether or not related to the existence of prior art.

[0481] Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation many equivalents to the specific embodiments described herein. The scope of the present embodiments described herein is not intended to be limited to the above Description, but rather is as set forth in the appended claims. Those of ordinary skill in the art will appreciate that various changes and modifications to this description may be made without departing from the spirit or scope of the present disclosure, as defined in the following claims.

CLAIMS

What is claimed is:

1. An engineered ribozyme represented by the structure of FIG. 1A.
2. An engineered ribozyme represented by the structure of FIG. 3B.
3. An engineered ribozyme comprising a deletion in the 3' terminal end sufficient to remove the self-insertion activity of the ribozyme.
4. The engineered ribozyme of claim 3, wherein the deletion in the 3' terminal end comprises a deletion of the terminal 1-5 nucleotides of the ribozyme.
5. The engineered ribozyme of claim 3, further comprising an active site that catalyzes the insertion of a nucleotide into target site of a substrate single strand DNA molecule.
6. The engineered ribozyme of claim 5, wherein the active site comprises a region that hybridizes to the substrate single strand DNA molecule.
7. The engineered ribozyme of claim 6, wherein the region is 5 nucleotides, or 6 nucleotides, or 7 nucleotides, or 8 nucleotides and whose sequence is complementary to the substrate single strand DNA molecule.
8. The engineered ribozyme of claim 5, wherein the active site comprises a nucleotide that forms a wobble base pair with the substrate single strand DNA molecule.
9. The engineered ribozyme of claim 5, wherein the active site comprises an unpaired nucleotide.
10. The engineered ribozyme of claim 5, wherein the active site comprises in a 5'-3' direction a region that hybridizes to the substrate single strand DNA molecule, a nucleotide that forms a wobble base pair with the substrate single strand DNA molecule, and an unpaired nucleotide.
11. The engineered ribozyme of claim 10, wherein the ribozyme inserts a nucleotide immediate adjacent to the wobble base pair.

12. A ribozyme-mediated programmable nucleic acid editing construct comprising a ribozyme and a nucleic acid programmable DNA binding protein (napDNAbp) which is capable of installing an insertion of one or more nucleotides at a target site in a DNA molecule.
13. The editing construct of claim 12, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.
14. The editing construct of claim 13, wherein the one or more nucleotides is a G or A.
15. The editing construct of claim 13, wherein the one or more nucleotides is a C or T.
16. The editing construct of claim 12, wherein the ribozyme is represented by the structure of FIG. 1A or FIG. 3B.
17. The editing construct of claim 12, wherein the ribozyme is a modified group I intron from *Tetrahymena thermophila*.
18. The editing construct of claim 12, wherein the ribozyme further comprises a targeting moiety.
19. The editing construct of claim 18, wherein the targeting moiety is an MS2 hairpin structure.
20. The editing construct of claim 12, wherein the ribozyme and the napDNAbp are not fusion proteins.
21. The editing construct of claim 12, wherein the napDNAbp further comprises a targeting moiety receptor capable of binding to a ribozyme comprising a cognate targeting moiety.
22. The editing construct of claim 12, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
23. The editing construct of claim 12, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).

24. The editing construct of claim 12, wherein the napDNAbp is selected from the group consisting of: Cas9, CasX, CasY, Cpf1, C2c1, C2c2, C2C3, and Argonaute and optionally has a nickase activity
25. The editing construct of claim 12, wherein the napDNAbp when complexed with a guide RNA functions to bind to the target site in the DNA molecule and form an R-loop.
26. The editing construct of claim 24, wherein the R-loop comprise a single strand DNA region comprising the target site for binding the ribozyme.
27. A complex comprising the editing construct of any of claims 12-26 and a guide RNA.
28. The complex of claim 27, wherein the guide RNA is fused to the ribozyme.
29. The complex of claim 27, wherein the guide RNA is bound to the napDNAbp.
30. A polynucleotide encoding the ribozyme of any of claims 1-11.
31. A polynucleotide encoding the editing construct of any of claims 12-26.
32. A vector comprising the polynucleotide of claim 30.
33. A vector comprising the polynucleotide of claim 31.
34. A cell comprising an editing construct of any of claims 12-26.
35. A cell comprising a ribozyme of any of claims 1-11.
36. A pharmaceutical composition comprising a ribozyme of any of claims 1-11, an editing construct of any of claims 12-26, or a vector of any of claims 32-33.
37. A method for introducing a new nucleobase pair into a target site of a DNA molecule, comprising contacting a single-stranded R-loop formed in the DNA molecule by a bound napDNAbp with an engineered ribozyme, wherein the engineered ribozyme is configured to insert a nucleobase into an insertion site located in the R-loop.
38. The method of claim 37, wherein DNA repair and/or replication of a cell process the nucleobase insertion to form the new nucleobase pair in the DNA molecule.

39. The method of claim 37, wherein the engineered ribozyme is represented by the structure of FIG. 1A.
40. The method of claim 37, wherein the engineered ribozyme is represented by the structure of FIG. 3B.
41. The method of claim 37, wherein the engineered ribozyme comprises a deletion in the 3' terminal end sufficient to remove the self-insertion activity of the ribozyme.
42. The method of claim 37, wherein the engineered ribozyme comprises an active site that catalyzes the insertion of the nucleobase.
43. The method of claim 37, wherein the engineered ribozyme comprises an active site having a region that hybridizes to the single-stranded R-loop.
44. The method of claim 37, wherein the engineered ribozyme comprises a nucleotide that forms a wobble base pair with the single-stranded R-loop.
45. The method of claim 37, wherein the engineered ribozyme comprises an unpaired nucleotide.
46. The method of claim 37, wherein the engineered ribozyme comprises an active site comprising in a 5'-3' direction a region that hybridizes to the single-stranded R-loop, a nucleotide that forms a wobble base pair with the the single-stranded R-loop, and an unpaired nucleotide.
47. The method of claim 37, wherein the ribozyme inserts the nucleobase immediate adjacent a wobble base pair formed between the ribozyme and the single-stranded R-loop.
48. The method of claim 37, wherein the ribozyme further comprises a targeting moiety.
49. The method of claim 48, wherein the targeting moiety is an MS2 hairpin structure.
50. The method of claim 37, wherein the ribozyme and the napDNAbp are not fusion proteins.
51. The method of claim 37, wherein the napDNAbp further comprises a targeting moiety receptor capable of binding to a ribozyme comprising a cognate targeting moiety.

52. The method of claim 37, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
53. The method of claim 37, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).
54. The method of claim 37, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.
55. An engineered ribozyme comprising SEQ ID NO: 88, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 88.
56. An engineered ribozyme comprising SEQ ID NO: 89, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 89.
57. An engineered ribozyme comprising SEQ ID NO: 156, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 156.
58. An engineered ribozyme comprising SEQ ID NO: 157, or a ribozyme comprising a nucleotide sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to SEQ ID NO: 157.
59. A genome editing system comprising a nucleic acid programmable DNA binding protein (napDNAbp), a guide RNA, and a ribozyme.
60. The genome editing system of claim 59, wherein the ribozyme comprises any of SEQ ID NOs: 88, 89, 156, or 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least

97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 88, 89, 156, or 157.

61. The genome editing system of claim 59, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.

62. The genome editing system of claim 61, wherein the one or more nucleotides is a G or A.

63. The genome editing system of claim 61, wherein the one or more nucleotides is a C or T.

64. The genome editing system of claim 59, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.

65. The genome editing system of claim 59, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).

66. The genome editing system of claim 59, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.

67. The genome editing system of claim 59, wherein the napDNAbp comprises a recruitment domain.

68. The genome editing system of claim 67, wherein the recruitment domain is a MS2 bacteriophage coat protein.

69. The genome editing system of claim 67, wherein the MS2 bacteriophage coat protein comprises SEQ ID NO: 94, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO: 94.

70. The genome editing system of claim 67, wherein the ribozyme comprises the SEQ ID NO: 89, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 89.

71. The genome editing system of claim 67, wherein the ribozyme comprises the SEQ ID NO: 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 157.
72. The genome editing system of claim 59, wherein the napDNABp comprise an additional one or more functional domains.
73. The genome editing system of claim 72, wherein the one or more functional domains is an NLS.
74. The genome editing system of claim 72, wherein the one or more functional domains is an intein or a split-intein.
75. The genome editing system of claim 72, wherein the one or more functional domains are coupled via one or more linkers.
76. The genome editing system of claim 73, wherein the NLS comprises SEQ ID NOs: 9, 118, 10, 119, or 121-126, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 9, 118, 10, 119, or 121-126.
77. The genome editing system of claim 74, wherein the intein or split-intein comprises SEQ ID NOs: 1-8, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 1-8.
78. The genome editing system of claim 75, wherein the linker comprises SEQ ID NOs: 102-113, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity to any of SEQ ID NOs: 102-113.
79. The genome editing system of claim 59, wherein the napDNABp when complexed with the guide RNA functions to bind to a target site in a DNA molecule, forming an R-loop.

80. The genome editing system of claim 79, wherein the R-loop comprises a single strand DNA region comprising a complementary region that binds to the ribozyme.
81. The genome editing system of claim 80, wherein the complementary region binds to the P0 site of the ribozyme.
82. One or more polynucleotides encoding the genome editing system of any of claims 59-81.
83. A vector comprising the polynucleotide of claim 82.
84. The vector of claim 83, wherein the vector is an rAAV.
85. The vector of claim 84, wherein the rAAV is an rAAV2, rAAV6, rAAV8, rPHP.B, rPHP.eB, or rAAV9.
86. A cell comprising the vector of any of claims 83-85.
87. A pharmaceutical composition comprising a genome editing system of any of claims 59-81, a polynucleotide of claim 82, or a vector of claims 83-85, and a pharmaceutically acceptable excipient.
88. A method for installing one or more nucleobases at a target site in a DNA sequence, comprising contacting the DNA sequence with a genome editing system of any of claims 59-80.
89. The method of claim 88, wherein the genome editing system comprises a nucleic acid programmable DNA binding protein (napDNAbp), a guide RNA, and a ribozyme.
90. The method of claim 89, wherein the ribozyme comprises any of SEQ ID NOs: 88, 89, 156, or 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 88, 89, 156, or 157.
91. The method of claim 89, wherein the ribozyme is capable of inserting one or more nucleotides at the target site.
92. The method of claim 88, wherein the method installs a G, A, T, or C, or a combination thereof.

93. The method of claim 88, wherein the method installs a frameshift mutation.
94. The method of claim 89, wherein the napDNAbp is a Cas9 protein or functional equivalent thereof.
95. The method of claim 89, wherein the napDNAbp is a nuclease active Cas9, a nuclease inactive Cas9 (dCas9), or a Cas9 nickase (nCas9).
96. The method of claim 89, wherein the napDNAbp is selected from the group consisting of: Cas9, Cas12e, Cas12d, Cas12a, Cas12b1, Cas13a, Cas12c, and Argonaute and optionally has a nickase activity.
97. The method of claim 89, wherein the napDNAbp comprises a recruitment domain.
98. The method of claim 89, wherein the recruitment domain is a MS2 bacteriophage coat protein.
99. The method of claim 98, wherein the MS2 bacteriophage coat protein comprises SEQ ID NO: 94, or an amino acid sequence having at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% sequence identity with SEQ ID NO: 94.
100. The method of claim 98, wherein the ribozyme comprises the SEQ ID NO: 89, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 89.
101. The method of claim 98, wherein the ribozyme comprises the SEQ ID NO: 157, or a ribozyme having a sequence that is at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% identical to any of SEQ ID NOs: 157.
102. An engineered ribozyme that catalyzes the insertion of a nucleotide into a single-stranded DNA molecule.
103. The engineered ribozyme of claim 102, wherein the nucleotide is G.
104. The engineered ribozyme of claim 102, wherein the nucleotide is A.

- 105. The engineered ribozyme of claim 102, wherein the nucleotide is T.
- 106. The engineered ribozyme of claim 102, wherein the nucleotide is C.

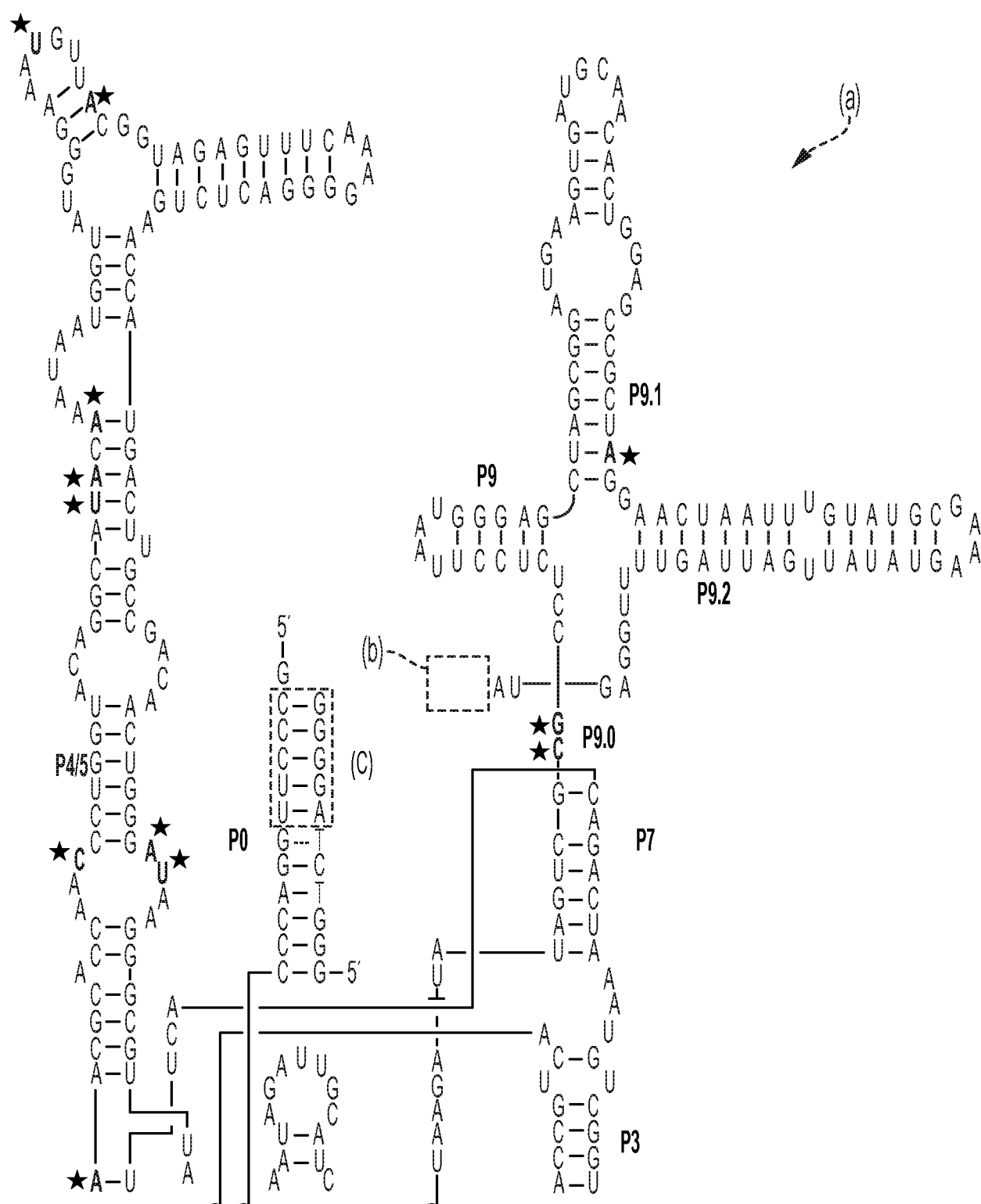
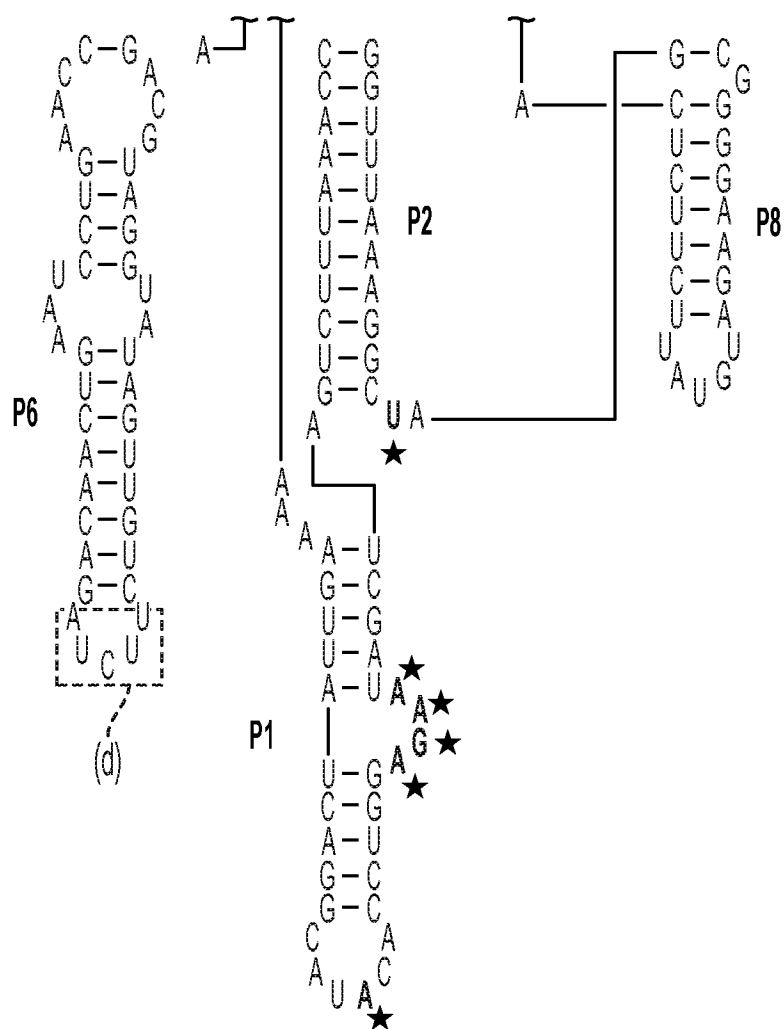


FIG. 1A

FIG. 1A
CONTINUED

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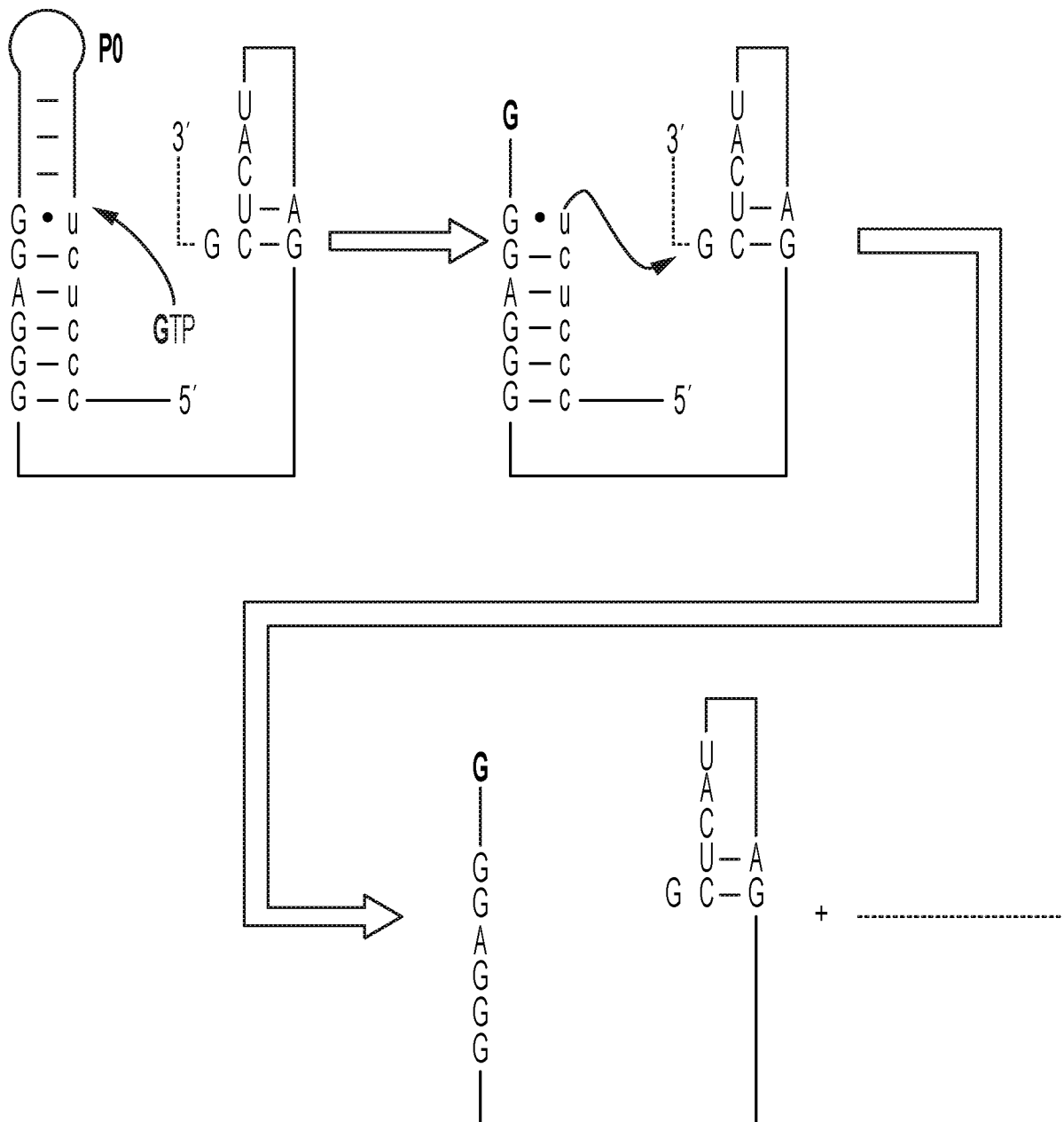


FIG. 1B

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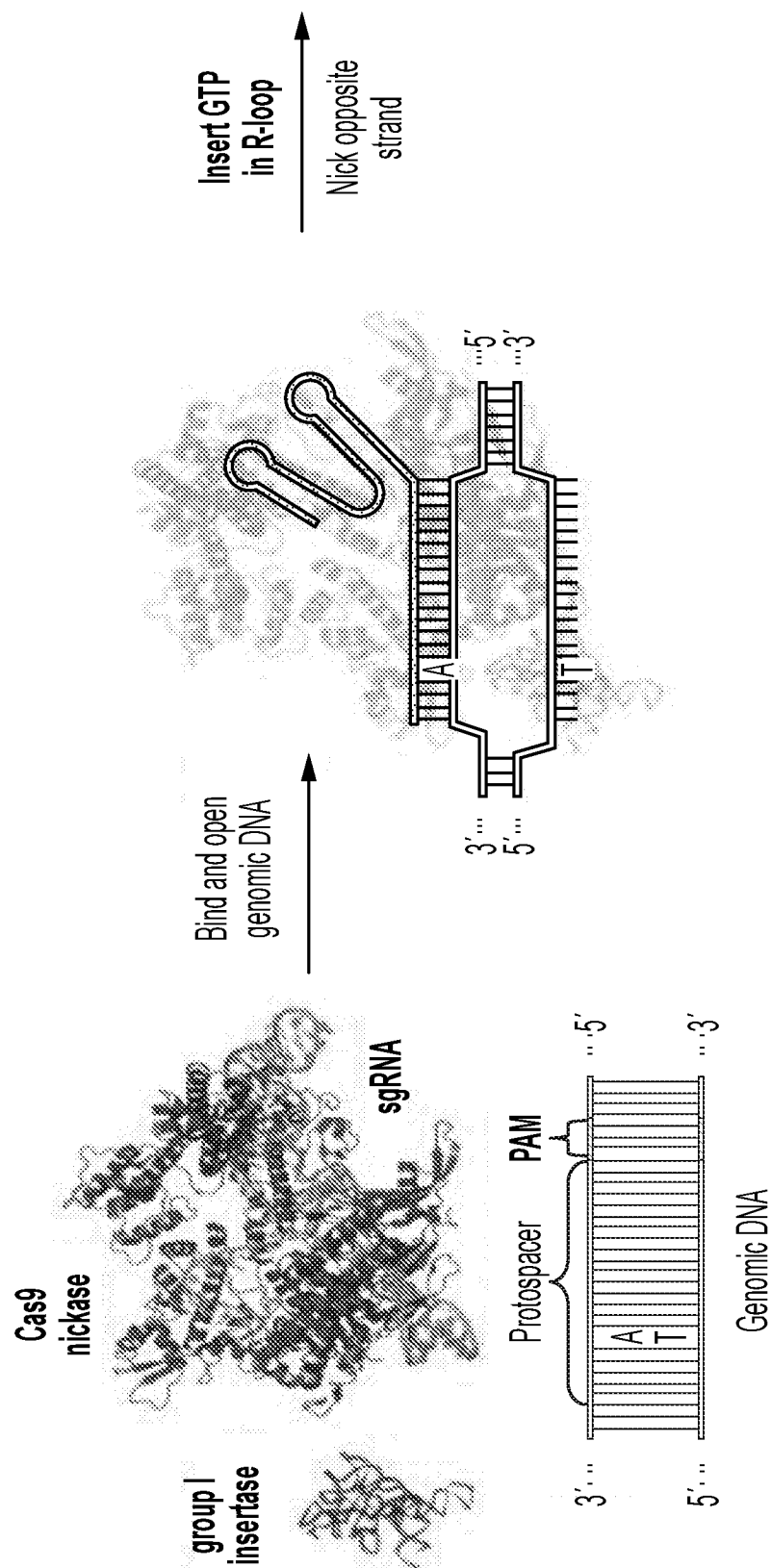


FIG. 2A

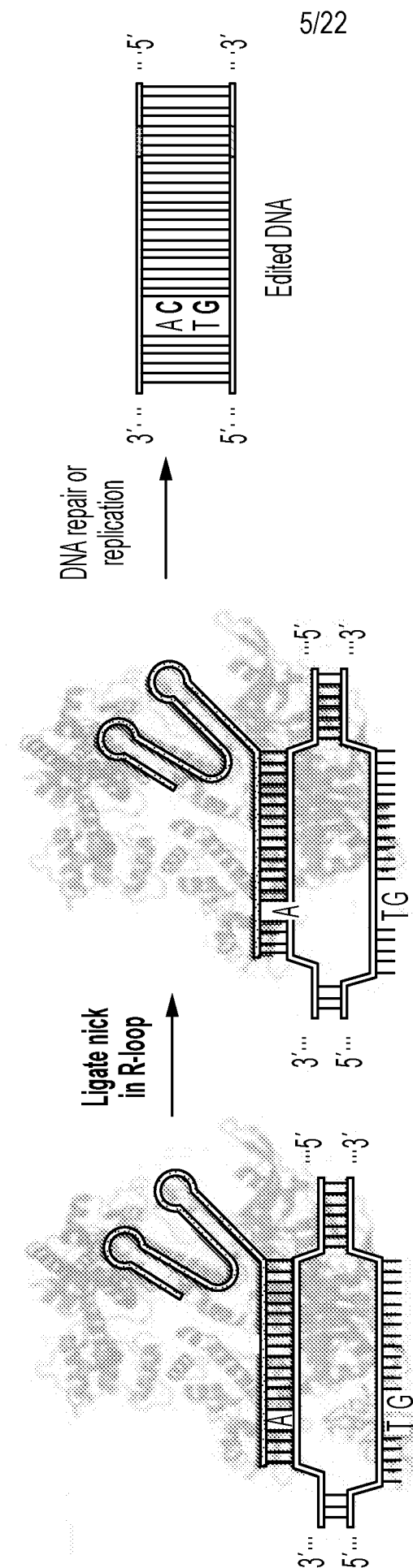


FIG. 2A
CONTINUED

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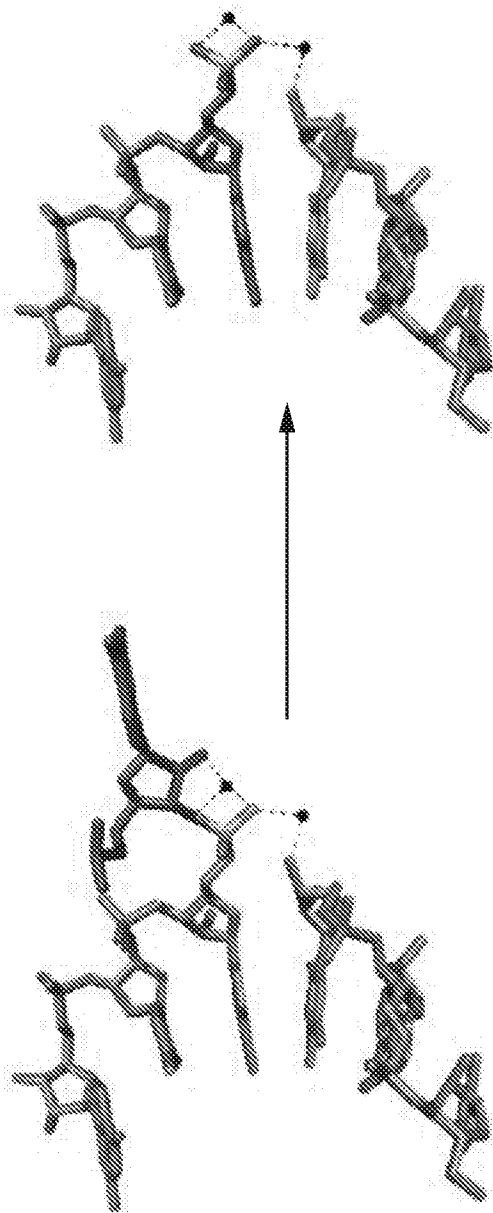
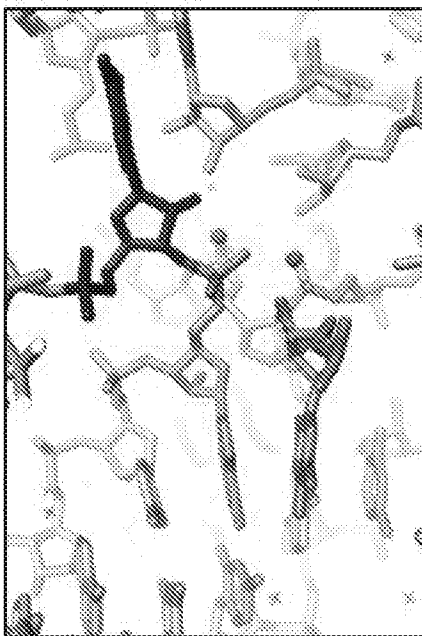


FIG. 2C

Azoarcus Ribozyme



T7 DNA Polymerase

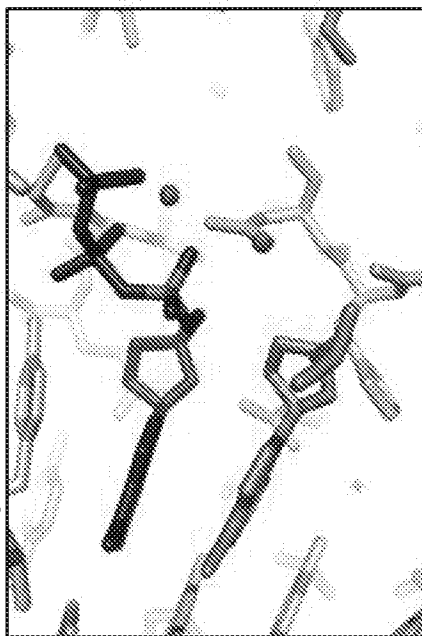


FIG. 2B

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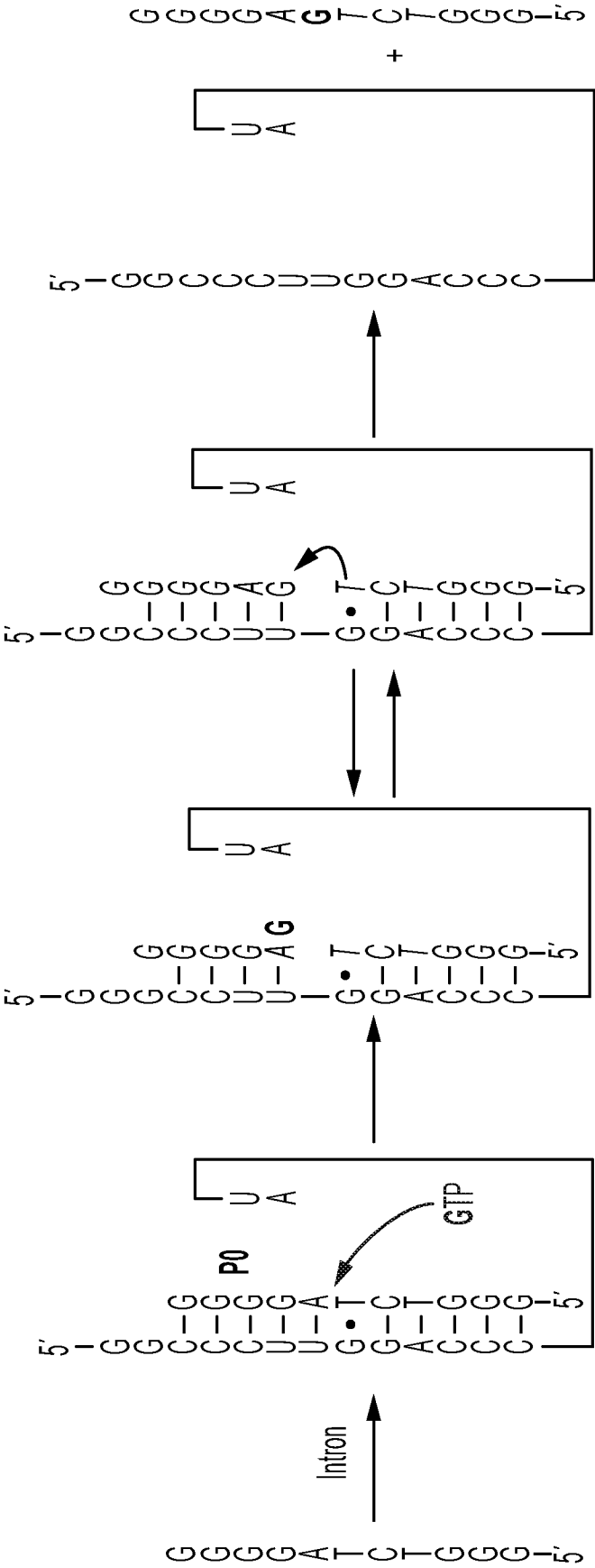


FIG. 2D

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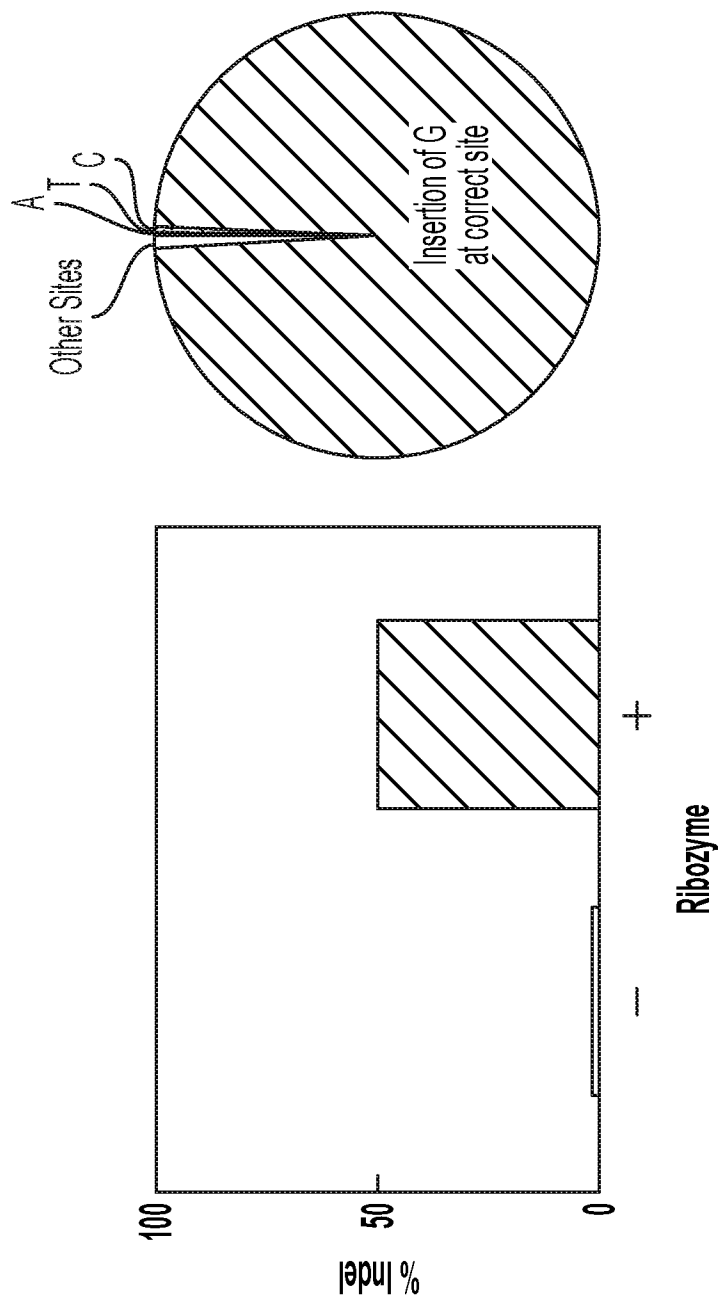


FIG. 3A

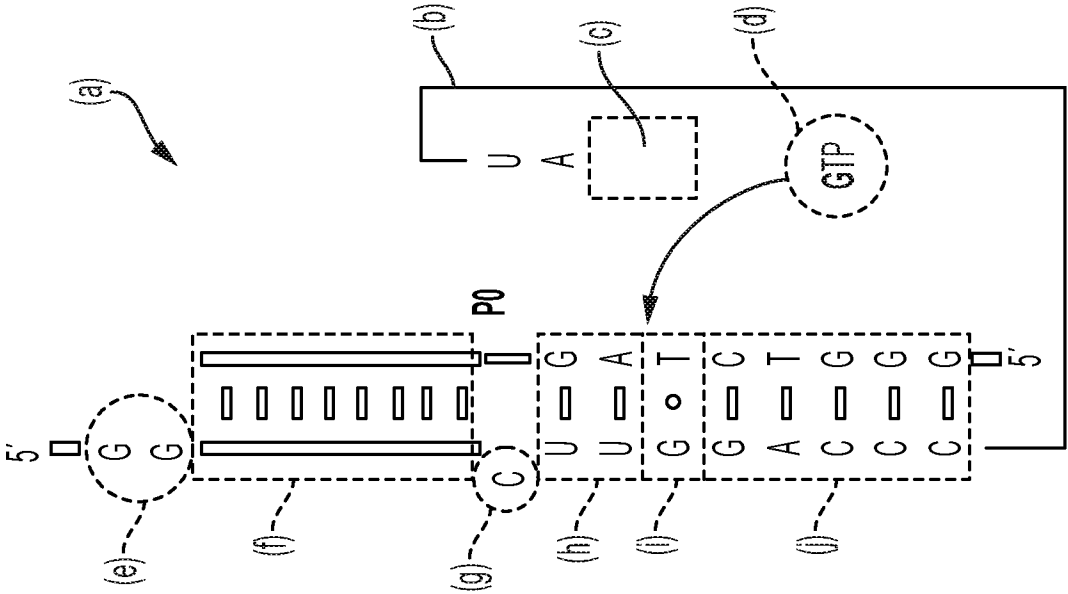
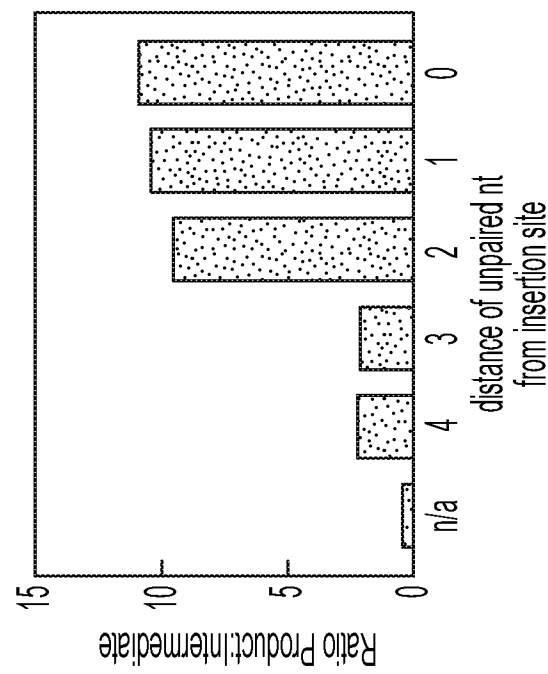


FIG. 3B

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Product
Starting Material
Cleaved Intermediates

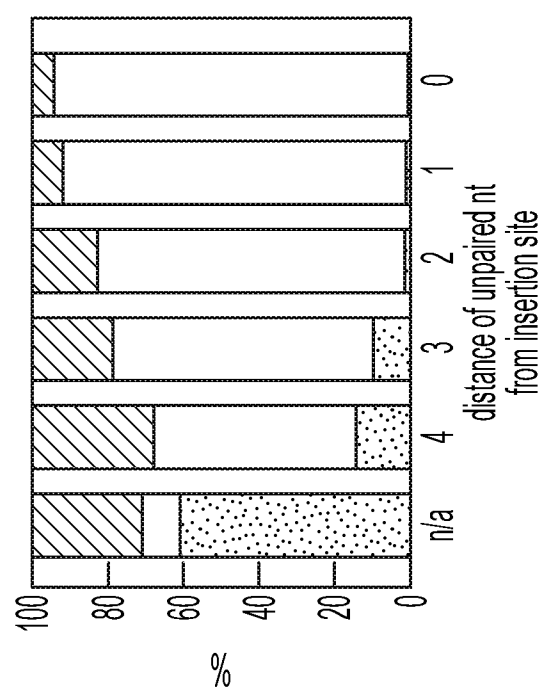


FIG. 3C

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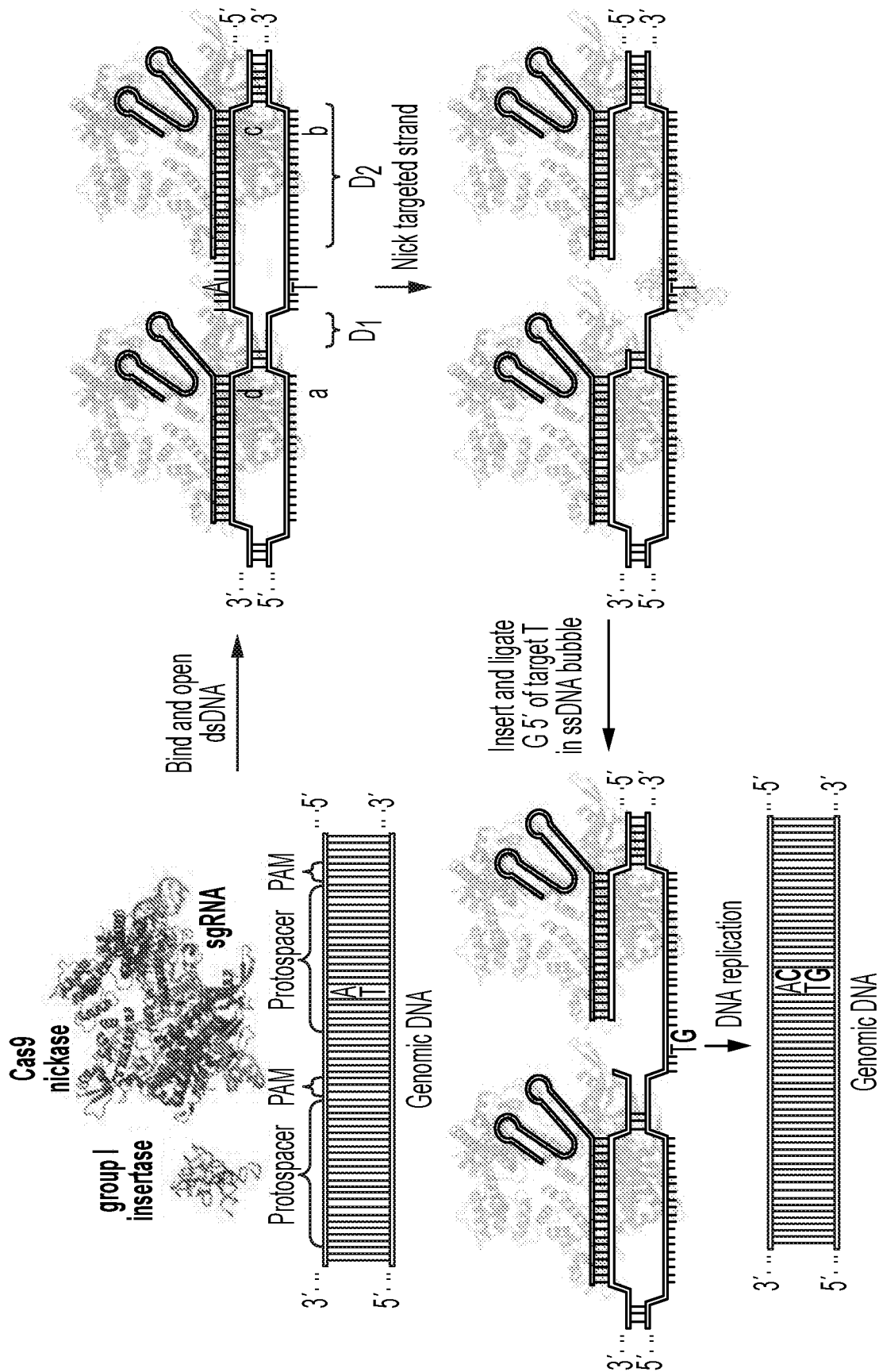


FIG. 4

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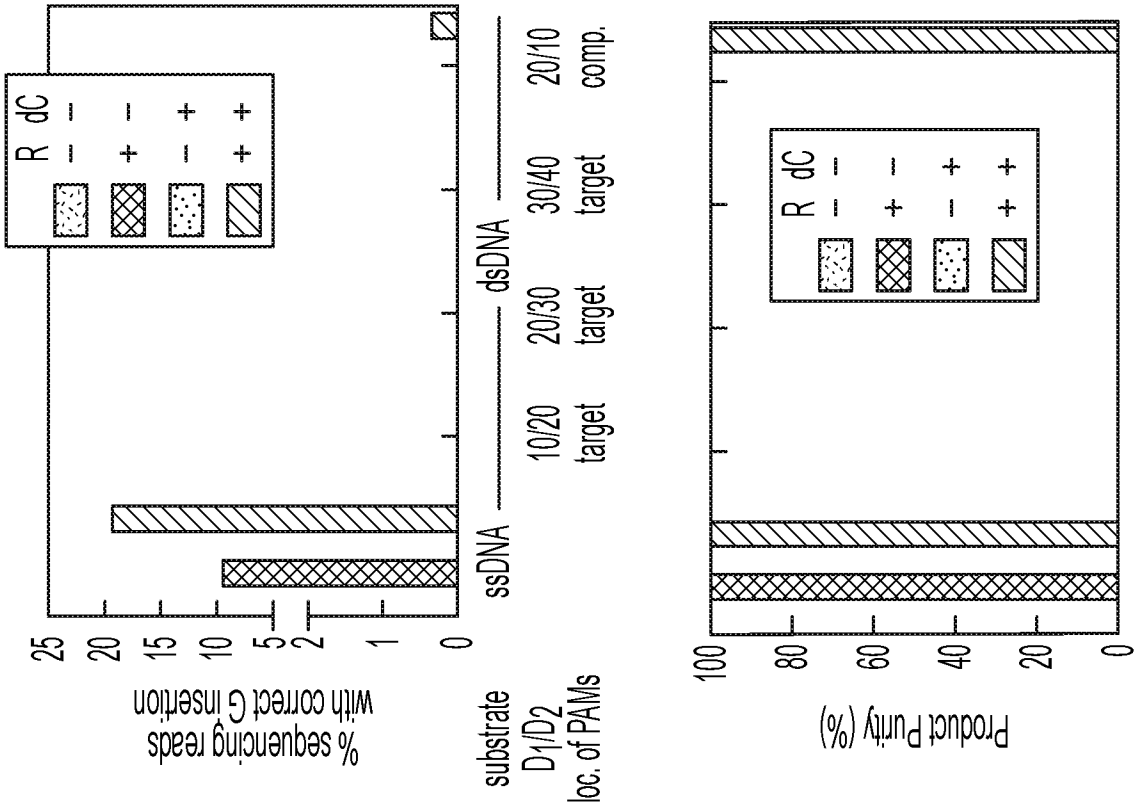


FIG. 5A

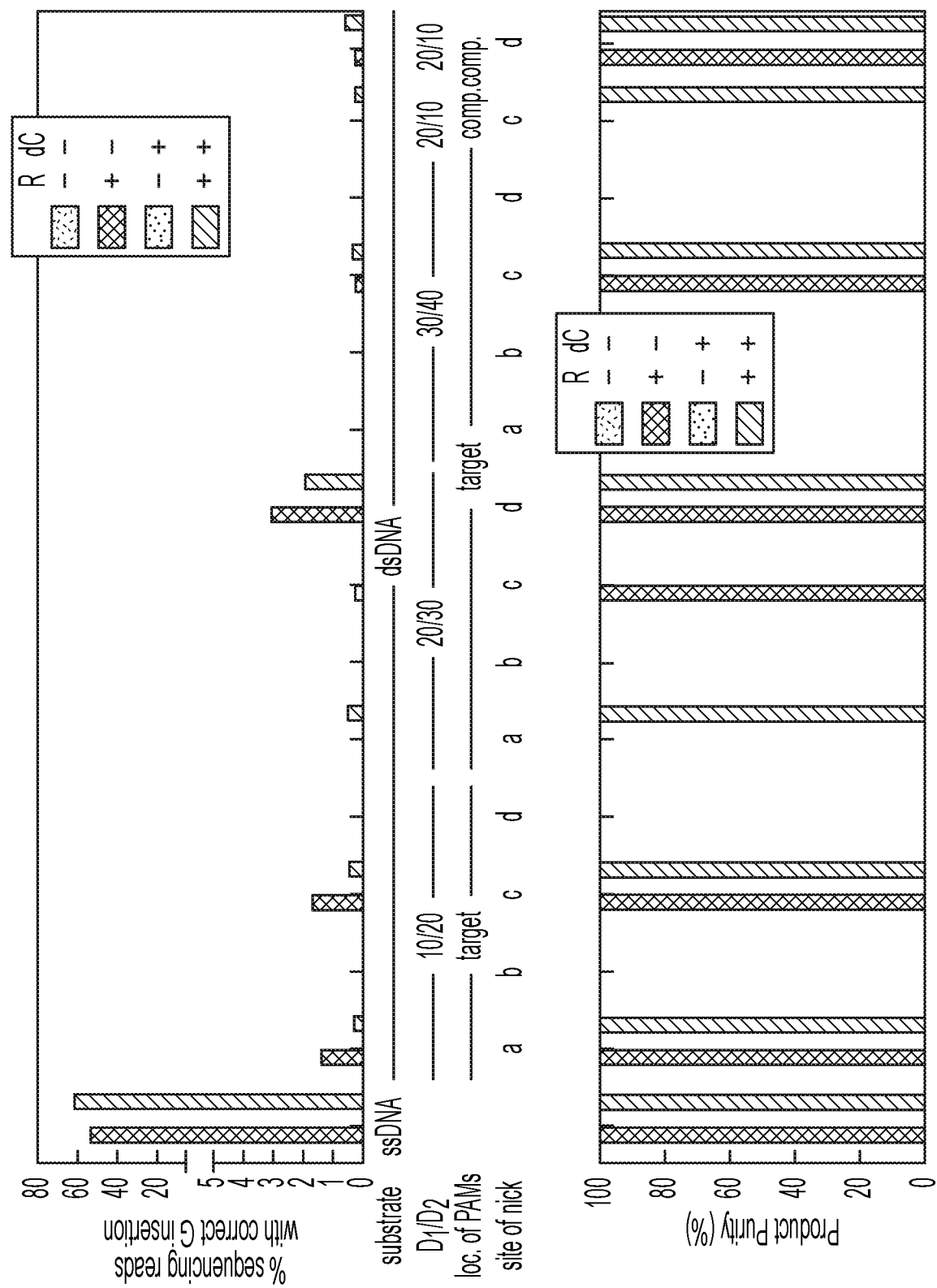


FIG. 5B

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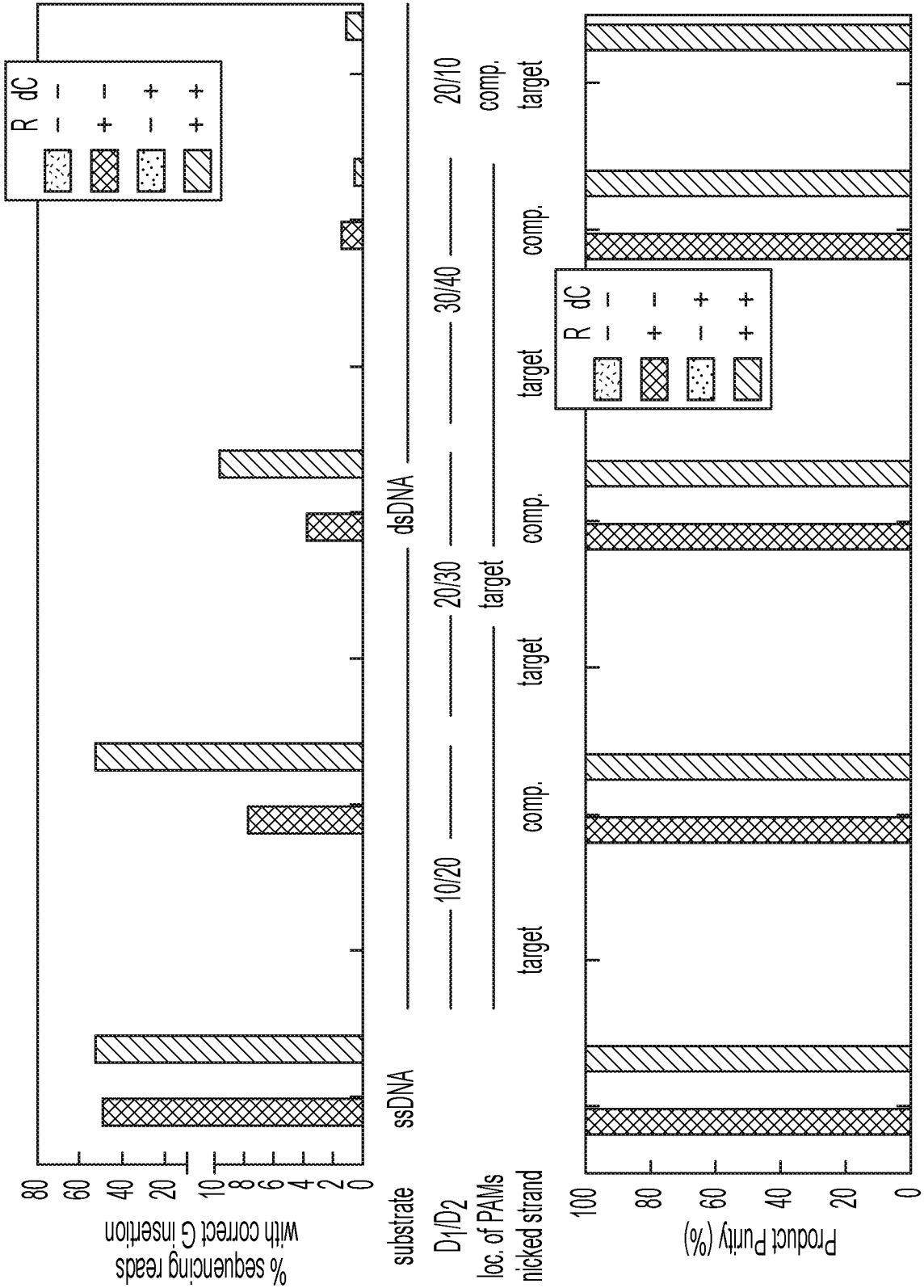


FIG. 5C

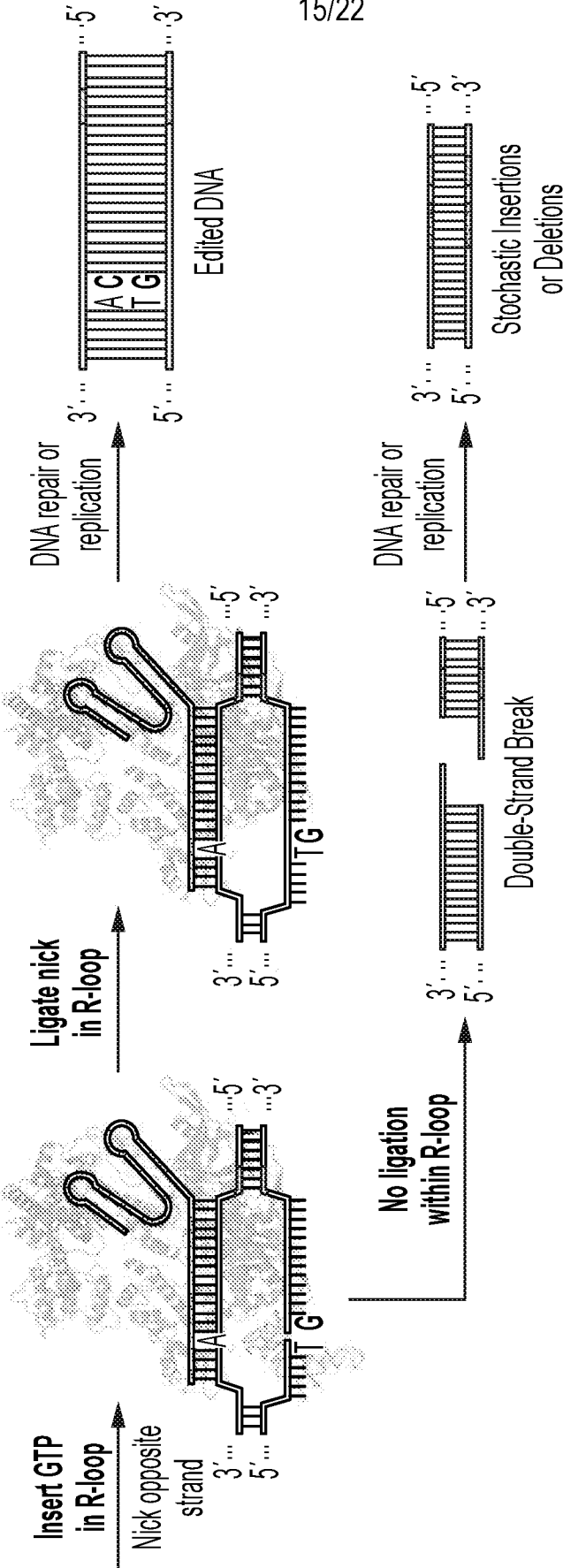


FIG. 6A

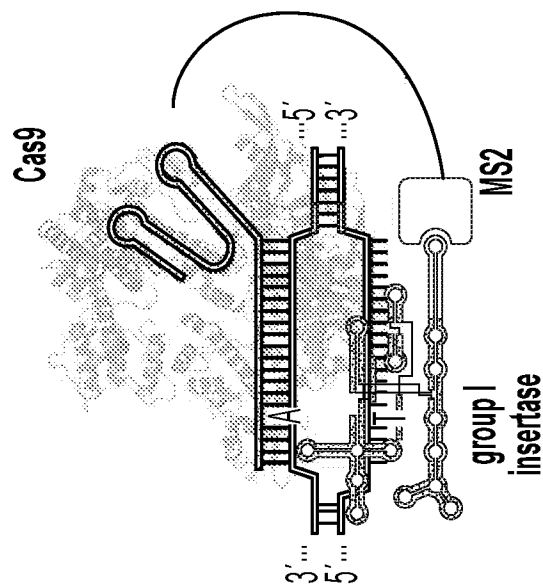


FIG. 7A

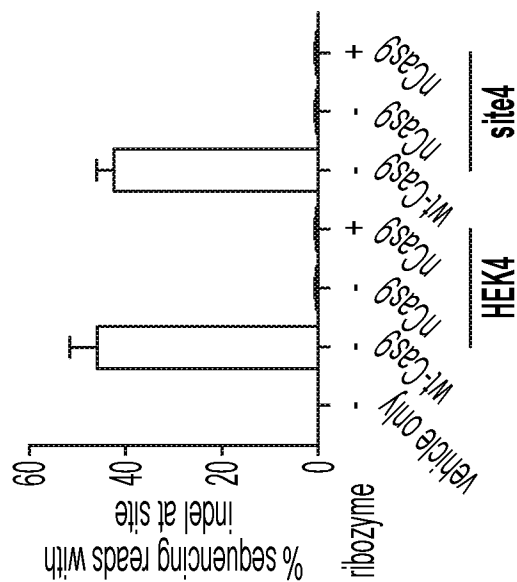
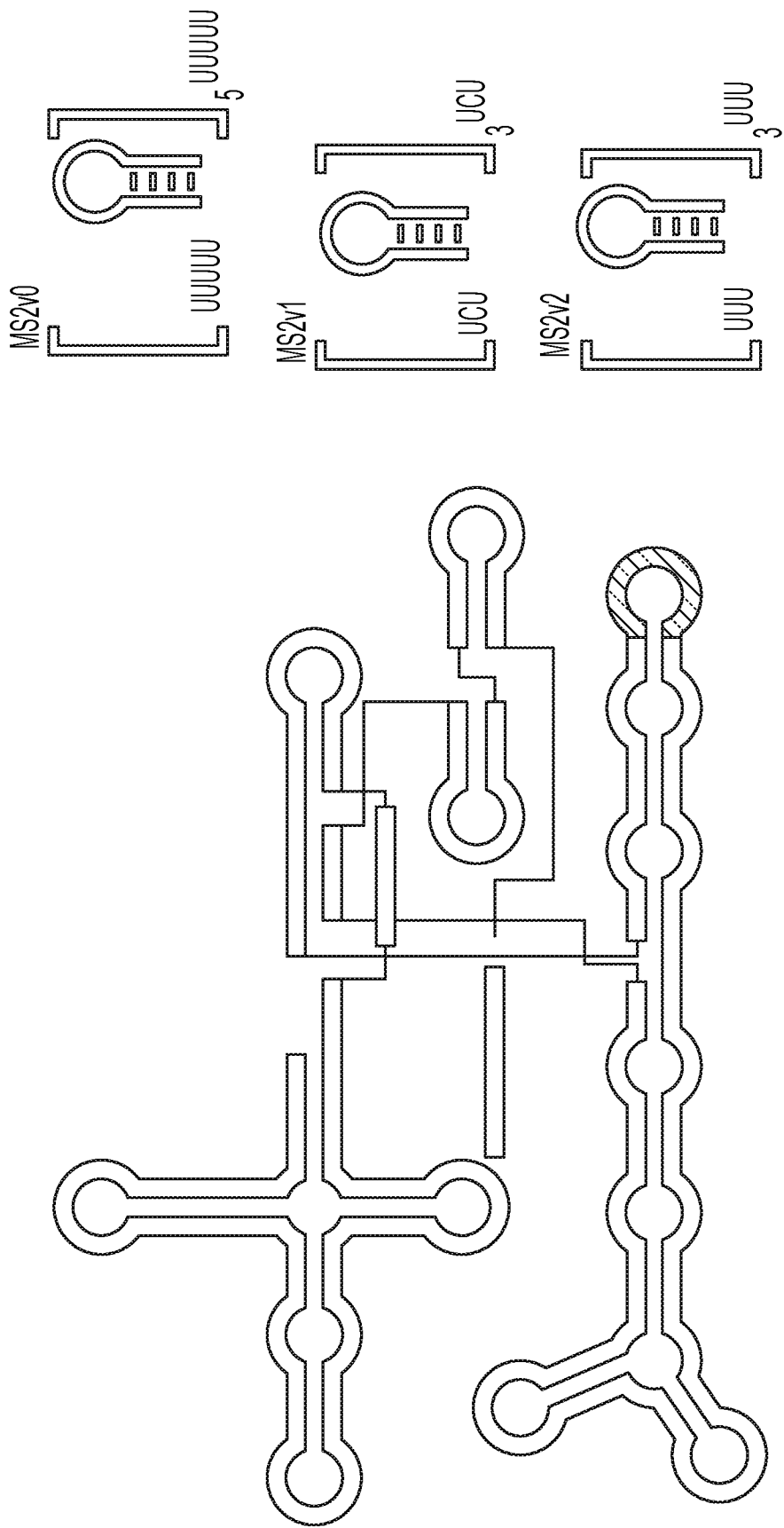


FIG. 6B



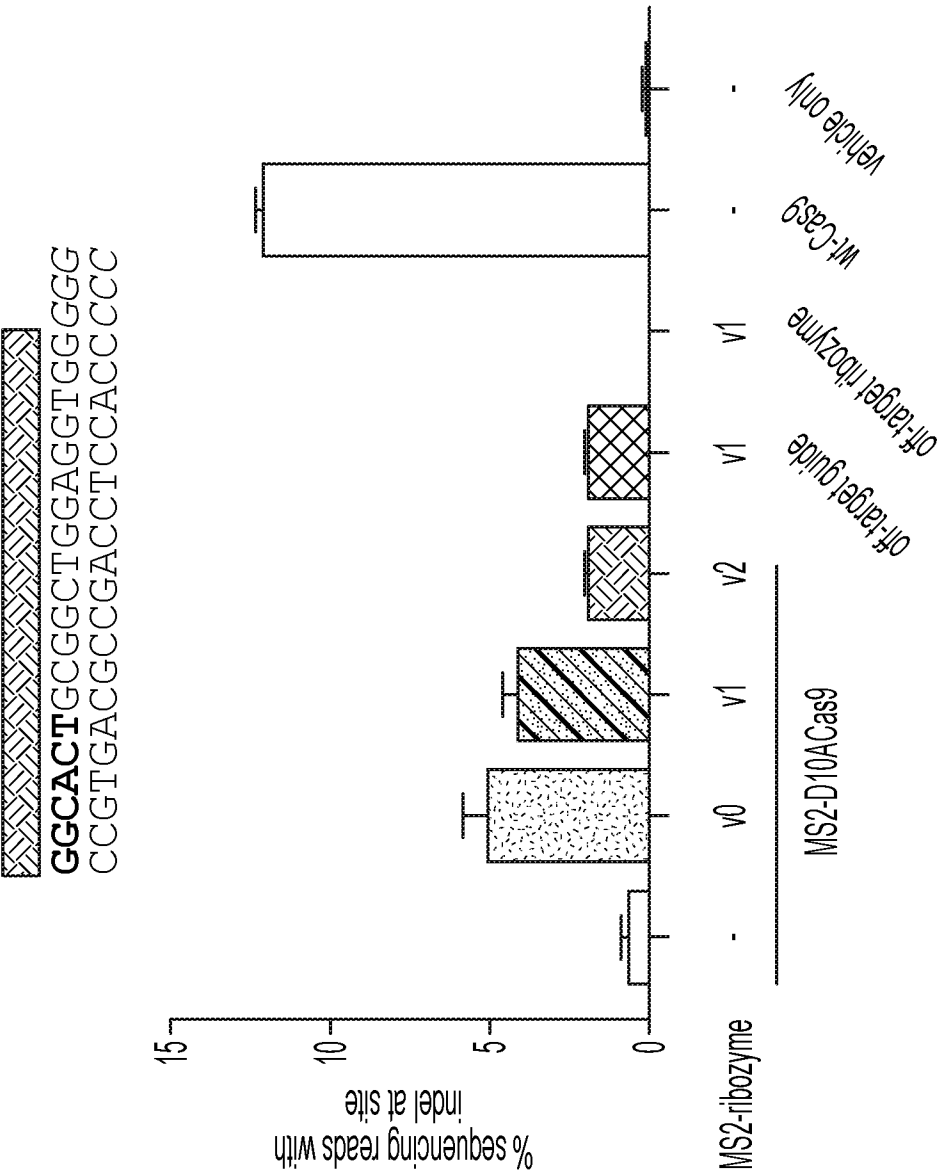


FIG. 7C

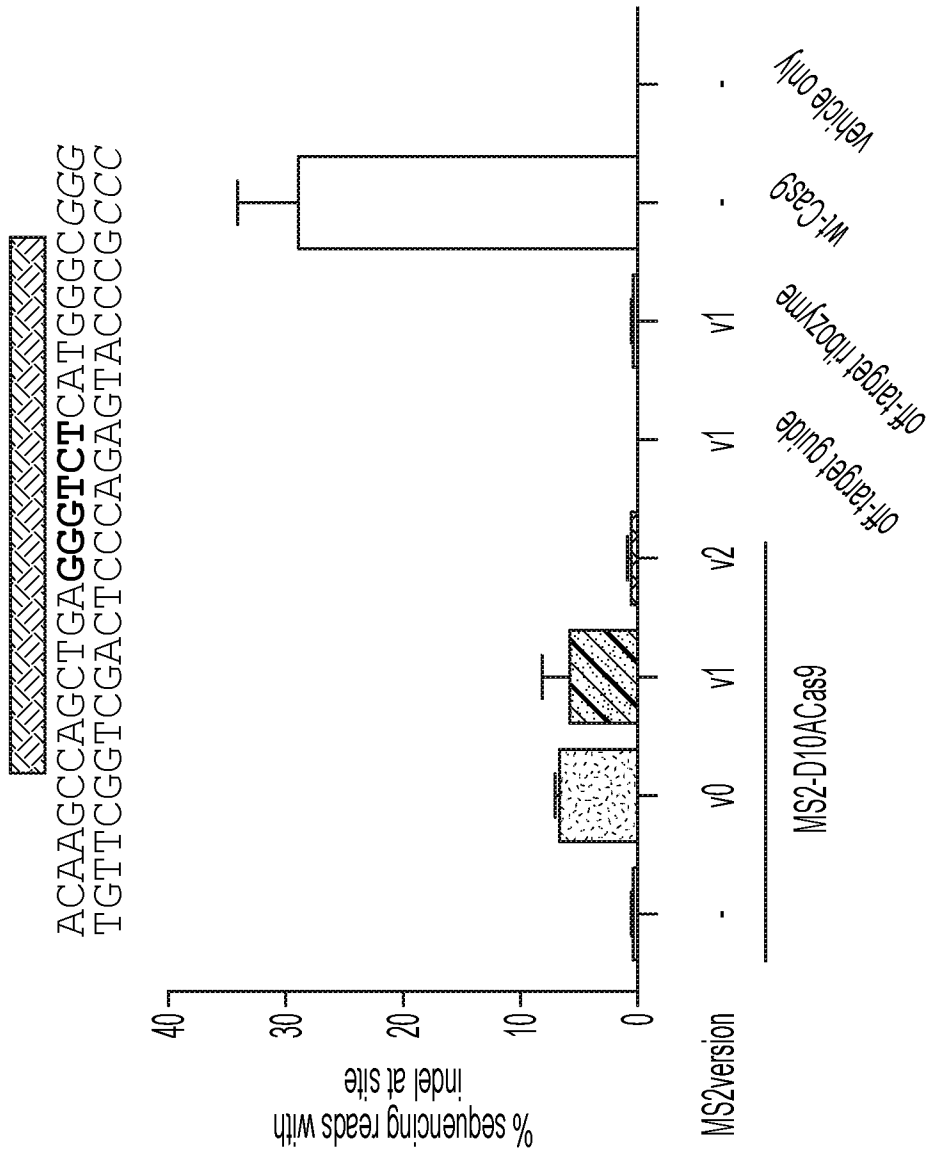


FIG. 7D

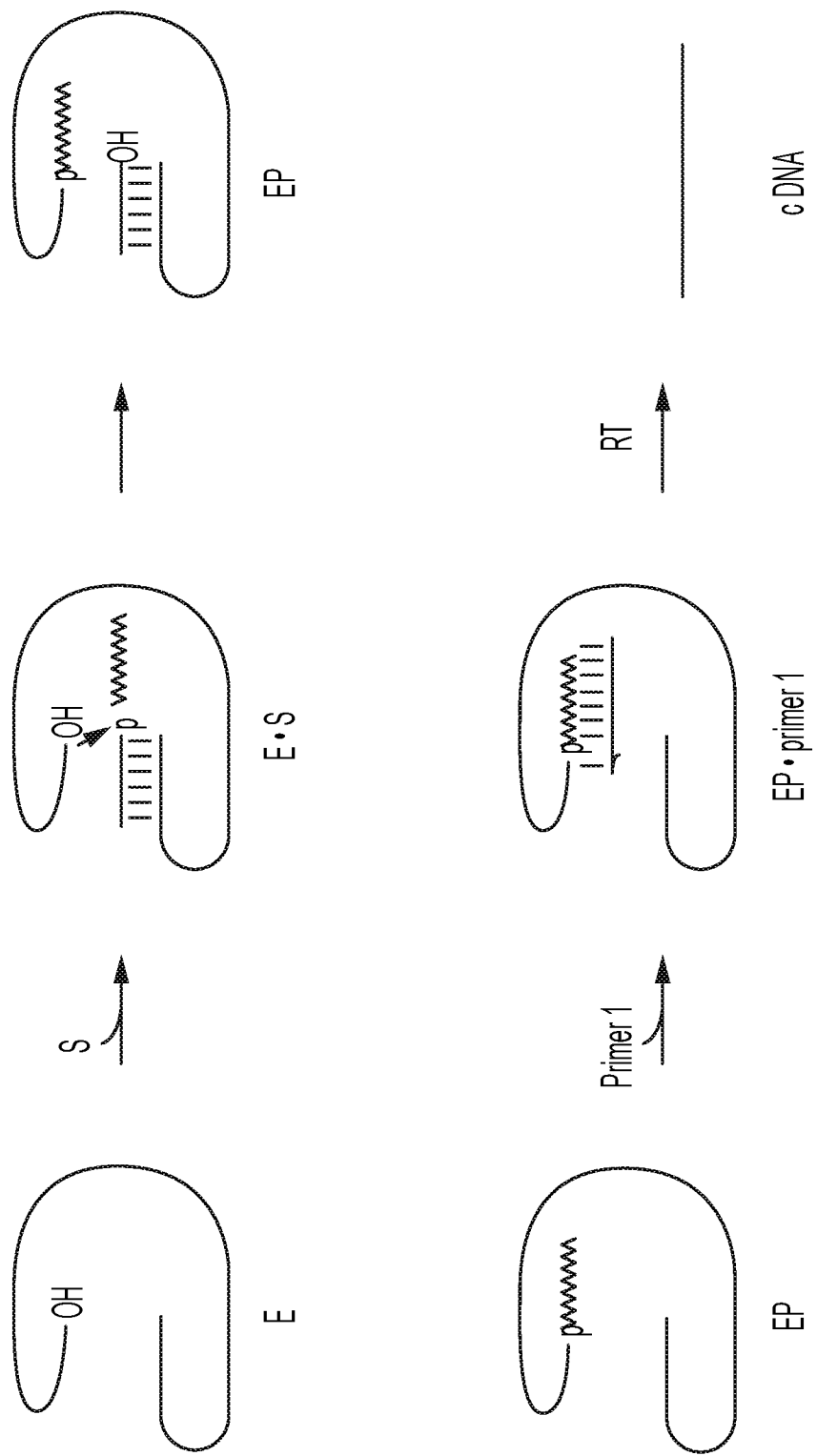
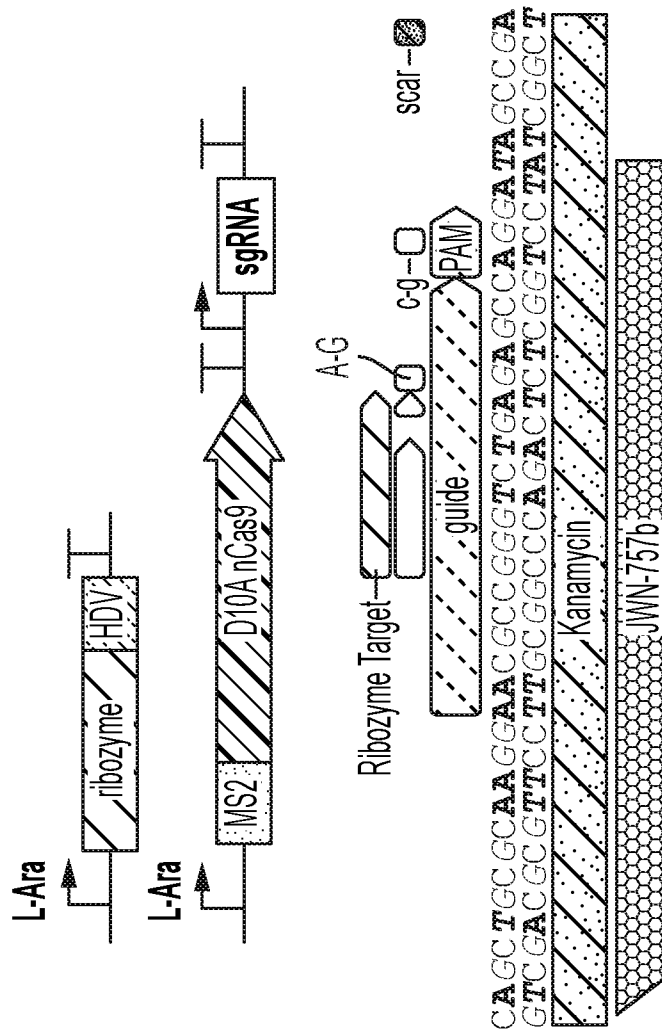


FIG. 8



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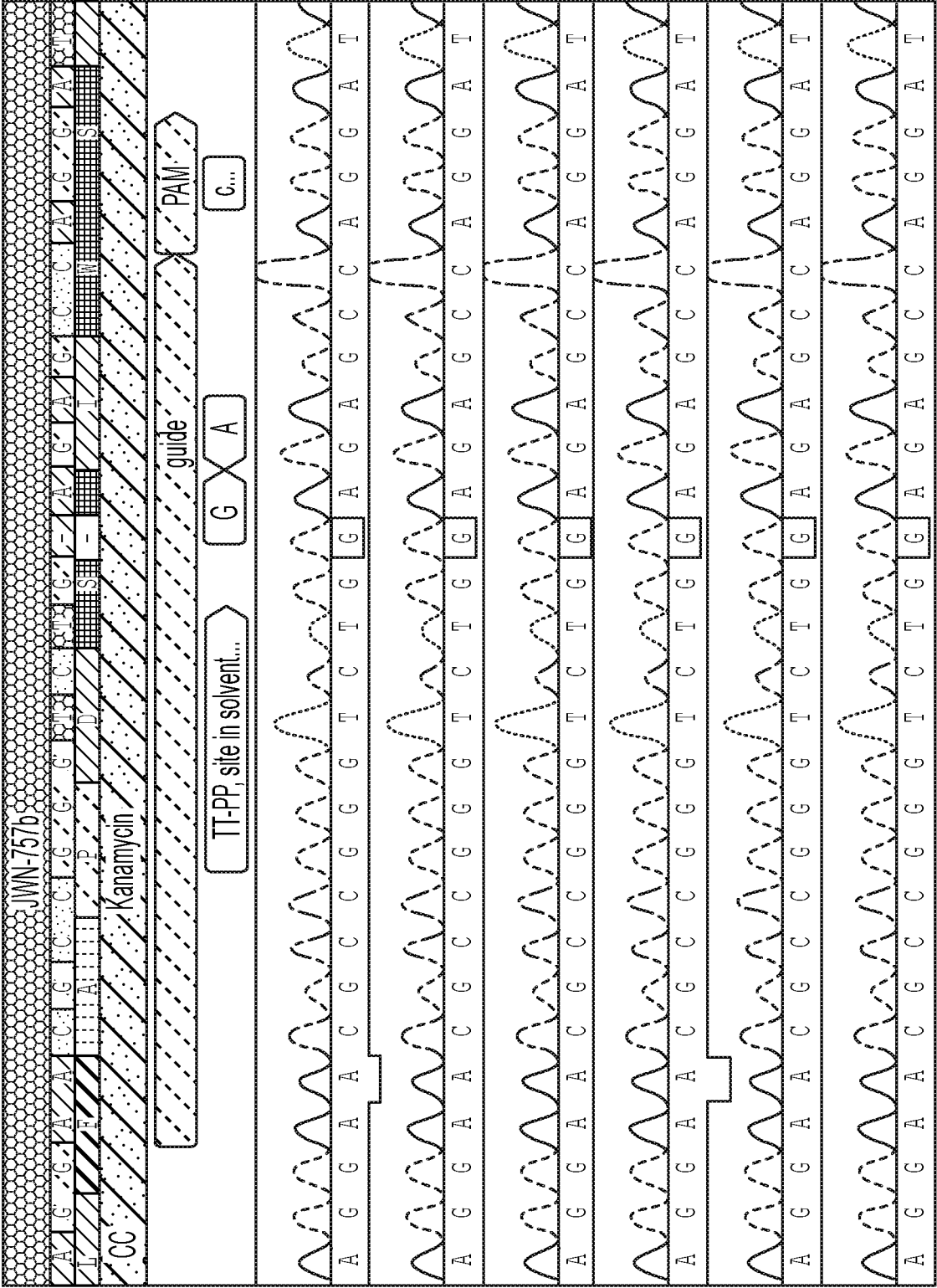


FIG. 9
CONTINUED

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2020/027836

A. CLASSIFICATION OF SUBJECT MATTER INV. C12N15/113 A61K47/54 C12N9/22 C12N15/11 ADD.														
According to International Patent Classification (IPC) or to both national classification and IPC														
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) A61K C12N Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EPO-Internal, BIOSIS, EMBASE, WPI Data, Sequence Search														
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1"> <thead> <tr> <th>Category*</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>X</td> <td> WO 2018/209320 A1 (HARVARD COLLEGE [US]) 15 November 2018 (2018-11-15) the whole document </td> <td> 2-38, 40-66, 68-106 </td> </tr> <tr> <td>X</td> <td> WEIXIN TANG ET AL: "Aptazyme-embedded guide RNAs enable ligand-responsive genome editing and transcriptional activation", NATURE COMMUNICATIONS, vol. 8, 28 June 2017 (2017-06-28), page 15939, XP055459755, DOI: 10.1038/ncomms15939 cited in the application Methods; figure 2 </td> <td> 59, 64-66, 82,83,86 </td> </tr> <tr> <td></td> <td style="text-align: center;">----- -/-</td> <td></td> </tr> </tbody> </table>			Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	X	WO 2018/209320 A1 (HARVARD COLLEGE [US]) 15 November 2018 (2018-11-15) the whole document	2-38, 40-66, 68-106	X	WEIXIN TANG ET AL: "Aptazyme-embedded guide RNAs enable ligand-responsive genome editing and transcriptional activation", NATURE COMMUNICATIONS, vol. 8, 28 June 2017 (2017-06-28), page 15939, XP055459755, DOI: 10.1038/ncomms15939 cited in the application Methods; figure 2	59, 64-66, 82,83,86		----- -/-	
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.												
X	WO 2018/209320 A1 (HARVARD COLLEGE [US]) 15 November 2018 (2018-11-15) the whole document	2-38, 40-66, 68-106												
X	WEIXIN TANG ET AL: "Aptazyme-embedded guide RNAs enable ligand-responsive genome editing and transcriptional activation", NATURE COMMUNICATIONS, vol. 8, 28 June 2017 (2017-06-28), page 15939, XP055459755, DOI: 10.1038/ncomms15939 cited in the application Methods; figure 2	59, 64-66, 82,83,86												
	----- -/-													
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Date of the actual completion of the international search 10 June 2020		Date of mailing of the international search report 19/06/2020												
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016		Authorized officer Bradbrook, Derek												

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2020/027836

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	ARNOLD PARK ET AL: "Sendai virus, an RNA virus with no risk of genomic integration, delivers CRISPR/Cas9 for efficient gene editing", MOLECULAR THERAPY - METHODS & CLINICAL DEVELOP, vol. 3, 1 January 2016 (2016-01-01), page 16057, XP055675590, GB ISSN: 2329-0501, DOI: 10.1038/mtm.2016.57 the whole document	2-38, 40-106
X	JOYCE ET AL: "Amplification, mutation and selection of catalytic RNA", GENE, ELSEVIER, AMSTERDAM, NL, vol. 82, no. 1, 15 October 1989 (1989-10-15), pages 83-87, XP025736872, ISSN: 0378-1119, DOI: 10.1016/0378-1119(89)90033-4 [retrieved on 1989-10-15] figure 3	3,4,30, 55-58
X	DATABASE Geneseq [Online] 29 January 2004 (2004-01-29), "T. thermophila intron TetIVS2a DNA fragment.", XP55702370, retrieved from EBI accession no. GSN:ADE34233 Database accession no. ADE34233 abstract; sequence	55-58
X	TSANG JOYCE ET AL: "Specialization of the DNA-cleaving activity of a group I ribozyme through in vitro evolution", JOURNAL OF MOLECULAR BIOLOGY, ACADEMIC PRESS, UNITED KINGDOM, vol. 262, no. 1, 1 January 1996 (1996-01-01), pages 31-42, XP002160945, ISSN: 0022-2836, DOI: 10.1006/JMBI.1996.0496 cited in the application figure 1	55-58
X	US 2010/305197 A1 (CHE AUSTIN J [US]) 2 December 2010 (2010-12-02) SEQ ID NO.2; paragraph [0012] - paragraph [0053]	55-58

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2020/027836

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2018209320	A1	15-11-2018	NONE

US 2010305197	A1	02-12-2010	NONE
