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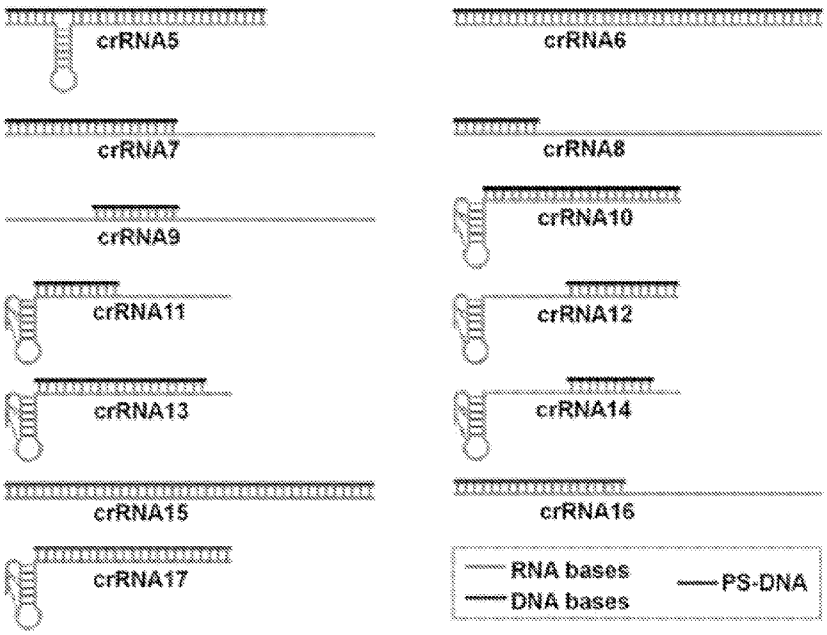

FIG. 1C

(57) Abstract: The present disclosure generally relates to genome editing systems and methods and compounds and compositions for use in Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) genome editing systems. Disclosed herein are modified nucleic acids that modulate the activity of genome editing.

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MODIFIED NUCLEIC ACIDS, HYBRID GUIDE RNAS, AND USES THEREOF

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application Serial No. 62/359,880, filed July 8, 2016 and U.S. Provisional Patent Application Serial No. 62/480,716 filed April 3, 2017, each of which are expressly incorporated herein by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

This invention was made with Government Support under Grant No. R01HL136652 awarded by the National Heart, Lung, and Blood Institute. The Government has certain rights to the invention.

FIELD

The present disclosure generally relates to compounds and methods for use in genome editing systems.

BACKGROUND

Cpf1 (CRISPR from *Prevotella* and *Francisella* 1) is one of the CRISPR associated effector endonucleases, which induces double stranded DNA breaks under the guidance of a single CRISPR RNA (crRNA). The wild-type crRNA of CRISPR-Cpf1 system comprises a 5'-handle engaging Cpf1 recognition and a guide segment interacting with targeted DNA sequences through complimentary bindings. Based on its unique gene editing properties, the CRISPR-Cpf1 system has recently been applied in diverse eukaryotic species including plants and animals to achieve targeted genome editing.

Although the CRISPR system offers a powerful platform for genome editing, a number of challenges exist for its therapeutic applications including gene editing efficiency and potential side effects. Previously, extensive efforts have been made to improve gene editing efficiency. Meanwhile, researchers have also investigated diverse approaches to modulate the activity of the CRISPR system. Due to the potential for severe side effects in these genome editing systems, it is essential to prepare an effective and fast mechanism to switch off its function. Recently, anti-CRISPR proteins from bacteriophage or bacteria were discovered to inhibit the function of *Listeria monocytogenes* or *Neisseria meningitidis* CRISPR-Cas9. In addition, multiple strategies such as chemical-, temperature- and light-triggered approaches were developed to regulate the CRISPR-

Cas9 system. However, no method is currently available to effectively regulate the CRISPR-Cpf1 system including upregulation, downregulation, and complete inactivation.

The compounds, compositions, and methods disclosed herein address these and other needs.

SUMMARY

The inventors have designed and synthesized a novel array of nucleic acid molecules for use as adjustable switches to upregulate, downregulate, and completely inactivate the cleavage activity of Cpf1 in the CRISPR genome editing system. In some embodiments, these nucleic acid molecules comprise chemically modified nucleotides and/or chimeric DNA/RNA guide molecules.

In one aspect, disclosed herein is an isolated nucleic acid comprising at least one chemically modified nucleotide, wherein the nucleic acid is complementary to a guide RNA of a CRISPR genome editing system.

In one aspect, disclosed herein is a method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

In another aspect, disclosed herein is a method for increasing the nuclease activity of a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid increases the activity of the nuclease of the CRISPR genome editing system.

In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof. In some embodiments, the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage. In some embodiments, the chemically modified phosphodiester linkage is phosphorothioate (PS).

In some embodiments, all the nucleotides comprise chemically modified phosphodiester linkages. In some embodiments, the chemically modified phosphodiester linkages are phosphorothioate (PS).

In some embodiments, the nucleic acid inhibits a nuclease activity of the CRISPR genome editing system. In some embodiments, the at least one chemically modified nucleotide is a chemically modified ribose. In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F). In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me). In some embodiments, the chemically modified ribose is 2'-fluoro (2'-F).

In some embodiments, the nucleic acid increases a nuclease activity of the CRISPR genome editing system.

In some embodiments, the complementary region between the nucleic acid and the guide RNA comprises at least 5 nucleotides. In some embodiments, the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid is RNA. In some embodiments, the nucleic acid is DNA. In some embodiments, the nuclease activity is from a Cpf1 protein.

In one aspect, disclosed herein is a chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide, wherein the chimeric guide nucleic acid inhibits a nuclease activity of a CRISPR genome editing system.

In a further aspect, disclosed herein is a method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide; and

wherein the chimeric guide nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

In some embodiments, the nucleic acid is comprised of at least 5% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 10% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 30% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 50% DNA nucleotides.

In some embodiments, the nuclease activity is from a Cpf1 protein. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid comprises at least one chemically modified nucleotide. In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying figures, which are incorporated in and constitute a part of this specification, illustrate several aspects described below.

FIGS. 1A-1G. Gene cutting efficiency of crRNA variants in human cells. Figure 1A, Schematic illustration of crRNA chimeras. Wild-type crRNA consists of a handle (pseudoknot structure) and a guide segment. crRNA chimeras were synthesized by substituting of ribonucleotides (gray) with corresponding deoxynucleotides (black). Figure 1B, Relative gene cutting efficiency of crRNA chimeras in the presence of AsCpf1 plasmid for the *DNMT1* locus in HEK293T cells. Figure 1C, Schematic illustration of DNA-crRNA duplexes. Duplexes were formed by hybridization of different lengths of unmodified (crRNA1 to crRNA14) or PS-modified (crRNA15, 16, 17) DNA oligonucleotides with various regions of the crRNA. Figure 1D, Relative Gene cutting efficiency of DNA-crRNA duplexes in the presence of AsCpf1 plasmid for the *DNMT1* locus in HEK293T cells. Figure 1E, Schematic illustration of RNA-crRNA duplexes. Duplexes were formed by hybridization of unmodified (crRNA18, 19, 20), 2'-fluoro modified (crRNA21, 22) or 2'-*O*-Methyl modified (crRNA23, 24, 25) RNA oligonucleotides with of the crRNA. Figure 1F, Relative Gene cutting efficiency of RNA-crRNA duplexes in the presence of AsCpf1 plasmid for the *DNMT1* locus in HEK293T cells (**$P < 0.01$, crRNA24 versus crRNA; two-tailed *t*-test). Figure 1G, Relative Gene cutting efficiency of PS-DNA-crRNA duplexes in the presence of AsCpf1 mRNA for the *DNMT1* locus in HEK293T cells. In all cases, relative gene cutting (%) was determined by the T7E1 cleavage assay, and normalized to that of the wild-type crRNA group. All data are expressed as the mean ± s.d. from three biological replicates. ND, not detectable.

FIGS. 2A-2F. Inhibition effects of phosphorothioated DNA oligonucleotides on Cpf1-mediated gene editing in human cells. Figure 2A,2B, Time- (2A) and dose- (2B) dependent effects of ps42DNA on AsCpf1-mediated *DNMT1* gene cutting in HEK293T cells. Figure 2C,2D, Time-dependent effects of ps42DNA-AAVS1 on AsCpf1-mediated gene cutting at the *AAVS1* locus (2C), and ps42DNA-FANCF on AsCpf1-mediated gene cutting at the *FANCF* locus (2D). Figure 2E, Time-dependent effects of ps42DNA on AsCpf1-mediated *DNMT1* gene cleavage in Hep3B cells. Figure 2F, Time-dependent effects of Lbps42DNA on LbCpf1-mediated gene cutting at the *DNMT1* locus in HEK293T cells. Relative gene cutting was determined by the T7E1 cleavage assay, normalized to that of the treatment with wild-type crRNA and AsCpf1 mRNA, and plotted versus time or dose. The corresponding gel images were shown in Fig.4.

FIG. 3. Overall structure of wild-type crRNA and its variants. The light grey letters denote the unmodified RNA base (see crRNA19 and 20). The black letters denote unmodified DNA base (see crRNA1 to crRNA14). The dark grey letters denote PS-linkage modified DNA (crRNA15, 16, 17). The intermediate grey letters denote 2'-fluoro modified RNA (crRNA21 and 22). The light black letters denote 2'-*O*-methyl modified RNA (crRNA23, 24, and 25). The dash represents the hydrogen-bond interaction between paired bases.

FIGS. 4A-4F. Inhibition effects of phosphorothioated DNA oligonucleotides on Cpf1-mediated gene editing in human cells. Figure 4A,4B, Time- (4A) and dose- (4B) dependent effects of ps42DNA on AsCpf1-mediated *DNMT1* gene cutting in HEK293T cells. Figure 4C,4D, Time-dependent effects of ps42DNA-AAVS1 on AsCpf1-mediated gene cutting at the *AAVS1* locus (4C), and ps42DNA-FANCF on AsCpf1-mediated gene cutting at the *FANCF* locus (4D). Figure 4E, Time-dependent effects of ps42DNA on AsCpf1-mediated *DNMT1* gene cleavage in Hep3B cells. Figure 4F, Time-dependent effects of Lbps42DNA on LbCpf1-mediated gene cutting at the *DNMT1* locus in HEK293T cells. Indels were determined by the T7E1 cleavage assay, normalized to that of the treatment with wild-type crRNA and AsCpf1 mRNA, and plotted versus time or dose. The lane marked with "×" is excluded for calculation of gene cutting efficiency. The asterisk denotes the non-specific band. The grey and black arrows denote the intact and cleaved product, respectively.

FIGS. 5A-5E. Gene cutting efficiency of fluorescently labeled crRNA and variants in human cells. Figure 5A, Schematic illustration of fluorescently labeled crRNA and variants. The light grey letters denote the unmodified RNA base. The black letter denotes unmodified DNA base. The dark grey letters denote PS-linkage modified DNA (see ps42DNA-Cy5crRNA). Figure 5B, Gene cutting efficiency of Cy5crRNA (left) and crRNA-Cy3uDNA (right) on *DNMT1* locus in HEK293T cells. Figure 5C, Effects of Cy3uDNA on AsCpf1-mediated *DNMT1* gene cleavage

in HEK293T cells. Figure 5D, Gene cutting efficiency of crRNA-Cy3uDNA-AAVS1 on *AAVS1* locus (left) and crRNA-Cy3uDNA-FANCF on *FANCF* locus (right) in HEK293T cells. Figure 5E, Gene cutting efficiency of crRNA-intCy3uDNA and crRNA-3'Cy3uDNA on *DNMT1* locus in HEK293T cells. Indels were determined by the T7E1 cleavage assay, normalized to that of the treatment with wild-type crRNA and AsCpf1 mRNA. The grey and black arrows denote the intact and cleaved product, respectively.

DETAILED DESCRIPTION

The inventors have designed and synthesized a novel array of nucleic acid molecules for use as adjustable switches to upregulate, downregulate, and completely inactivate the cleavage activity of Cpf1 in the CRISPR genome editing system. In some embodiments, these nucleic acid molecules comprise chemically modified nucleotides and/or chimeric DNA/RNA guide molecules.

Reference will now be made in detail to the embodiments of the invention, examples of which are illustrated in the drawings and the examples. This invention may, however, be embodied in many different forms and should not be construed as limited to the embodiments set forth herein.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this invention belongs. The following definitions are provided for the full understanding of terms used in this specification.

Terminology

As used herein, the article "a," "an," and "the" means "at least one," unless the context in which the article is used clearly indicates otherwise.

The term "nucleic acid" as used herein means a polymer composed of nucleotides, e.g. deoxyribonucleotides or ribonucleotides.

The terms "ribonucleic acid" and "RNA" as used herein mean a polymer composed of ribonucleotides.

The terms "deoxyribonucleic acid" and "DNA" as used herein mean a polymer composed of deoxyribonucleotides.

The term "oligonucleotide" denotes single- or double-stranded nucleotide multimers of from about 2 to up to about 100 nucleotides in length. Suitable oligonucleotides may be prepared by the phosphoramidite method described by Beaucage and Carruthers, *Tetrahedron Lett.*, 22:1859-1862 (1981), or by the triester method according to Matteucci, et al., *J. Am. Chem. Soc.*,

103:3185 (1981), both incorporated herein by reference, or by other chemical methods using either a commercial automated oligonucleotide synthesizer or VLSIPS™ technology. When oligonucleotides are referred to as "double-stranded," it is understood by those of skill in the art that a pair of oligonucleotides exist in a hydrogen-bonded, helical array typically associated with, for example, DNA. In addition to the 100% complementary form of double-stranded oligonucleotides, the term "double-stranded," as used herein is also meant to refer to those forms which include such structural features as bulges and loops, described more fully in such biochemistry texts as Stryer, *Biochemistry*, Third Ed., (1988), incorporated herein by reference for all purposes.

The term "polynucleotide" refers to a single or double stranded polymer composed of nucleotide monomers. In some embodiments, the polynucleotide is composed of nucleotide monomers of generally greater than 100 nucleotides in length and up to about 8,000 or more nucleotides in length.

The term "polypeptide" refers to a compound made up of a single chain of D- or L-amino acids or a mixture of D- and L-amino acids joined by peptide bonds.

The term "complementary" refers to the topological compatibility or matching together of interacting surfaces of a probe molecule and its target. Thus, the target and its probe can be described as complementary, and furthermore, the contact surface characteristics are complementary to each other.

The term "hybridization" refers to a process of establishing a non-covalent, sequence-specific interaction between two or more complementary strands of nucleic acids into a single hybrid, which in the case of two strands is referred to as a duplex.

The term "anneal" refers to the process by which a single-stranded nucleic acid sequence pairs by hydrogen bonds to a complementary sequence, forming a double-stranded nucleic acid sequence, including the reformation (renaturation) of complementary strands that were separated by heat (thermally denatured).

The term "melting" refers to the denaturation of a double-stranded nucleic acid sequence due to high temperatures, resulting in the separation of the double strand into two single strands by breaking the hydrogen bonds between the strands.

The term "target" refers to a molecule that has an affinity for a given probe. Targets may be naturally-occurring or man-made molecules. Also, they can be employed in their unaltered state or as aggregates with other species.

The term "promoter" or "regulatory element" refers to a region or sequence determinants located upstream or downstream from the start of transcription and which are involved in

recognition and binding of RNA polymerase and other proteins to initiate transcription. Promoters need not be of bacterial origin, for example, promoters derived from viruses or from other organisms can be used in the compositions, systems, or methods described herein. The term "regulatory element" is intended to include promoters, enhancers, internal ribosomal entry sites (IRES), and other expression control elements (e.g. transcription termination signals, such as polyadenylation signals and poly-U sequences). Such regulatory elements are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990). Regulatory elements include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). A tissue-specific promoter may direct expression primarily in a desired tissue of interest, such as muscle, neuron, bone, skin, blood, specific organs (e.g. liver, pancreas), or particular cell types (e.g. lymphocytes). Regulatory elements may also direct expression in a temporal-dependent manner, such as in a cell-cycle dependent or developmental stage-dependent manner, which may or may not also be tissue or cell-type specific. In some embodiments, a vector comprises one or more pol III promoter (e.g. 1, 2, 3, 4, 5, or more pol I promoters), one or more pol II promoters (e.g. 1, 2, 3, 4, 5, or more pol II promoters), one or more pol I promoters (e.g. 1, 2, 3, 4, 5, or more pol I promoters), or combinations thereof. Examples of pol III promoters include, but are not limited to, U6 and H1 promoters. Examples of pol II promoters include, but are not limited to, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g., Boshart et al, Cell, 41:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1α promoter. Also encompassed by the term "regulatory element" are enhancer elements, such as WPRE; CMV enhancers; the R-U5′ segment in LTR of HTLV-I (Mol. Cell. Biol., Vol. 8(1), p. 466-472, 1988); SV40 enhancer; and the intron sequence between exons 2 and 3 of rabbit β-globin (Proc. Natl. Acad. Sci. USA., Vol. 78(3), p. 1527-31, 1981). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression desired, etc.

The term "recombinant" refers to a human manipulated nucleic acid (e.g. polynucleotide) or a copy or complement of a human manipulated nucleic acid (e.g. polynucleotide), or if in reference to a protein (i.e, a "recombinant protein"), a protein encoded by a recombinant nucleic acid (e.g. polynucleotide). In embodiments, a recombinant expression cassette comprising a promoter operably linked to a second nucleic acid (e.g. polynucleotide) may include a promoter

that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation (e.g., by methods described in Sambrook et al., *Molecular Cloning—A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1989) or Current Protocols in Molecular Biology Volumes 1-3, John Wiley & Sons, Inc. (1994-1998)). In another example, a recombinant expression cassette may comprise nucleic acids (e.g. polynucleotides) combined in such a way that the nucleic acids (e.g. polynucleotides) are extremely unlikely to be found in nature. For instance, human manipulated restriction sites or plasmid vector sequences may flank or separate the promoter from the second nucleic acid (e.g. polynucleotide). One of skill will recognize that nucleic acids (e.g. polynucleotides) can be manipulated in many ways and are not limited to the examples above.

The term "expression cassette" refers to a nucleic acid construct, which when introduced into a host cell, results in transcription and/or translation of a RNA or polypeptide, respectively. In embodiments, an expression cassette comprising a promoter operably linked to a second nucleic acid (e.g. polynucleotide) may include a promoter that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation (e.g., by methods described in Sambrook et al., *Molecular Cloning—A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1989) or Current Protocols in Molecular Biology Volumes 1-3, John Wiley & Sons, Inc. (1994-1998)). In some embodiments, an expression cassette comprising a terminator (or termination sequence) operably linked to a second nucleic acid (e.g. polynucleotide) may include a terminator that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation. In some embodiments, the expression cassette comprises a promoter operably linked to a second nucleic acid (e.g. polynucleotide) and a terminator operably linked to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation. In some embodiments, the expression cassette comprises an endogenous promoter. In some embodiments, the expression cassette comprises an endogenous terminator. In some embodiments, the expression cassette comprises a synthetic (or non-natural) promoter. In some embodiments, the expression cassette comprises a synthetic (or non-natural) terminator.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%,94%, 95%, 96%, 97%, 98%, 99% or higher identity over a specified region when compared and aligned for maximum correspondence over a comparison window or designated

region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 10 amino acids or 20 nucleotides in length, or more preferably over a region that is 10-50 amino acids or 20-50 nucleotides in length. As used herein, percent (%) amino acid sequence identity is defined as the percentage of amino acids in a candidate sequence that are identical to the amino acids in a reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared can be determined by known methods.

For sequence comparisons, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nuc. Acids Res.* 25:3389-3402, and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score

can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=−4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=−4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01.

The phrase "codon optimized" as it refers to genes or coding regions of nucleic acid molecules for the transformation of various hosts, refers to the alteration of codons in the gene or coding regions of polynucleic acid molecules to reflect the typical codon usage of a selected organism without altering the polypeptide encoded by the DNA. Such optimization includes replacing at least one, or more than one, or a significant number, of codons with one or more codons that are more frequently used in the genes of that selected organism.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are near each other, and, in the case of a secretory leader, contiguous and in reading phase. However, operably linked nucleic acids (e.g. enhancers and coding sequences)

do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. In embodiments, a promoter is operably linked with a coding sequence when it is capable of affecting (e.g. modulating relative to the absence of the promoter) the expression of a protein from that coding sequence (i.e., the coding sequence is under the transcriptional control of the promoter).

The term "nucleobase" refers to the part of a nucleotide that bears the Watson/Crick base-pairing functionality. The most common naturally-occurring nucleobases, adenine (A), guanine (G), uracil (U), cytosine (C), and thymine (T) bear the hydrogen-bonding functionality that binds one nucleic acid strand to another in a sequence specific manner.

As used throughout, by a "subject" (or a “host”) is meant an individual. Thus, the "subject" can include, for example, domesticated animals, such as cats, dogs, etc., livestock (e.g., cattle, horses, pigs, sheep, goats, etc.), laboratory animals (e.g., mouse, rabbit, rat, guinea pig, etc.) mammals, non-human mammals, primates, non-human primates, rodents, birds, reptiles, amphibians, fish, and any other animal. The subject can be a mammal such as a primate or a human.

The terms “guide RNA”, “gRNA”, “CRISPR RNA”, or “crRNA” are used interchangeably throughout the specification and refers to the RNA associated with one of the CRISPR gene editing systems. This crRNA (or guide RNA) consists of a 5’-handle and a guide segment. Cpf1 protein interacts with the pseudoknot structure formed by the 5’-handle of crRNA (or guide RNA). The guide segment possesses complementary binding with the target DNA sequences.

The term “about” as used herein when referring to a measurable value such as an amount, a percentage, and the like, is meant to encompass variations of ±20%, ±10%, ±5%, or ±1% from the measurable value.

Modified Nucleic Acids, Hybrid Guide RNAs, and Methods of Use

In one aspect, disclosed herein is an isolated nucleic acid comprising at least one chemically modified nucleotide, wherein the nucleic acid is complementary to a guide RNA of a CRISPR genome editing system.

In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof. In some embodiments, the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage. In some embodiments, the chemically modified phosphodiester linkage is phosphorothioate (PS).

In some embodiments, all the nucleotides comprise chemically modified phosphodiester linkages. In some embodiments, the chemically modified phosphodiester linkages are phosphorothioate (PS).

In some embodiments, the nucleic acid inhibits a nuclease activity of the CRISPR genome editing system. In some embodiments, the at least one chemically modified nucleotide is a chemically modified ribose. In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F). In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me). In some embodiments, the chemically modified ribose is 2'-fluoro (2'-F).

In some embodiments, the nucleic acid increases a nuclease activity of the CRISPR genome editing system.

In some embodiments, the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid is RNA. In some embodiments, the nucleic acid is DNA. In some embodiments, the nuclease activity is from a Cpf1 protein.

In one aspect, disclosed herein is a method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof. In some embodiments, the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage. In some embodiments, the chemically modified phosphodiester linkage is phosphorothioate (PS).

In some embodiments, all the nucleotides comprise chemically modified phosphodiester linkages. In some embodiments, the chemically modified phosphodiester linkages are phosphorothioate (PS).

In some embodiments, the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid is RNA. In some embodiments, the nucleic acid is DNA. In some embodiments, the nuclease activity is from a Cpf1 protein.

In another aspect, disclosed herein is a method for increasing the nuclease activity of a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid increases the activity of the nuclease of the CRISPR genome editing system.

In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof. In some embodiments, the at least one chemically modified nucleotide is a chemically modified ribose. In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F). In some embodiments, the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me). In some embodiments, the chemically modified ribose is 2'-fluoro (2'-F).

In some embodiments, the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid is RNA. In some embodiments, the nucleic acid is DNA. In some embodiments, the nuclease activity is from a Cpf1 protein.

In yet a further aspect, disclosed herein is a chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide, wherein the chimeric guide nucleic acid inhibits a nuclease activity of a CRISPR genome editing system.

In some embodiments, the nucleic acid is comprised of at least 5% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 10% DNA nucleotides. In some

embodiments, the nucleic acid is comprised of at least 30% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 50% DNA nucleotides.

In some embodiments, the nuclease activity is from a Cpf1 protein. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid comprises at least one chemically modified nucleotide. In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

In one aspect, disclosed herein is a method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide; and

wherein the chimeric guide nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

In some embodiments, the nucleic acid is comprised of at least 5% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 10% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 30% DNA nucleotides. In some embodiments, the nucleic acid is comprised of at least 50% DNA nucleotides.

In some embodiments, the nuclease activity is from a Cpf1 protein. In some embodiments, the nucleic acid is about 10 to about 43 nucleotides in length.

In some embodiments, the nucleic acid comprises at least one chemically modified nucleotide. In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

In some embodiments, the CRISPR genome editing system comprises:

a) a guide RNA that hybridizes with a target sequence of a DNA molecule in a eukaryotic cell that contains the DNA molecule, and

b) a DNA vector comprising a regulatory element operable in a eukaryotic cell operably linked to a nucleotide sequence encoding a Cpf1 protein; an mRNA encoding a Cpf1 protein; or a Cpf1 protein.

In one aspect, disclosed herein is a method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

In another aspect, disclosed herein is a method for increasing the nuclease activity of a CRISPR genome editing system in a cell comprising:

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid increases the activity of the nuclease of the CRISPR genome editing system.

In one aspect, disclosed herein is an isolated deoxyribonucleic acid, wherein the deoxyribonucleic acid is complementary to a guide RNA of a CRISPR genome editing system, wherein the deoxyribonucleic acid inhibits a nuclease activity of the CRISPR genome editing system.

The class II CRISPR system bearing single protein effector, such as CRISPR-Cas9 and CRISPR-Cpf1, has been shown to induce precise genome cleavage in human cells. Given that guide RNA (gRNA) plays a critical role in capturing endonucleases and subsequent targeting to specific genomic regions, a series of short or full-length oligodeoxynucleotides (ODNs) that are complementary with guide DNA, and forged DNA-RNA heteroduplexes via base-pairing between ODNs and guide RNA were designed and disclosed herein.

In some embodiments, disclosed herein is a nucleic acid composition comprising an oligonucleotide selected from the group consisting of any of the oligonucleotides listed in Table 1. In some embodiments, disclosed herein is an isolated nucleic acid selected from the group consisting of any of oligodeoxynucleotides (ODNs) listed in Table 1. Also disclosed herein is an isolated hybrid guide RNA composition as described herein and a method of inducing genome cleavage as described herein. In some embodiments, disclosed herein a nucleic acid (hybrid guide RNA) composition selected from the group consisting of any of the oligonucleotides shown Figure

1. Also provided are methods for eukaryotic genome editing utilizing nucleic acid molecules in complex with a class II CRISPR endonuclease, including Cpfl or Cas9, as described herein.

In some embodiments, the nuclease activity is from a Cpf1 protein. In some embodiments, the nuclease activity is from a Cas9 protein.

In some embodiments, the nucleic acid molecule (for example, DNA) is complementary to the entire guide RNA molecule. The complementary molecule forms a double stranded DNA/RNA hybrid guide molecule with the guide RNA (hybrid guide RNA). In some embodiments, the nucleic acid molecule is complementary over a portion of the guide RNA molecule. In some embodiments, the nucleic acid molecule is complementary to the guide portion of the guide RNA molecule. In some embodiments, the nucleic acid molecule is complementary to the handle portion of the guide RNA molecule. In some embodiments, the nucleic acid molecule is complementary over at least 10 nucleotides (for example at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40) of the guide RNA molecule. In some embodiments, the nucleic acid molecule is complementary over about 10 to about 20 nucleotides, over about 15 to about 30 nucleotides, over about 20 to about 35 nucleotides of the guide RNA molecule.

Chemically Modified Nucleotides

In some embodiments, the nucleic acids disclosed herein comprise at least one chemically modified nucleotide. In some embodiments, the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

In some embodiments, the mRNA encoding a Cpf1 protein comprises at least one chemically modified nucleotide selected from a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

In some embodiments, the guide RNA comprises at least one chemically modified nucleotide selected from a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

Chemically modified nucleobases

In one embodiment, the at least one chemically modified nucleotide is a chemically modified nucleobase.

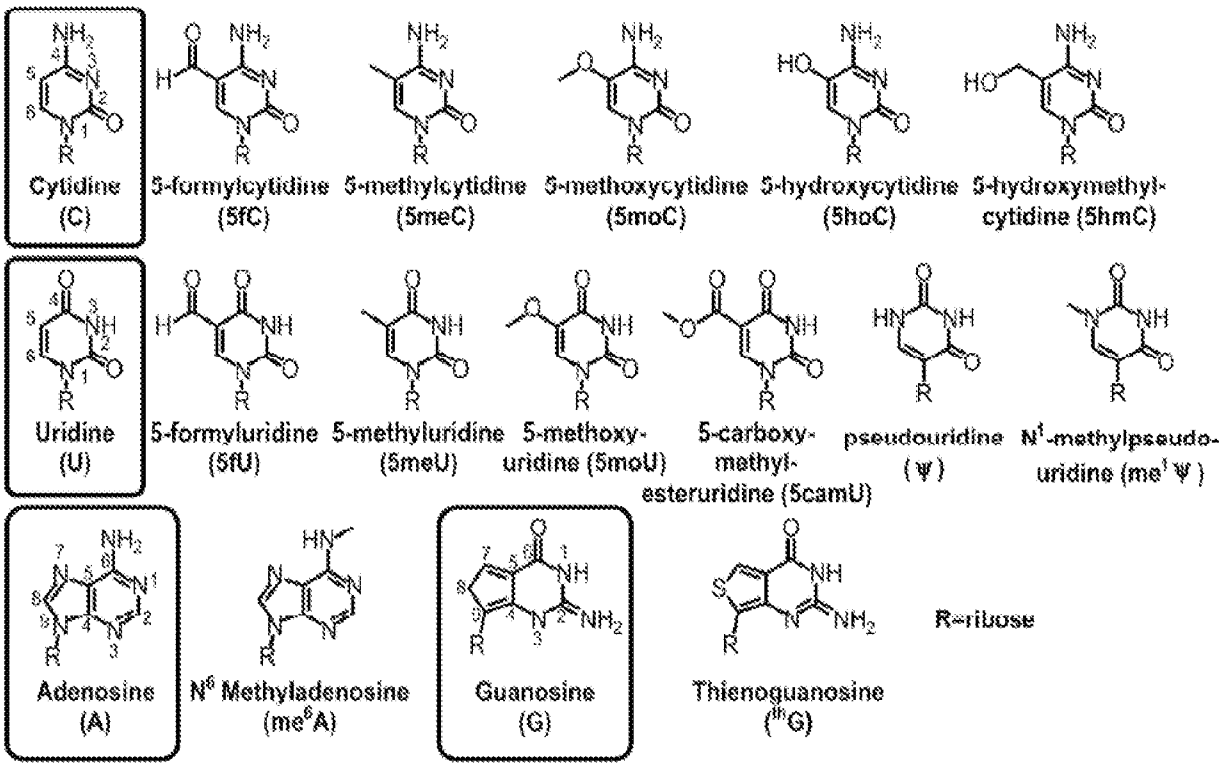
In one embodiment, the chemically modified nucleobase is selected from 5-formylcytidine (5fC), 5-methylcytidine (5meC), 5-methoxycytidine (5moC), 5-hydroxycytidine (5hoC), 5-hydroxymethylcytidine (5hmC), 5-formyluridine (5fU), 5-methyluridine (5-meU), 5-

methoxyuridine (5moU), 5-carboxymethylesteruridine (5camU), pseudouridine (Ψ), N^1-methylpseudouridine ($me^1\Psi$), N^6-methyladenosine (me^6A), or thienoguanosine (^{th}G).

In some embodiments, the chemically modified nucleobase is selected from 5-methoxyuridine (5moU), pseudouridine (Ψ), and N^1-methylpseudouridine ($me^1\Psi$). In some embodiments, the chemically modified nucleobase is 5-methoxyuridine (5moU). In some embodiments, the chemically modified nucleobase is pseudouridine (Ψ). In some embodiments, the chemically modified nucleobase is N^1-methylpseudouridine ($me^1\Psi$).

In some embodiments, the at least one chemically modified nucleobase comprises N^1-methylpseudouridine ($me^1\Psi$) and 5-methylcytidine (5meC). In some embodiments, the at least one chemically modified nucleobase comprises pseudouridine (Ψ) and 5-methylcytidine (5meC). In some embodiments, the at least one chemically modified nucleobase comprises 5-methyluridine (5-meU) and 5-methoxycytidine (5moC). In some embodiments, the at least one chemically modified nucleobase comprises 5-methyluridine (5-meU) and 5-hydroxymethylcytidine (5hmC).

The structures of these modified nucleobases are shown below:



In addition to a chemically modified nucleobase in the complementary RNAs that form hybrid guide RNAs and/or in the novel chimeric nucleic acids disclosed herein, a chemically

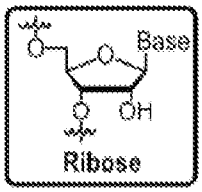
modified nucleobase can also be used in the mRNA encoding a Cpf1 protein and/or the guide RNA of the CRISPR genome editing systems. In some embodiments, the mRNA encoding a Cpf1 protein comprises a chemically modified nucleobase. In some embodiments, the guide RNA comprises a chemically modified nucleobase.

Chemically modified ribose moieties

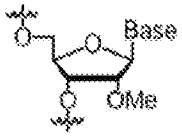
In one embodiment, the at least one chemically modified nucleotide is a chemically modified ribose.

In one embodiment, the chemically modified ribose is selected from 2′-*O*-methyl (2′-*O*-Me), 2′-Fluoro (2′-F), 2′-deoxy-2′-fluoro-beta-D-arabino-nucleic acid (2′F-ANA), 4′-S, 4′-SFANA, 2′-azido, UNA, 2′-*O*-methoxy-ethyl (2′-*O*-ME), 2′-*O*-Allyl, 2′-*O*-Ethylamine, 2′-*O*-Cyanoethyl, Locked nucleic acid (LAN), Methylene-cLAN, N-MeO-amino BNA, or N-MeO-aminooxy BNA. In one embodiment, the chemically modified ribose is selected from 2′-O-methyl (2′-O-Me) or 2′-Fluoro (2′-F). In one embodiment, the chemically modified ribose is 2′-O-methyl (2′-O-Me). In one embodiment, the chemically modified ribose is 2′-Fluoro (2′-F).

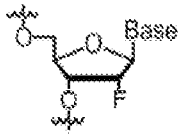
The structures of these modified riboses are shown below:



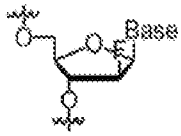
Ribose



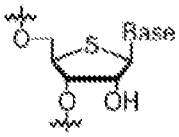
2'-O-methyl (2'-O-Me)



2'-Fluoro (2'-F)



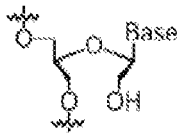
2'-deoxy-2'-fluoro-beta-D-arabino-nucleic acid (2'F-ANA)



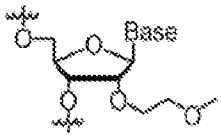
4'-S

4'-SFANA

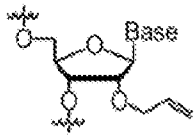
2'-azido



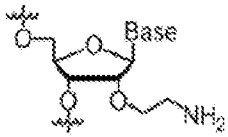
UNA



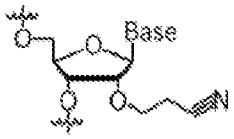
2'-O-methoxy-ethyl (2'-O-ME)



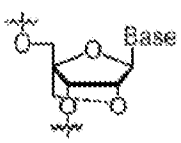
2'-O-Allyl



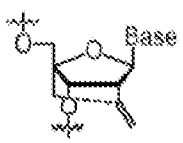
2'-O-Ethylamine



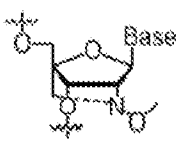
2'-O-Cyanoethyl



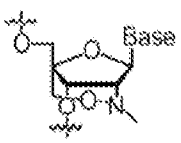
Locked nucleic acid (LAN)



Methylene-cLAN



N-MeO-amino BNA



N-MeO-aminooxy BNA

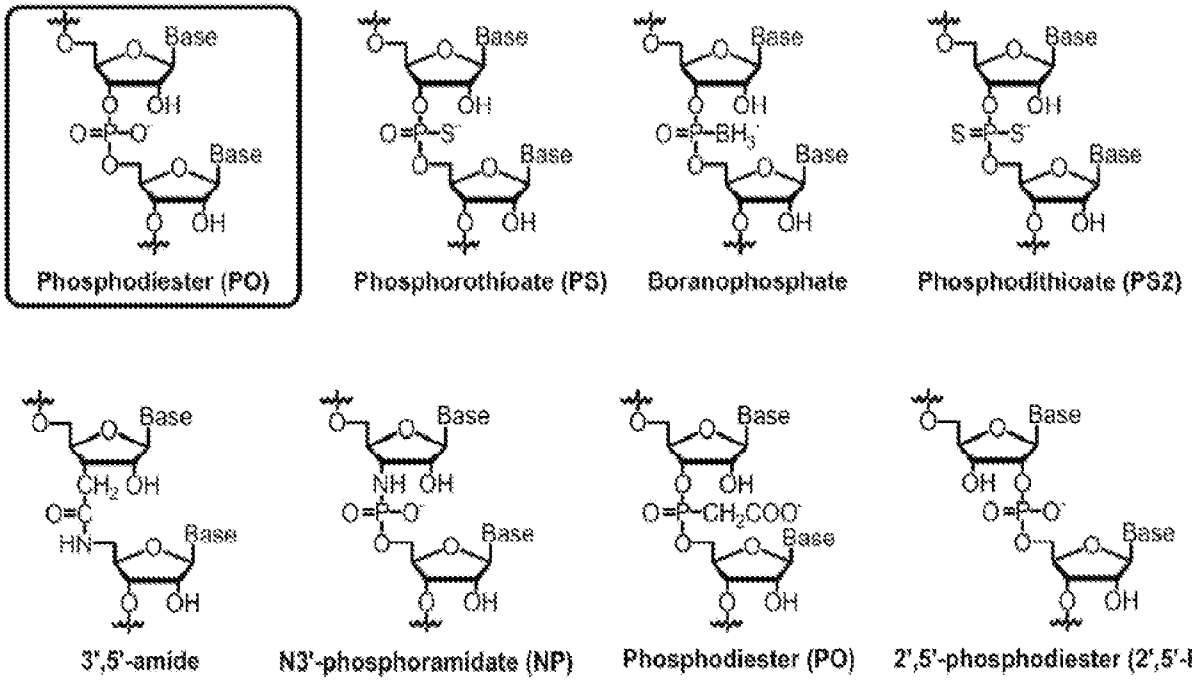
In addition to a chemically modified ribose in the complementary RNAs that form hybrid guide RNAs and/or in the novel chimeric nucleic acids disclosed herein, a chemically modified ribose can also be used in the mRNA encoding a Cpf1 protein and/or the guide RNA of the CRISPR genome editing systems. In some embodiments, the mRNA encoding a Cpf1 protein comprises a chemically modified ribose. In some embodiments, the guide RNA comprises a chemically modified ribose.

Chemically modified phosphodiester backbone

In one embodiment, the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage.

In one embodiment, the chemically modified phosphodiester linkage is selected from phosphorothioate (PS), boranophosphate, phosphodithioate (PS2), 3′,5′-amide, N3′-phosphoramidate (NP), Phosphodiester (PO), or 2′,5′-phosphodiester (2′,5′-PO). In one embodiment, the chemically modified phosphodiester linkage is phosphorothioate.

The structures of these modified phosphodiester linkages are shown below:



In addition to a chemically modified phosphodiester linkage in the complementary RNAs that form hybrid guide RNAs and/or in the novel chimeric nucleic acids disclosed herein, a chemically modified phosphodiester linkage can also be used in the mRNA encoding a Cpf1

protein and/or the guide RNA of the CRISPR genome editing systems. In some embodiments, the mRNA encoding a Cpf1 protein comprises a chemically modified phosphodiester linkage. In some embodiments, the guide RNA comprises a chemically modified phosphodiester linkage.

Cpf1 protein

In one embodiment, the Cpf1 protein is encoded by SEQ ID NO:1. This sequence can be codon optimized, can differ due to the degeneracy of the genetic code, can be similar, or share substantial identity, to SEQ ID NO:1, but still retain nuclease activity.

AsCpf1 sequence (SEQ ID NO:1)

ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCACACA
GTTCGAGGGCTTTACCAACCTGTATCAGGTGAGCAAGACACTGCGGTTTGAGCTGAT
CCCACAGGGCAAGACCCTGAAGCACATCCAGGAGCAGGGCTTCATCGAGGAGGACA
AGGCCCGCAATGATCACTACAAGGAGCTGAAGCCCATCATCGATCGGATCTACAAG
ACCTATGCCGACCAGTGCCTGCAGCTGGTGCAGCTGGATTGGGAGAACCTGAGCGC
CGCCATCGACTCCTATAGAAAGGAGAAAACCGAGGAGACAAGGAACGCCCTGATCG
AGGAGCAGGCCACATATCGCAATGCCATCCACGACTACTTCATCGGCCGGACAGAC
AACCTGACCGATGCCATCAATAAGAGACACGCCGAGATCTACAAGGGCCTGTTCAA
GGCCGAGCTGTTTAATGGCAAGGTGCTGAAGCAGCTGGGCACCGTGACCACAACCG
AGCACGAGAACGCCCTGCTGCGGAGCTTCGACAAGTTTACAACCTACTTCTCCGGCT
TTTATGAGAACAGGAAGAACGTGTTCAGCGCCGAGGATATCAGCACAGCCATCCCA
CACCGCATCGTGCAGGACAACTTCCCCAAGTTTAAGGAGAATTGTCACATCTTCACA
CGCCTGATCACCGCCGTGCCCAGCCTGCGGGAGCACTTTGAGAACGTGAAGAAGGC
CATCGGCATCTTCGTGAGCACCTCCATCGAGGAGGTGTTTTCCTTCCCTTTTTATAAC
CAGCTGCTGACACAGACCCAGATCGACCTGTATAACCAGCTGCTGGGAGGAATCTC
TCGGGAGGCAGGCACCGAGAAGATCAAGGGCCTGAACGAGGTGCTGAATCTGGCCA
TCCAGAAGAATGATGAGACAGCCCACATCATCGCCTCCCTGCCACACAGATTCATCC
CCCTGTTTAAGCAGATCCTGTCCGATAGGAACACCCTGTCTTTCATCCTGGAGGAGT
TTAAGAGCGACGAGGAAGTGATCCAGTCCTTCTGCAAGTACAAGACACTGCTGAGA
AACGAGAACGTGCTGGAGACAGCCGAGGCCCTGTTTAACGAGCTGAACAGCATCGA
CCTGACACACATCTTCATCAGCCACAAGAAGCTGGAGACAATCAGCAGCGCCCTGT
GCGACCACTGGGATACACTGAGGAATGCCCTGTATGAGCGGAGAATCTCCGAGCTG
ACAGGCAAGATCACCAAGTCTGCCAAGGAGAAGGTGCAGCGCAGCCTGAAGCACG
AGGATATCAACCTGCAGGAGATCATCTCTGCCGCAGGCAAGGAGCTGAGCGAGGCC
TTCAAGCAGAAAACCAGCGAGATCCTGTCCCACGCACACGCCGCCCTGGATCAGCC
ACTGCCTACAACCCTGAAGAAGCAGGAGGAGAAGGAGATCCTGAAGTCTCAGCTGG
ACAGCCTGCTGGGCCTGTACCACCTGCTGGACTGGTTTGCCGTGGATGAGTCCAACG
AGGTGGACCCCGAGTTCTCTGCCCGGCTGACCGGCATCAAGCTGGAGATGGAGCCT
TCTCTGAGCTTCTACAACAAGGCCAGAAATTATGCCACCAAGAAGCCCTACTCCGTG
GAGAAGTTCAAGCTGAACTTTCAGATGCCTACACTGGCCTCTGGCTGGGACGTGAAT
AAGGAGAAGAACAATGGCGCCATCCTGTTTGTGAAGAACGGCCTGTACTATCTGGG

CATCATGCCAAAGCAGAAGGGCAGGTATAAGGCCCTGAGCTTCGAGCCCACAGAGA
AAACCAGCGAGGGCTTTGATAAGATGTACTATGACTACTTCCCTGATGCCGCCAAGA
TGATCCCAAAGTGCAGCACCCAGCTGAAGGCCGTGACAGCCCACTTTCAGACCCAC
ACAACCCCCATCCTGCTGTCCAACAATTTCATCGAGCCTCTGGAGATCACAAAGGAG
ATCTACGACCTGAACAATCCTGAGAAGGAGCCAAAGAAGTTTCAGACAGCCTACGC
CAAGAAAACCGGCGACCAGAAGGGCTACAGAGAGGCCCTGTGCAAGTGGATCGAC
TTCACAAGGGATTTTCTGTCCAAGTATACCAAGACAACCTCTATCGATCTGTCTAGC
CTGCGGCCATCCTCTCAGTATAAGGACCTGGGCGAGTACTATGCCGAGCTGAATCCC
CTGCTGTACCACATCAGCTTCCAGAGAATCGCCGAGAAGGAGATCATGGATGCCGT
GGAGACAGGCAAGCTGTACCTGTTCCAGATCTATAACAAGGACTTTGCCAAGGGCC
ACCACGGCAAGCCTAATCTGCACACACTGTATTGGACCGGCCTGTTTTCTCCAGAGA
ACCTGGCCAAGACAAGCATCAAGCTGAATGGCCAGGCCGAGCTGTTCTACCGCCCT
AAGTCCAGGATGAAGAGGATGGCACACCGGCTGGGAGAGAAGATGCTGAACAAGA
AGCTGAAGGATCAGAAAACCCCAATCCCCGACACCCTGTACCAGGAGCTGTACGAC
TATGTGAATCACAGACTGTCCCACGACCTGTCTGATGAGGCCAGGGCCCTGCTGCCC
AACGTGATCACCAAGGAGGTGTCTCACGAGATCATCAAGGATAGGCGCTTTACCAG
CGACAAGTTCTTTTTCCACGTGCCTATCACACTGAACTATCAGGCCGCCAATTCCCC
ATCTAAGTTCAACCAGAGGGTGAATGCCTACCTGAAGGAGCACCCCGAGACACCTA
TCATCGGCATCGATCGGGGCGAGAGAAACCTGATCTATATCACAGTGATCGACTCC
ACCGGCAAGATCCTGGAGCAGCGGAGCCTGAACACCATCCAGCAGTTTGATTACCA
GAAGAAGCTGGACAACAGGGAGAAGGAGAGGGTGGCAGCAAGGCAGGCCTGGTCT
GTGGTGGGCACAATCAAGGATCTGAAGCAGGGCTATCTGAGCCAGGTCATCCACGA
GATCGTGGACCTGATGATCCACTACCAGGCCGTGGTGGTGCTGGAGAACCTGAATTT
CGGCTTTAAGAGCAAGAGGACCGGCATCGCCGAGAAGGCCGTGTACCAGCAGTTCG
AGAAGATGCTGATCGATAAGCTGAATTGCCTGGTGCTGAAGGACTATCCAGCAGAG
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CGGCGACTTCATCCTGCACTTTAAGATGAACAGAAATCTGTCCTTCCAGAGGGGCCT
GCCCGGCTTTATGCCTGCATGGGATATCGTGTTCGAGAAGAACGAGACACAGTTTGA
CGCCAAGGGCACCCCTTTCATCGCCGGCAAGAGAATCGTGCCAGTGATCGAGAATC
ACAGATTCACCGGCAGATACCGGGACCTGTATCCTGCCAACGAGCTGATCGCCCTGC
TGGAGGAGAAGGGCATCGTGTTCAGGGATGGCTCCAACATCCTGCCAAAGCTGCTG
GAGAATGACGATTCTCACGCCATCGACACCATGGTGGCCCTGATCCGCAGCGTGCTG
CAGATGCGGAACTCCAATGCCGCCACAGGCGAGGACTATATCAACAGCCCCGTGCG
CGATCTGAATGGCGTGTGCTTCGACTCCCGGTTTCAGAACCCAGAGTGGCCCATGGA
CGCCGATGCCAATGGCGCCTACCACATCGCCCTGAAGGGCCAGCTGCTGCTGAATC
ACCTGAAGGAGAGCAAGGATCTGAAGCTGCAGAACGGCATCTCCAATCAGGACTGG
CTGGCCTACATCCAGGAGCTGCGCAACAAGCGTCCTGCTGCTACTAAGAAAGCTGG
TCAAGCTAAGAAAAGAAATAA(SEQ ID NO:1).

In one embodiment, the Cpf1 protein is encoded by SEQ ID NO:2. This sequence can be codon optimized, can differ due to the degeneracy of the genetic code, can be similar, or share substantial identity, to SEQ ID NO:2, but still retain nuclease activity.

LbCpf1 sequence (SEQ ID NO:2)

ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCAGCA
AGCTGGAGAAGTTTACAAACTGCTACTCCCTGTCTAAGACCCTGAGGTTCAAGGCCA
TCCCTGTGGGCAAGACCCAGGAGAACATCGACAATAAGCGGCTGCTGGTGGAGGAC
GAGAAGAGAGCCGAGGATTATAAGGGCGTGAAGAAGCTGCTGGATCGCTACTATCT
GTCTTTTATCAACGACGTGCTGCACAGCATCAAGCTGAAGAATCTGAACAATTACAT
CAGCCTGTTCCGGAAGAAAACCAGAACCGAGAAGGAGAATAAGGAGCTGGAGAAC
CTGGAGATCAATCTGCGGAAGGAGATCGCCAAGGCCTTCAAGGGCAACGAGGGCTA
CAAGTCCCTGTTTAAGAAGGATATCATCGAGACAATCCTGCCAGAGTTCCTGGACGA
TAAGGACGAGATCGCCCTGGTGAACAGCTTCAATGGCTTTACCACAGCCTTCACCGG
CTTCTTTGATAACAGAGAGAATATGTTTTCCGAGGAGGCCAAGAGCACATCCATCGC
CTTCAGGTGTATCAACGAGAATCTGACCCGCTACATCTCTAATATGGACATCTTCGA
GAAGGTGGACGCCATCTTTGATAAGCACGAGGTGCAGGAGATCAAGGAGAAGATCC
TGAACAGCGACTATGATGTGGAGGATTTCTTTGAGGGCGAGTTCTTTAACTTTGTGC
TGACACAGGAGGGCATCGACGTGTATAACGCCATCATCGGCGGCTTCGTGACCGAG
AGCGGCGAGAAGATCAAGGGCCTGAACGAGTACATCAACCTGTATAATCAGAAAAC
CAAGCAGAAGCTGCCTAAGTTTAAGCCACTGTATAAGCAGGTGCTGAGCGATCGGG
AGTCTCTGAGCTTCTACGGCGAGGGCTATACATCCGATGAGGAGGTGCTGGAGGTG
TTTAGAAACACCCTGAACAAGAACAGCGAGATCTTCAGCTCCATCAAGAAGCTGGA
GAAGCTGTTCAAGAATTTTGACGAGTACTCTAGCGCCGGCATCTTTGTGAAGAACGG
CCCCGCCATCAGCACAATCTCCAAGGATATCTTCGGCGAGTGGAACGTGATCCGGG
ACAAGTGGAATGCCGAGTATGACGATATCCACCTGAAGAAGAAGGCCGTGGTGACC
GAGAAGTACGAGGACGATCGGAGAAAGTCCTTCAAGAAGATCGGCTCCTTTTCTCT
GGAGCAGCTGCAGGAGTACGCCGACGCCGATCTGTCTGTGGTGGAGAAGCTGAAGG
AGATCATCATCCAGAAGGTGGATGAGATCTACAAGGTGTATGGCTCCTCTGAGAAG
CTGTTCGACGCCGATTTTGTGCTGGAGAAGAGCCTGAAGAAGAACGACGCCGTGGT
GGCCATCATGAAGGACCTGCTGGATTCTGTGAAGAGCTTCGAGAATTACATCAAGG
CCTTCTTTGGCGAGGGCAAGGAGACAAACAGGGACGAGTCCTTCTATGGCGATTTTG
TGCTGGCCTACGACATCCTGCTGAAGGTGGACCACATCTACGATGCCATCCGCAATT
ATGTGACCCAGAAGCCCTACTCTAAGGATAAGTTCAAGCTGTATTTTCAGAACCCTC
AGTTCATGGGCGGCTGGGACAAGGATAAGGAGACAGACTATCGGGCCACCATCCTG
AGATACGGCTCCAAGTACTATCTGGCCATCATGGATAAGAAGTACGCCAAGTGCCT
GCAGAAGATCGACAAGGACGATGTGAACGGCAATTACGAGAAGATCAACTATAAG
CTGCTGCCCGGCCCTAATAAGATGCTGCCAAAGGTGTTCTTTTCTAAGAAGTGGATG
GCCTACTATAACCCCAGCGAGGACATCCAGAAGATCTACAAGAATGGCACATTCAA
GAAGGGCGATATGTTTAACCTGAATGACTGTCACAAGCTGATCGACTTCTTTAAGGA
TAGCATCTCCCGGTATCCAAAGTGGTCCAATGCCTACGATTTCAACTTTTCTGAGAC
AGAGAAGTATAAGGACATCGCCGGCTTTTACAGAGAGGTGGAGGAGCAGGGCTATA
AGGTGAGCTTCGAGTCTGCCAGCAAGAAGGAGGTGGATAAGCTGGTGGAGGAGGG

CAAGCTGTATATGTTCCAGATCTATAACAAGGACTTTTCCGATAAGTCTCACGGCAC
ACCCAATCTGCACACCATGTACTTCAAGCTGCTGTTTGACGAGAACAATCACGGACA
GATCAGGCTGAGCGGAGGAGCAGAGCTGTTCATGAGGCGCGCCTCCCTGAAGAAGG
AGGAGCTGGTGGTGCACCCAGCCAACTCCCCTATCGCCAACAAGAATCCAGATAAT
CCCAAGAAAACCACAACCCTGTCCTACGACGTGTATAAGGATAAGAGGTTTTCTGA
GGACCAGTACGAGCTGCACATCCCAATCGCCATCAATAAGTGCCCCAAGAACATCT
TCAAGATCAATACAGAGGTGCGCGTGCTGCTGAAGCACGACGATAACCCCTATGTG
ATCGGCATCGATAGGGGCGAGCGCAATCTGCTGTATATCGTGGTGGTGGACGGCAA
GGGCAACATCGTGGAGCAGTATTCCCTGAACGAGATCATCAACAACTTCAACGGCA
TCAGGATCAAGACAGATTACCACTCTCTGCTGGACAAGAAGGAGAAGGAGAGGTTC
GAGGCCCGCCAGAACTGGACCTCCATCGAGAATATCAAGGAGCTGAAGGCCGGCTA
TATCTCTCAGGTGGTGCACAAGATCTGCGAGCTGGTGGAGAAGTACGATGCCGTGA
TCGCCCTGGAGGACCTGAACTCTGGCTTTAAGAATAGCCGCGTGAAGGTGGAGAAG
CAGGTGTATCAGAAGTTCGAGAAGATGCTGATCGATAAGCTGAACTACATGGTGGA
CAAGAAGTCTAATCCTTGTGCAACAGGCGGCGCCCTGAAGGGCTATCAGATCACCA
ATAAGTTCGAGAGCTTTAAGTCCATGTCTACCCAGAACGGCTTCATCTTTTACATCC
CTGCCTGGCTGACATCCAAGATCGATCCATCTACCGGCTTTGTGAACCTGCTGAAAA
CCAAGTATACCAGCATCGCCGATTCCAAGAAGTTCATCAGCTCCTTTGACAGGATCA
TGTACGTGCCCGAGGAGGATCTGTTCGAGTTTGCCCTGGACTATAAGAACTTCTCTC
GCACAGACGCCGATTACATCAAGAAGTGGAAGCTGTACTCCTACGGCAACCGGATC
AGAATCTTCCGGAATCCTAAGAAGAACAACGTGTTCGACTGGGAGGAGGTGTGCCT
GACCAGCGCCTATAAGGAGCTGTTCAACAAGTACGGCATCAATTATCAGCAGGGCG
ATATCAGAGCCCTGCTGTGCGAGCAGTCCGACAAGGCCTTCTACTCTAGCTTTATGG
CCCTGATGAGCCTGATGCTGCAGATGCGGAACAGCATCACAGGCCGCACCGACGTG
GATTTTCTGATCAGCCCTGTGAAGAACTCCGACGGCATCTTCTACGATAGCCGGAAC
TATGAGGCCCAGGAGAATGCCATCCTGCCAAAGAACGCCGACGCCAATGGCGCCTA
TAACATCGCCAGAAAGGTGCTGTGGGCCATCGGCCAGTTCAAGAAGGCCGAGGACG
AGAAGCTGGATAAGGTGAAGATCGCCATCTCTAACAAGGAGTGGCTGGAGTACGCC
CAGACCAGCGTGAAGCACAAGCGTCCTGCTGCTACTAAGAAAGCTGGTCAAGCTAA
GAAAAAGAAATAA(SEQ ID NO:2).

EXAMPLES

The following examples are set forth below to illustrate the compounds, compositions, methods, and results according to the disclosed subject matter. These examples are not intended to be inclusive of all aspects of the subject matter disclosed herein, but rather to illustrate representative methods and results. These examples are not intended to exclude equivalents and variations of the present invention which are apparent to one skilled in the art.

Example 1. Tunable oligonucleotide switches to modulate CRISPR-Cpf1 mediated genome editing

The CRISPR-Cpf1 system employs a single stranded CRISPR RNA (crRNA) to guide genome editing of target DNA sequences. To modulate genome editing activity of Cpf1, a series of crRNA variants were designed containing crRNA chimeras and duplexes. Single-stranded crRNA chimeras composed of mixed DNA and RNA nucleotides completely lost gene-cutting activity and crRNA is not well-tolerated for deoxynucleotide substitutions. Furthermore, crRNA duplexes formed by introduction of oligonucleotides (10-43 nucleotides) complementary to various regions of crRNA were capable of regulating activity of the Cpf1 endonuclease. For example, phosphorothioate (PS)-modified DNA/crRNA hybrid blocked the function of the Cpf1. More importantly, this PS-modified DNA was able to regulate Cpf1 activity in a time- and dose-dependent manner. Consequently, oligonucleotides provide tunable switches to modulate Cpf1 mediated genome editing.

Cpf1 (CRISPR from *Prevotella* and *Francisella* 1) is one of the CRISPR associated effector endonucleases, which induces double stranded DNA breaks under the guidance of a single CRISPR RNA (crRNA)[1]. The wild-type crRNA of CRISPR-Cpf1 system comprises a 5'-handle engaging Cpf1 recognition and a guide segment interacting with targeted DNA sequences through complimentary bindings[1-3]. Crystal structure of the Cpf1-crRNA-dsDNA complex uncovers the unique T-rich PAM recognition and cleavage mechanism by Cpf1[2,4-7]. Based on its unique gene editing properties, the CRISPR-Cpf1 system has recently been applied in diverse eukaryotic species including plants and animals to achieve targeted genome editing[8-18].

Although the CRISPR system offers a powerful platform for genome editing, a number of challenges exist for its therapeutic applications including gene editing efficiency and potential side effects[19]. Previously, extensive efforts have been made to improve gene editing efficiency[2,20-22]. Meanwhile, researchers investigated diverse approaches to modulate the activity of the CRISPR system. Especially, when severe side effects occur for the system, it is essential to prepare an effective and fast mechanism to switch off its function. Recently, anti-CRISPR proteins from bacteriophage or bacteria were discovered to inhibit the function of *Listeria monocytogenes* or *Neisseria meningitidis* CRISPR-Cas9[23,24]. In addition, multiple strategies such as chemical-, temperature- and light-triggered approaches were developed to regulate the CRISPR-Cas9 system[25,26]. However, no method is currently available to effectively regulate the CRISPR-Cpf1 system including upregulation, downregulation, and complete inactivation. In this example, an array of oligonucleotides is reported as adjustable switches to fine-tune the Cpf1 activity. First, in

order to understand the applicability of Cpf1 crRNA, three crRNA chimeras crRNA1-crRNA3 were designed (Fig. 1a), by substituting crRNA nucleotides (full crRNA, 5'-handle or guide segment) with their corresponding DNA bases. Their activity to mediate *DNMT1* gene cleavage in HEK293T cells was tested in the presence of AsCpf1 plasmid. The wild-type crRNA targeting *DNMT1* site 3 served as a control group. None of the three substitution patterns resulted in detectable gene cutting (Fig. 1b). Meanwhile, in the crystal structure of crRNA-AsCpf1-DNA complex, twenty-one nucleotides were identified which displayed trivial interactions with the Cpf1 and target DNA sequences. These nucleotides were replaced with DNA bases and synthesized crRNA4 chimera (Fig. 1a), which also showed undetectable activity (Fig. 1b). These results indicate that a relatively large portion of deoxynucleotides substitution on the crRNA is not favorable for Cpf1 mediated gene cutting.

Next, in attempts to effectively regulate Cpf1-mediated genome editing, oligonucleotides were likely important regulators for gene cutting activity of the Cpf1. Oligonucleotides are short single stranded DNA or RNA molecules which have been widely used for diverse application[27]. Given the crucial role of crRNA in the Cpf1-crRNA-DNA complex, a series of oligonucleotides complimentary to crRNA were designed and synthesized (10-43 nucleotides, Table 1). Their corresponding crRNA duplexes are shown in Fig. 3.

The first set is DNA-crRNA duplexes formed by hybridization of unmodified or phosphorothioate (PS)-modified DNA oligonucleotides with crRNA at different regions (crRNA5 to crRNA17, Fig. 1c). As shown in Fig. 1d, several crRNA duplexes including crRNA7, crRNA8, crRNA9, crRNA11 and crRNA14 showed comparable or slightly higher activity compared to the crRNA, while the rest duplexes crRNA5, crRNA6, crRNA10, crRNA12, crRNA13, crRNA15, crRNA16 and crRNA17 down-regulated the gene cutting. Interestingly, all three duplexes bearing PS linkages in DNA oligonucleotides dramatically reduced the gene cutting efficiency (Fig. 1d). Moreover, crRNA15 and crRNA17 completely blocked the function of Cpf1 (Fig. 1d). These results implied that oligonucleotides complimentary to the guide segment of crRNA may greatly affect the Cpf1 activity (crRNA15 and crRNA17 vs crRNA16). On the basis of DNA-crRNA duplexes, a second type of RNA-crRNA duplexes were examined (Fig. 1e). In this case, unmodified, 2'-*O*-methyl and 2'-fluoro RNA oligonucleotides were used to produce unmodified RNA-crRNA (crRNA18-crRNA20), 2'-fluoro RNA-crRNA (crRNA21 and crRNA22), and 2'-OMe RNA-crRNA (crRNA23 and crRNA24) duplexes. The activity of crRNA18-crRNA20 was comparable to that of crRNA (Fig. 1f), showing that unmodified RNA oligonucleotides had little effects on gene cutting activity. crRNA21 and crRNA22 dramatically reduced the activity (Fig.

1f), therefore 2'-fluoro RNA oligonucleotides may not be preferred modifications to enhance gene cutting.

Recent studies reported that co-delivery of chemically modified Cpf1 mRNA and crRNA improved genome editing efficiency of Cpf1[21]. In order to further examine the effects of crRNA15 and crRNA17, HEK293T cells were treated with these crRNAs in the presence of Ψ-modified Cpf1 mRNA. crRNA17 induced much lower gene cutting compared to crRNA, while crRNA15 fully switched off the Cpf1 activity under the same condition (Fig. 1g). These results show that PS-DNA covering both the handle and the guide segment of crRNA may be essential to fully inhibit the Cpf1 function. Hence, duplex crRNA15 containing 42-PS modified DNA oligonucleotide (termed as ps42DNA) was selected for further studies.

Considering the switch-off function of crRNA15, ps42DNA could serve as an effective inhibitor for the Cpf1 system. To further investigate this concept, three components (crRNA targeting *DNMT1* locus, AsCpf1 mRNA, and ps42DNA) were separately formulated using Lipofectamine 3000 reagent, and then treated HEK293T cells. Amazingly, the process of genome editing was effectively interrupted when ps42DNA was added together with the other two components (time = 0h, Fig. 2a). Subsequently, cells were treated with crRNA plus AsCpf1 mRNA followed by the addition of Lipofectamine 3000 complexed ps42DNA at different time points in order to evaluate inhibition properties of ps42DNA. As shown in Fig. 2a, ps42DNA-treated groups gradually lost its inhibition activity on gene cutting. At the 10h time point, ps42DNA was not able to affect the Cpf1 function. Next, the dose-dependency effects of ps42DNA were investigated at the 5h time point. ps42DNA was found to act in a dose-dependent manner to regulate gene cutting (Fig. 2b). These observations indicated that time to add ps42DNA and dose of ps42DNA are two crucial factors to exert its switch-off function.

To investigate the applicability of ps42DNA, two additional phosphorothioated oligonucleotides complementary to crRNAs targeting the *AAVS1* and *FANCF* genes were synthesized (termed ps42DNA-AAVS1 and ps42DNA-FANCF, respectively; Table 1)[28,29]. Consistent with the results mentioned above, both ps42DNA-AA and ps42DNA-FA showed time-dependent inhibition of gene cutting for their corresponding sequences. Their inhibition potency were higher than that of ps42DNA targeting *DNMT1*, as evidenced by undetectable cleavage at the time points 1, 3 and 5h (Fig. 2c,d). In addition to HEK293T cell line, the effects of ps42DNA in Hep3B cells was evaluated. Similarly, ps42DNA showed dramatic inhibition of gene cutting in Hep3B cells (Fig. 2e). Next, the same strategy for LbCpf1 was examined (another one of the Cpf1 orthologues) using Lbps42DNA, which exhibited strong inhibition of gene cutting in a time dependent manner similar to ps42DNA (Fig. 2f). Collectively, ps42 modified DNA

oligonucleotides are broadly applicable to inhibit Cpf1 activity at different gene loci in human cell lines.

In order to differentiate different components in the Cpf1 system, the 3'-end of crRNA was labeled with a Cy5 fluorescent probe and 5'-end of the unmodified DNA oligonucleotide (termed uDNA) with a Cy3 fluorescent probe (Fig. 5a). The function of Cy5-labeled crRNA (Cy5crRNA) and Cy3-labeled uDNA (Cy3 uDNA, hybridized into Cy3uDNA-crRNA duplex form, Fig. 5a) was tested in HEK293T cells. Cy5crRNA showed equivalent activity to crRNA, while Cy3uDNA-crRNA completely lost gene cutting function (Fig. 5b). Similarly, neither Cy3uDNA-AAVS1 nor Cy3uDNA-FANCF in dulpex form (Fig. 5a) was able to induce gene cleavage at the *AAVS1* and *FANCF* locus (Fig. 5c). Cy3uDNA may also be an inhibitor as psDNA for the Cpf1 system and its inhibition activity in HEK293T cells was tetsed. However, Cy3uDNA was unable to inhibit the gene cutting activity (Fig. 5d). In addition, the results were the same when Cy3 was installed in the middle or at the 3'-end of uDNA (intCy3uDNA and 3'Cy3uDNA; Fig. 5a,e). These findings revealed that Cy5 probe was feasible to label the 3'-end of crRNA, while Cy3 probe was not suitable for labeling the complementary oligonucleotide.

In summary, chimeric crRNAs comprised of both deoxynucleotides and ribonucleotides were investigated and their gene cleavage activity was tested. Current results show that a large amount of deoxynucleotide substitutions are not applicable to gene cutting by the AsCpf1. Moreover, a series of oligonucleotides were designed in order to regulate the activity of Cpf1. Intriguingly, phosphorothioate (ps)-modified DNA oligonucleotides are effective inhibitors for Cpf1. These PS-modified DNA oligonucleotides enabled us to switch off gene cutting of both AsCpf1 and LbCpf1. Also, similar phenomenon was observed in three genomic loci. The inhibition effect is time- and dose-dependent in human cells. Further studies on the mechanism of action are needed to elucidate the regulation effects of oligonucleotides on the Cpf1 function. Overall, these results provide new tools to understand and modulate the CRISPR-Cpf1 system. In cases of acute toxic effects of the CRISPR system occur in clinical use, this strategy can serve as an important antidote.

Methods

Generation of crRNA variants. crRNAs (Fig. 3) were synthesized by TriLink BioTechnologies via a solid-phase DNA/RNA synthesizer, purified by polyacrylamide gel electrophoresis system, and characterized by electrospray-ionization mass spectrometry. Chimeric crRNAs (crRNA1-crRNA4, Fig. 3) were obtained from Integrated DNA Technologies by substituting the crRNA sequence with corresponding DNA sequence at the following regions: 5'-

handle, guide segment or full-length wild-type crRNA. Unmodified oligonucleotides were obtained from Eurofins Genomics, and chemically modified oligonucleotides were obtained from Integrated DNA Technologies. crRNA duplexes (crRNA5-crRNA24, Fig. 3) were generated by hybridization of an equivalent molar of AsCpf1 crRNA targeting *DNMT1* and the customized oligonucleotides. The mixture was heated to 95°C for 30 s in Tris-EDTA buffer, followed by gradient cooling to room temperate at a rate of 0.1 °C/s. crRNA duplexes derived from AsCpf1 crRNAs targeting *AAVS* and *FANCF* locus, and LbCpf1 crRNAs targeting *DNMT1* locus were obtained through the same procedure. The sequences of all ONs used were listed in Table 1.

Gene cutting induced by crRNA variants. HEK293T or Hep3B cells (American Type Culture Collection, ATCC) were seeded in 24-well plates in medium (Dulbecco's Modified Eagle's Medium for HEK-293T cells and Eagle's Minimum Essential Medium for Hep3B cells) supplement with 10% FBS for 24h. Cells were then treated with 38 or 114 pmol crRNA variants formulated with Lipofectamine 3000 (Life Technologies) in Opti-MEM I reduced serum medium following manufacturer's instructions. Meanwhile, 500 or 1500 ng of Cpf1 plasmid (generously provided by Dr. F. Zhang) or mRNA (TriLink BioTechnologies) were formulated with the same protocol and add to each well. Cells treated with the wild-type crRNA plus Cpf1 served as the control group.

Time- and dose-dependent inhibition of Cpf1 activity. In order to study the effects of time interval, 2.5 times molar excess of PS-modified DNA over wild-type crRNA was added to cells treated with the wild-type crRNA plus Cpf1 mRNA at different time points (0, 1, 3, 5 and 10 h). In the case of dose-dependence study, crRNA and Cpf1 mRNA-treated cells were exposed with different molar of PS-modified DNA (the molar ratio of PS-DNA:crRNA ranged from 1:6.25 to 6.25:1) at 5 hrs. In both situations, the end point was 48 h after the addition of a combination of wild-type crRNA and Cpf1 mRNA.

T7E1 enzymatic cleavage assay. Two days after treatment, genomic DNA was harvested from treated cells with the DNeasy Blood & Tissue Kit (QIAGEN). Polymerase chain reactions (PCRs) were then performed using Q5 Hot-start High-Fidelity DNA Polymerase (New England Biolabs). Primers (Eurofins Genomics) flanking the targeted region were used. The PCR products were then annealed in NEBuffer 2 (50 mM NaCl, 10 mM Tris-HCl, 10 mM $MgCl_2$, 1 mM DTT, New England Biolabs) and subsequently digested by T7 Endonuclease I (T7E1, New England Biolabs) at 37°C for 30 min. The fraction cleaved was separated on 2% agarose gels, visualized on the ChemiDoc MP imaging system (Bio-Rad Laboratories), and analyzed by the Image Lab 5.2 analysis software (Bio-Rad Laboratories).

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Table 1. crRNAs and oligonucleotides

Name of oligonucleotides	Length (nt)	Sequence (5' to 3')
crRNA targeting *DNMT1*	43	UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC (SEQ ID NO:3)
Oligo 1 (crRNA1)	43	TAATTTCTACTCTTGTAGATCTGATGGTCCATGTCTGTTACTC (SEQ ID NO:4)
Oligo 2 (crRNA2)	43	TAATTTCTACTCTTGTAGAUCUGAUGGUCCAUGUCUGUUACUC (SEQ ID NO:5)
Oligo 3 (crRNA3)	43	UAAUUUCUACUCUUGUAGAUCTGATGGTCCATGTCTGTTACTC (SEQ ID NO:6)
Oligo 4 (crRNA4)	43	UAAUTTCUACUCTTGTAGAUCUGAUGGUCCATGUCUGUTACTC (SEQ ID NO:7)
Oligo 5 (crRNA5)	29	GAGTAACAGACATGGACCATCAGAAATTA (SEQ ID NO:8)
Oligo 6 (uDNA)	43	GAGTAACAGACATGGACCATCAGATCTACAAGAGTAGAAATTA (SEQ ID NO:9)
Oligo 7	20	ATCTACAAGAGTAGAAATTA (SEQ ID NO:10)
Oligo 8	10	GTAGAAATTA (SEQ ID NO:11)
Oligo 9	10	ATCTACAAGA (SEQ ID NO:12)
Oligo 10	23	GAGTAACAGACATGGACCATCAG (SEQ ID NO:13)
Oligo 11	10	GGACCATCAG (SEQ ID NO:14)
Oligo 12	13	GAGTAACAGACAT (SEQ ID NO:15)
Oligo 13	20	TAACAGACATGGACCATCAG (SEQ ID NO:16)
Oligo 14	10	TAACAGACAT (SEQ ID NO:17)
Oligo 15 (ps42DNA)	43	**GAGTAACAGACATGGACCATCAGATCTACAAGAGTAGAAATTA** (SEQ ID NO:18)
Oligo 16	20	**ATCTACAAGAGTAGAAATTA** (SEQ ID NO:19)
Oligo 17	23	**GAGTAACAGACATGGACCATCAG** (SEQ ID NO:20)
Oligo 18	43	GAGUAACAGACAUGGACCAUCAGAUCUACAAGAGUAGAAAUUA (SEQ ID NO:21)
Oligo 19	20	AUCUACAAGAGUAGAAAUUA (SEQ ID NO:22)
Oligo 20	13	GAGUAACAGACAU (SEQ ID NO:23)
Oligo 21	20	*AUCUACAAGAGUAGAAAUUA* (SEQ ID NO:24)
Oligo 22	13	*GAGUAACAGACAU* (SEQ ID NO:25)
Oligo 23	20	AUCUACAAGAGUAGAAAUUA (SEQ ID NO:33)
Oligo 24	13	GAGUAACAGACAU (SEQ ID NO:26)
Oligo 25	5	GAGUA
crRNA targeting *AAVS*	43	UAAUUUCUACUCUUGUAGAUCUUACGAUGGAGCCAGAGAGGAU (SEQ ID NO:27)
ps42DNA-AAVS1	43	**ATCCTCTCTGGCTCCATCGTAAGATCTACAAGAGTAGAAATTA** (SEQ ID NO:28)
crRNA targeting	43	UAAUUUCUACUCUUGUAGAUGUCGGCAUGGCCCC

FANCF		AUUCGCACG (SEQ ID NO:29)
ps42DNA-FANCF	43	**CGTGCGAATGGGGCCATGCCGACATCTACAAGAG TAGAAATTA** (SEQ ID NO:30)
LbcrRNA targeting *DNMT1*	43	AAUUUCUACUAAGUGUAGAUCUGAUGGUCCAUGU CUGUUACUC (SEQ ID NO:31)
Lbps42DNA	43	**GAGTAACAGACATGGACCATCAGATCTACAAGAG TAGAAATTA** (SEQ ID NO:32)

Unmodified RNA base is shown with underlined text. Unmodified DNA base is shown with unmodified text. PS-linkage modified DNA is shown with bold text. 2'-fluoro modified RNA is shown with italicized text. 2'-O-methyl modified RNA is shown with double-underlined text.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of skill in the art to which the disclosed invention belongs. Publications cited herein and the materials for which they are cited are specifically incorporated by reference.

Those skilled in the art will appreciate that numerous changes and modifications can be made to the preferred embodiments of the invention and that such changes and modifications can be made without departing from the spirit of the invention. It is, therefore, intended that the appended claims cover all such equivalent variations as fall within the true spirit and scope of the invention.

CLAIMS

We claim:

1. An isolated nucleic acid comprising at least one chemically modified nucleotide, wherein the nucleic acid is complementary to a guide RNA of a CRISPR genome editing system.
2. The nucleic acid of claim 1, wherein the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.
3. The nucleic acid of claim 2, wherein the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage.
4. The nucleic acid of claim 3, wherein the chemically modified phosphodiester linkage is phosphorothioate (PS).
5. The nucleic acid of claim 2, wherein all the nucleotides comprise chemically modified phosphodiester linkages.
6. The nucleic acid of claim 5, wherein the chemically modified phosphodiester linkages are phosphorothioate (PS).
7. The nucleic acid of any one of claims 3 to 6, wherein the nucleic acid inhibits a nuclease activity of the CRISPR genome editing system.
8. The nucleic acid of claim 2, wherein the at least one chemically modified nucleotide is a chemically modified ribose.
9. The nucleic acid of claim 8, wherein the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F).
10. The nucleic acid of claim 2, wherein all the nucleotides comprise chemically modified riboses.
11. The nucleic acid of claim 10, wherein the chemically modified riboses are 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F).
12. The nucleic acid of claim any one of claims 8 to 11, wherein the nucleic acid increases a nuclease activity of the CRISPR genome editing system.
13. The nucleic acid of any one of claims 1 to 12, wherein the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides.
14. The nucleic acid of claim 13, wherein the nucleic acid is about 10 to about 43 nucleotides in length.
15. The nucleic acid of any one of claims 1 to 14, wherein the nucleic acid is RNA or DNA.
16. The nucleic acid of claim 7 or 12, wherein the nuclease activity is from a Cpf1 protein.
17. A method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

18. The method of claim 17, wherein the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.
19. The method of claim 18, wherein the at least one chemically modified nucleotide is a chemically modified phosphodiester linkage.
20. The method of claim 19, wherein the chemically modified phosphodiester linkage is phosphorothioate (PS).
21. The method of claim 18, wherein all the nucleotides comprise chemically modified phosphodiester linkages.
22. The method of claim 21, wherein the chemically modified phosphodiester linkages are phosphorothioate (PS).
23. The method of any one of claims 17 to 22, wherein the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides.
24. The method of claim 23, wherein the nucleic acid is about 10 to about 43 nucleotides in length.
25. The method of any one of claims 17 to 24, wherein the nucleic acid is RNA or DNA.
26. The method of any one of claims 17 to 25, wherein the nuclease is a Cpf1 protein.
27. A method for increasing the nuclease activity of a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chemically modified nucleic acid comprising at least one chemically modified nucleotide;

wherein the nucleic acid is complementary to the guide RNA; and

wherein the chemically modified nucleic acid increases the activity of the nuclease of the CRISPR genome editing system.

28. The method of claim 27, wherein the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.
29. The method of claim 28, wherein the at least one chemically modified nucleotide is a chemically modified ribose.
30. The method of claim 29, wherein the chemically modified ribose is 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F).
31. The method of claim 28, wherein all the nucleotides comprise chemically modified riboses.
32. The method of claim 31, wherein the chemically modified riboses are 2'-*O*-methyl (2'-*O*-Me) or 2'-fluoro (2'-F).
33. The method of any one of claims 27 to 32, wherein the complementary region between the nucleic acid and the guide RNA comprises at least 10 nucleotides.
34. The method of claim 33, wherein the nucleic acid is about 10 to about 43 nucleotides in length.
35. The method of any one of claims 27 to 34, wherein the nucleic acid is RNA or DNA.
36. The method of any one of claims 27 to 35, wherein the nuclease is a Cpf1 protein.
37. A chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide, wherein the chimeric guide nucleic acid inhibits a nuclease activity of a CRISPR genome editing system.
38. The nucleic acid of claim 37, wherein the nucleic acid is comprised of at least 10% DNA nucleotides.
39. The nucleic acid of claim 38, wherein the nucleic acid is comprised of at least 30% DNA nucleotides.
40. The nucleic acid of any one of claims 37 to 39, wherein the nucleic acid is about 10 to about 43 nucleotides in length.
41. The nucleic acid of any one of claims 37 to 40, wherein the nuclease activity is from a Cpf1 protein.
42. The nucleic acid of any one of claims 37 to 41, wherein the nucleic acid comprises at least one chemically modified nucleotide.
43. The nucleic acid of claim 42, wherein the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.
44. A method for inhibiting a CRISPR genome editing system in a cell comprising:

contacting the cell with a CRISPR genome editing system, wherein the system comprises a guide RNA and a nuclease;

contacting the cell with a chimeric guide nucleic acid comprising at least one RNA nucleotide and at least one DNA nucleotide; and

wherein the chimeric guide nucleic acid inhibits the activity of the nuclease of the CRISPR genome editing system.

45. The method of claim 44, wherein the nucleic acid is comprised of at least 10% DNA nucleotides.

46. The method of claim 45, wherein the nucleic acid is comprised of at least 30% DNA nucleotides.

47. The method of any one of claims 44 to 46, wherein the nucleic acid is about 10 to about 43 nucleotides in length.

48. The method of any one of claims 44 to 47, wherein the nuclease activity is from a Cpf1 protein.

49. The method of any one of claims 44 to 48, wherein the nucleic acid comprises at least one chemically modified nucleotide.

50. The method of claim 49, wherein the at least one chemically modified nucleotide comprises a chemically modified nucleobase, a chemically modified ribose, a chemically modified phosphodiester linkage, or a combination thereof.

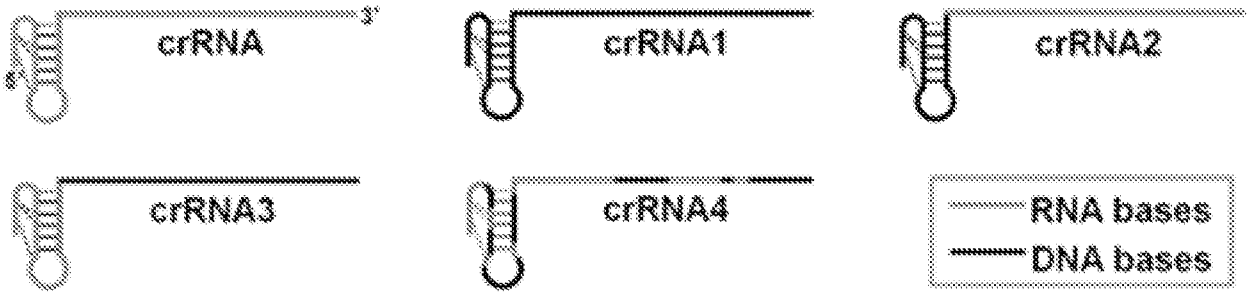


FIG. 1A

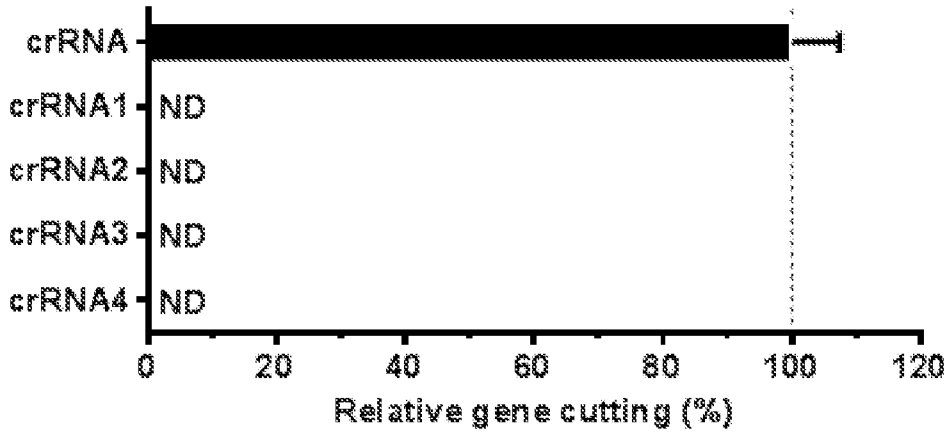


FIG. 1B

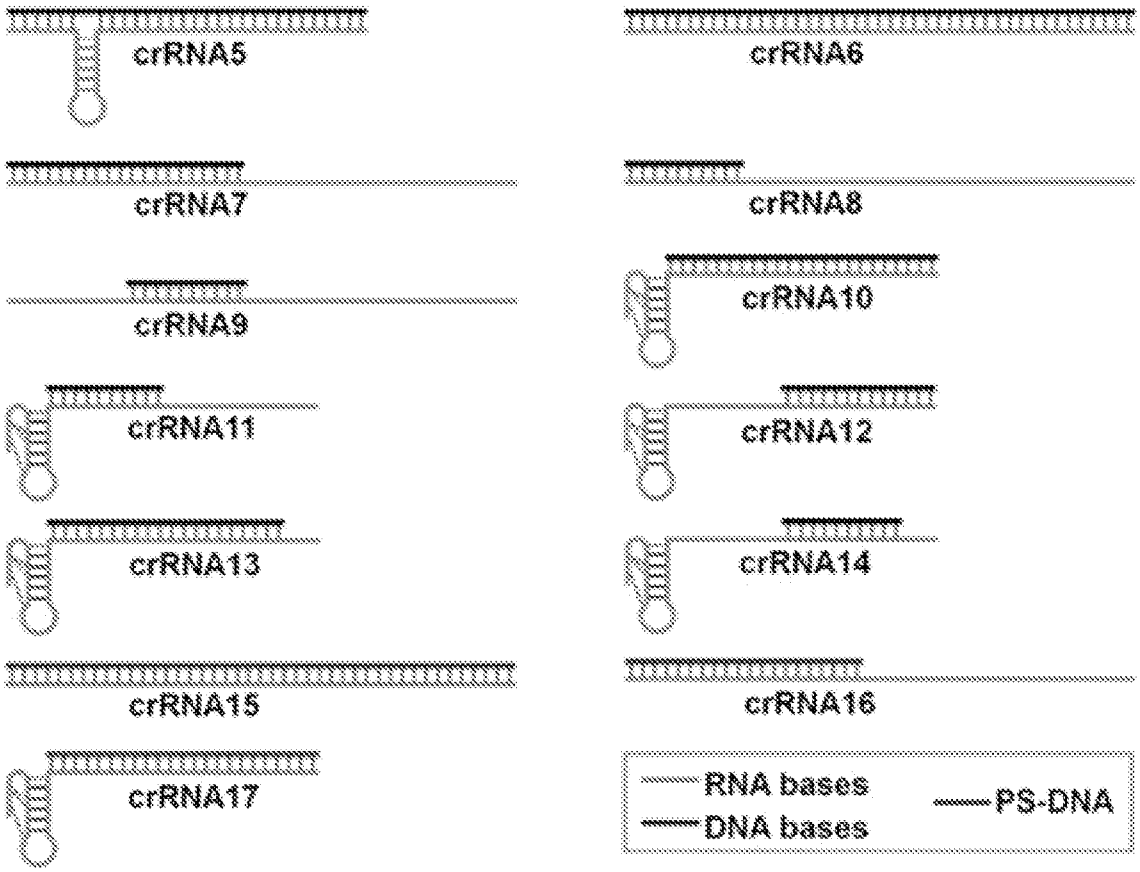


FIG. 1C

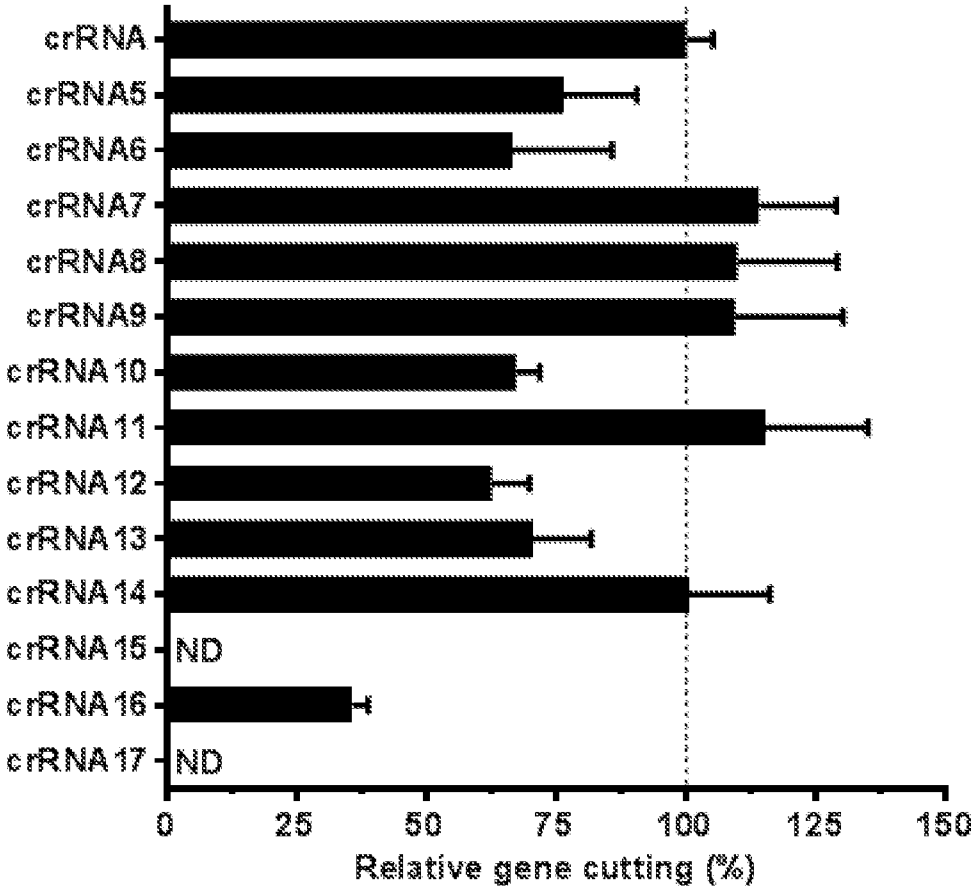

crRNA
crRNA5
crRNA6
crRNA7
crRNA8
crRNA9
crRNA10
crRNA11
crRNA12
crRNA13
crRNA14
crRNA15
ND
crRNA16
crRNA17
ND
0
25
50
75
100
125
150
Relative gene cutting (%)

FIG. 1D

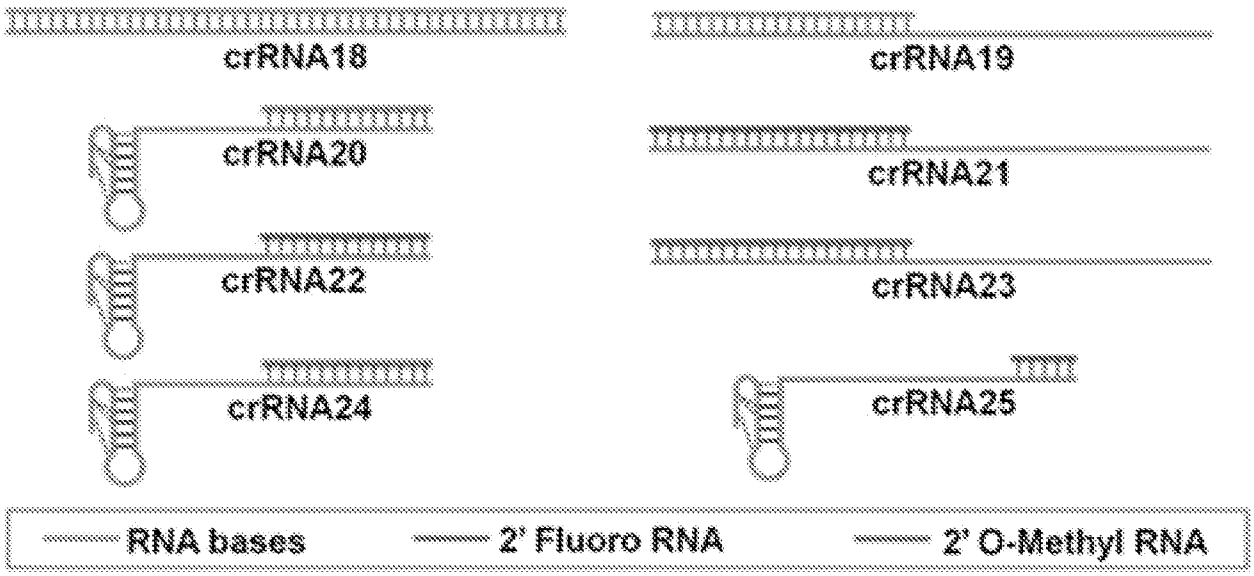

crRNA18
crRNA19
crRNA20
crRNA21
crRNA22
crRNA23
crRNA24
crRNA25
RNA bases
2' Fluoro RNA
2' O-Methyl RNA

FIG. 1E

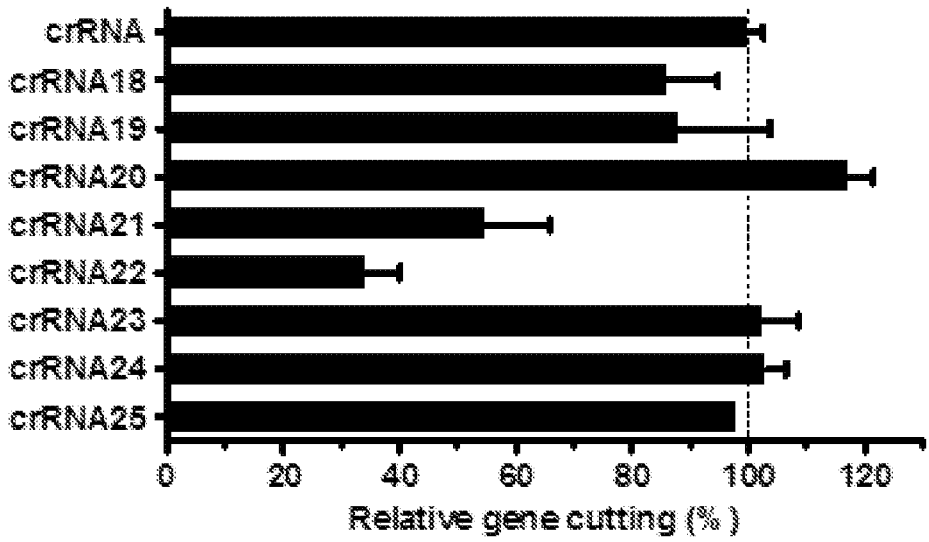


FIG. 1F

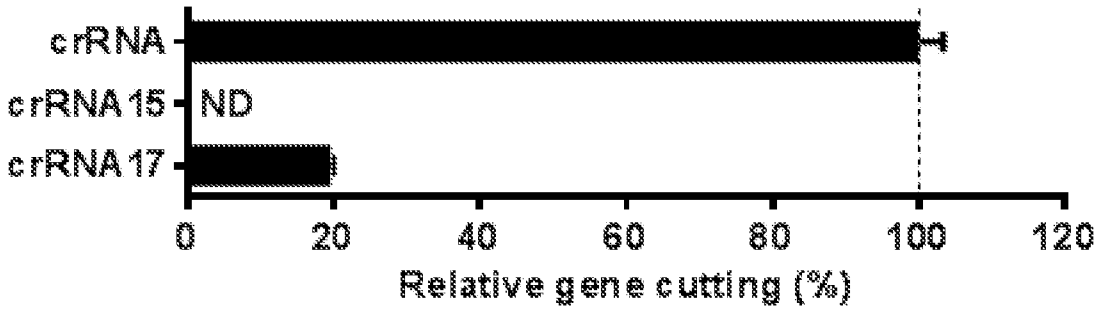


FIG. 1G

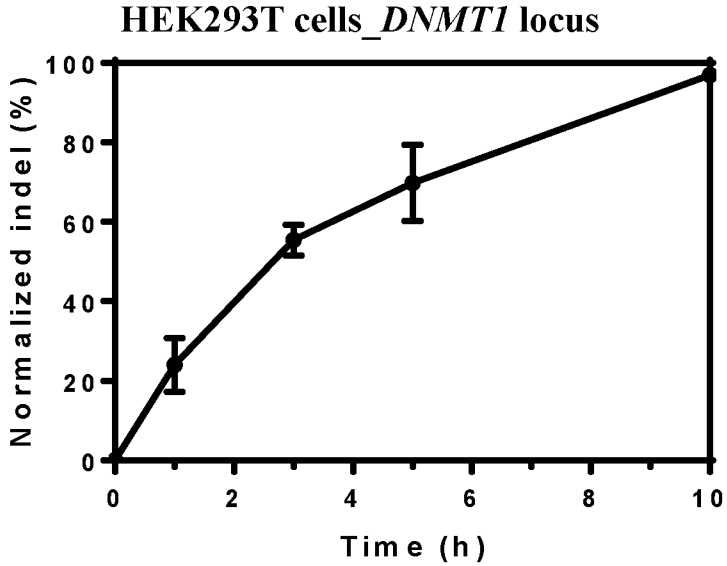


FIG. 2A

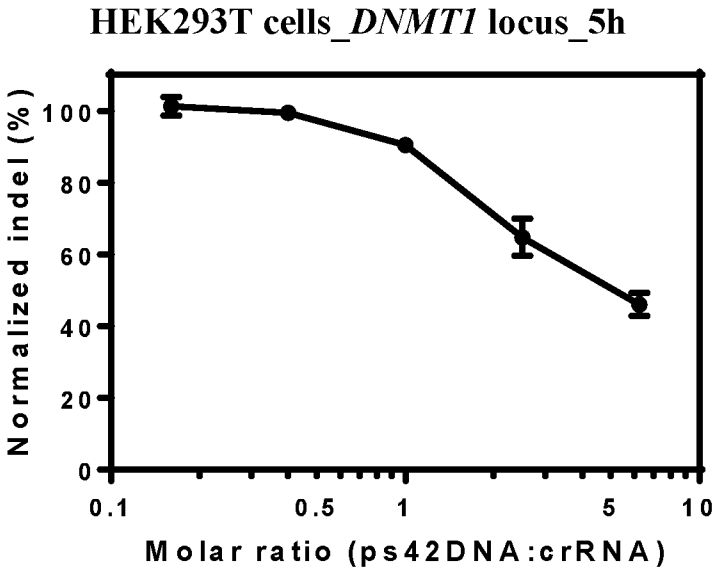

HEK293T cells_DNMT1 locus_5h
Normalized indel (%)
100
80
60
40
20
0
0.1
0.5
1
5
10
Molar ratio (ps42DNA:crRNA)

FIG. 2B

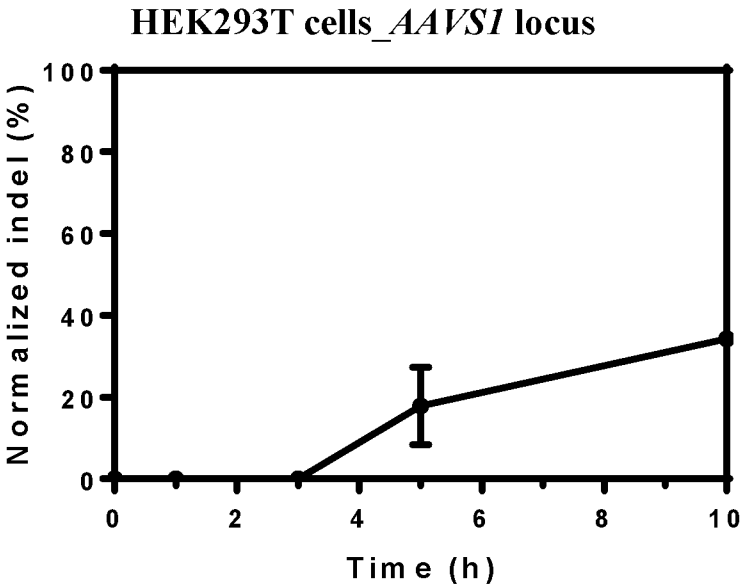

HEK293T cells_AAVS1 locus
Normalized indel (%)
100
80
60
40
20
0
0
2
4
6
8
10
Time (h)

FIG. 2C

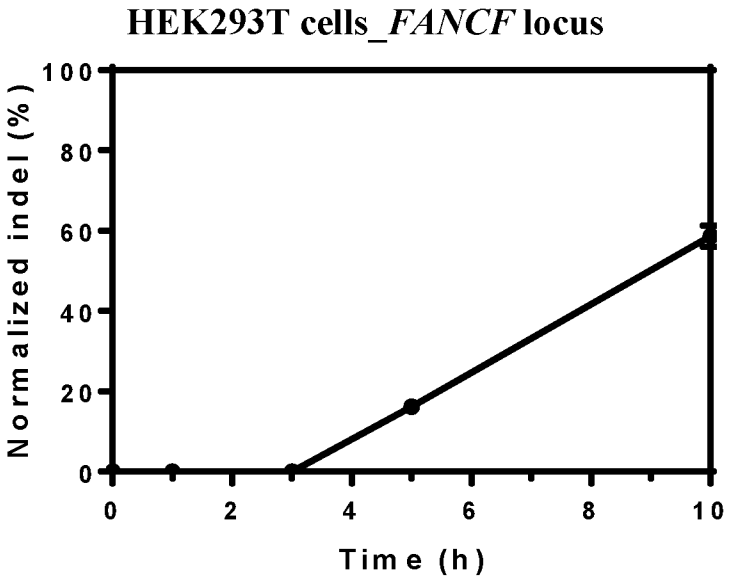

HEK293T cells_*FANCF* locus
Normalized indel (%)
100
80
60
40
20
0
0
2
4
6
8
10
Time (h)

FIG. 2D

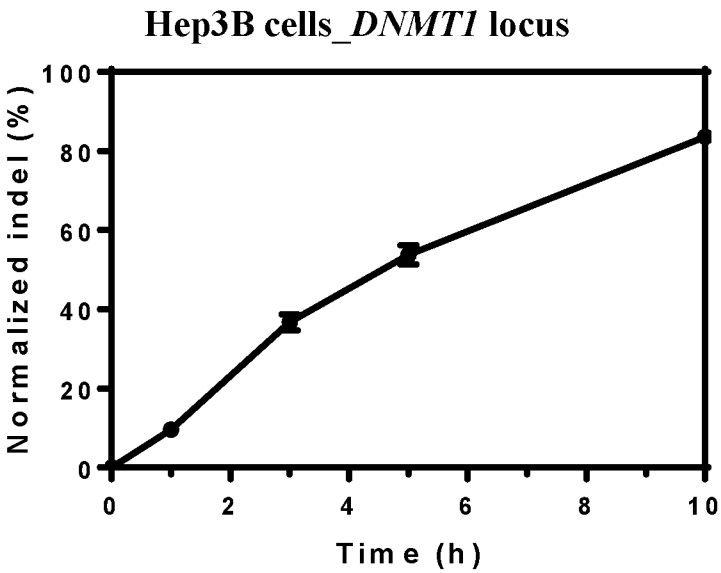

Hep3B cells_*DNMT1* locus
Normalized indel (%)
100
80
60
40
20
0
0
2
4
6
8
10
Time (h)

FIG. 2E

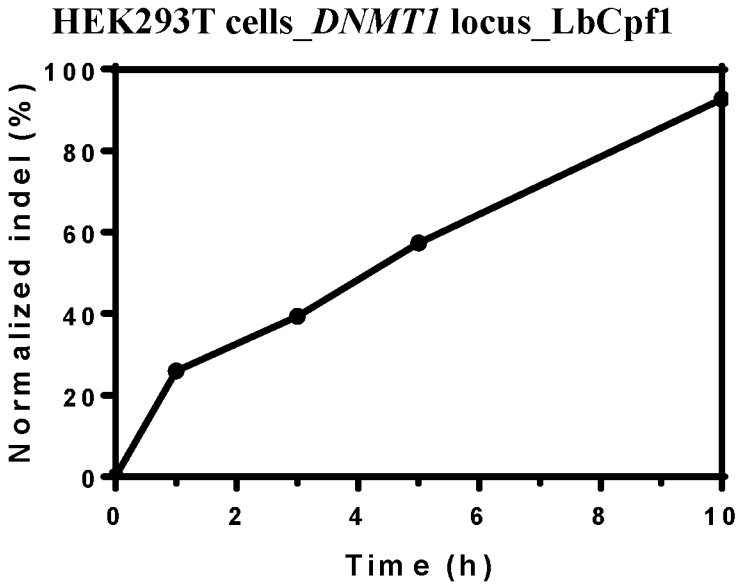

HEK293T cells_DNMT1 locus_LbCpf1
Normalized indel (%)
100
80
60
40
20
0
0
2
4
6
8
10
Time (h)

FIG. 2F

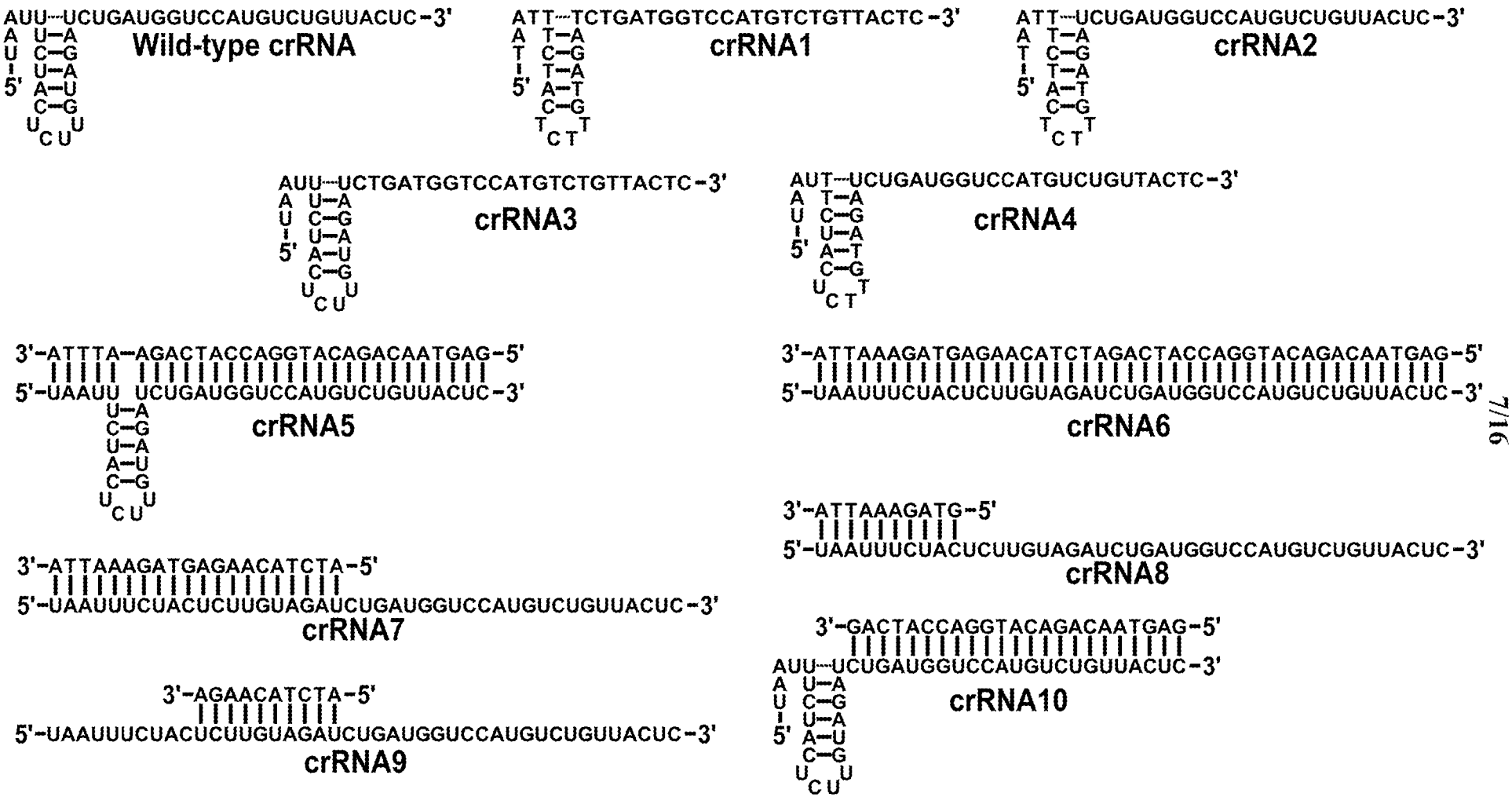

AUU---UCUGAUGGUCCAUGUCUGUUACUC-3'
Wild-type crRNA
ATT---TCTGATGGTCCATGTCTGTTACTC-3'
crRNA1
ATT---UCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA2
AUU---UCTGATGGTCCATGTCTGTTACTC-3'
crRNA3
AUT---UCUGAUGGUCCATGUCUGUTACTC-3'
crRNA4
3'-ATTTA-AGACTACCAGGTACAGACAATGAG-5'
5'-UAAUU UCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA5
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA6
3'-ATTAAAGATGAGAACATCTA-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA7
3'-ATTAAAGATG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA8
3'-AGAACATCTA-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA9
3'-GACTACCAGGTACAGACAATGAG-5'
AUU---UCUGAUGGUCCAUGUCUGUUACUC-3'
crRNA10

FIG. 3

FIG. 3 continued

FIG. 3 continued

FIG. 4A

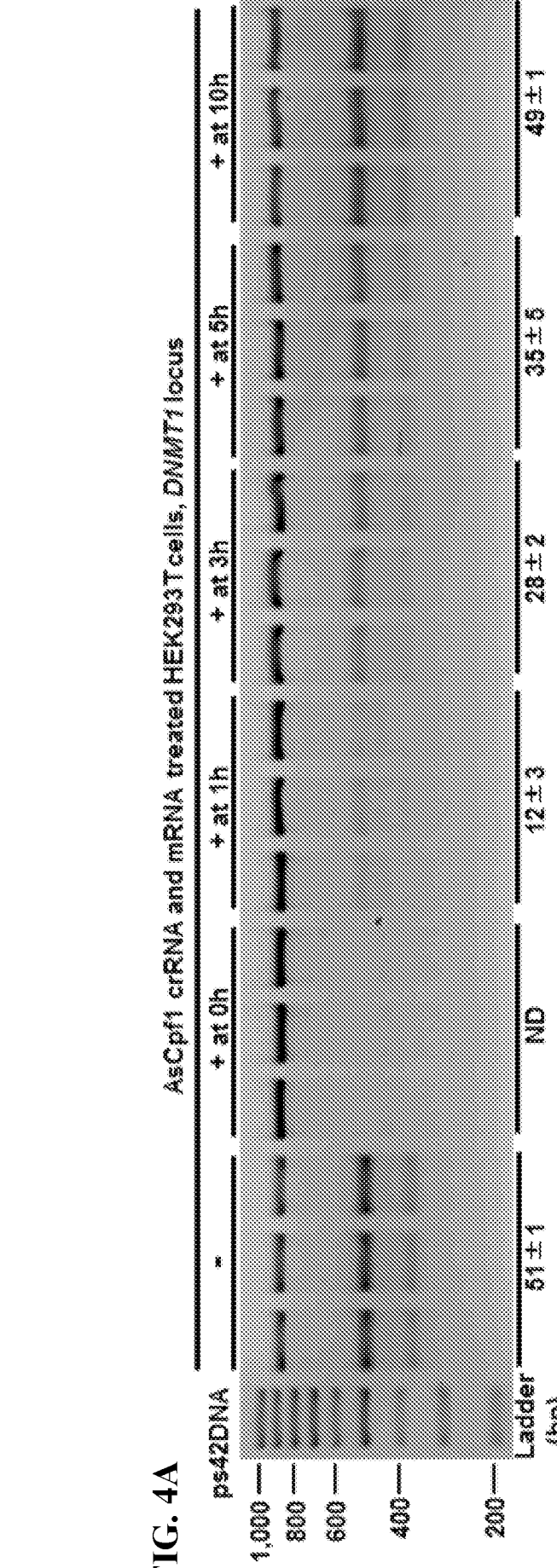

AsCpf1 crRNA and mRNA treated HEK293T cells, DNMT1 locus
ps42DNA
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
1,000
800
600
400
200
Ladder (bp)
51 ± 1
ND
12 ± 3
28 ± 2
35 ± 5
49 ± 1

FIG. 4B

AsCpf1 crRNA and mRNA treated HEK293T cells, DNMT1 locus, ps42DNA was added at 5 h
ps42DNA
-
+ 0.16-fold
+ at 0.4-fold
+ at 1-fold
+ at 2.5-fold
+ at 6.25-fold
1,000
800
600
400
200
56 ± 2
57 ± 1
56 ± 1
51 ± 1
36 ± 3
26 ± 2

FIG. 4C

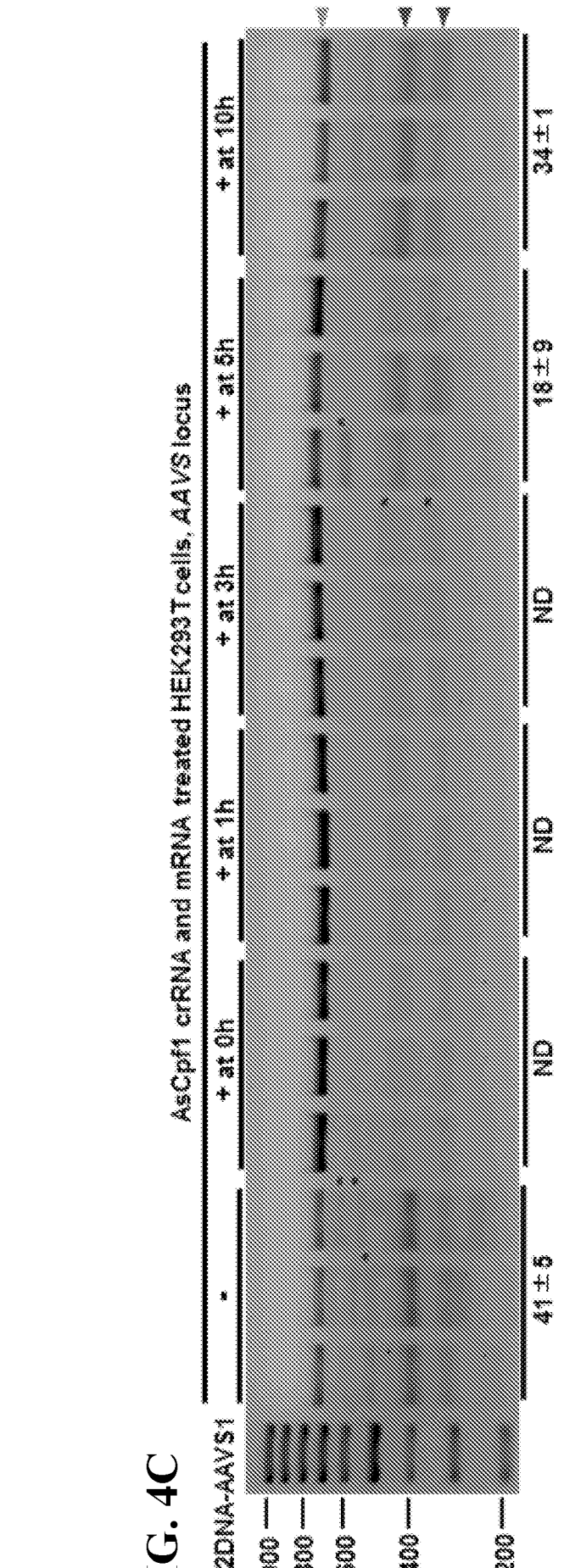

AsCpf1 crRNA and mRNA treated HEK293T cells, AAVS locus
ps42DNA-AAVS1
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
1,000
800
600
400
200
41 ± 5
ND
ND
ND
18 ± 9
34 ± 1

FIG. 4D

AsCpf1 crRNA and mRNA treated HEK293T cells, FANCF locus
ps42DNA-FANCF
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
1,000
800
600
400
200
39 ± 2
ND
ND
ND
6 ± 0.1
23 ± 1

FIG. 4E

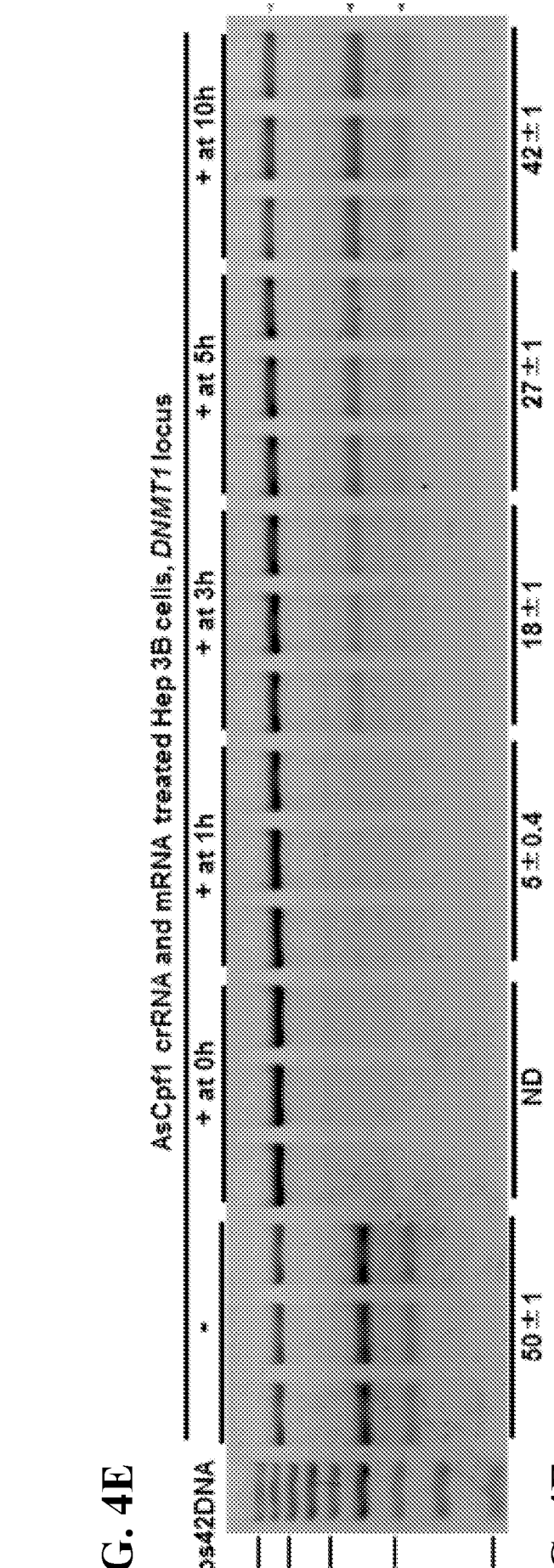
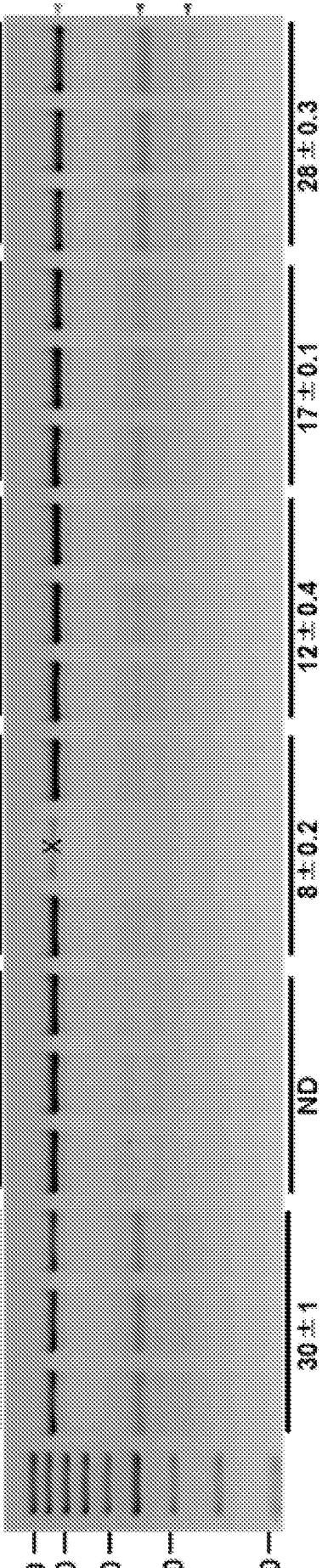

AsCpf1 crRNA and mRNA treated Hep 3B cells, DNMT1 locus
ps42DNA
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
1,000
800
600
400
200
50 ± 1
ND
5 ± 0.4
18 ± 1
27 ± 1
42 ± 1

FIG. 4F


LbCpf1 crRNA and mRNA treated HEK293T cells, DNMT1 locus
Lbps42DNA
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
1,000
800
600
400
200
30 ± 1
ND
8 ± 0.2
12 ± 0.4
17 ± 0.1
28 ± 0.3

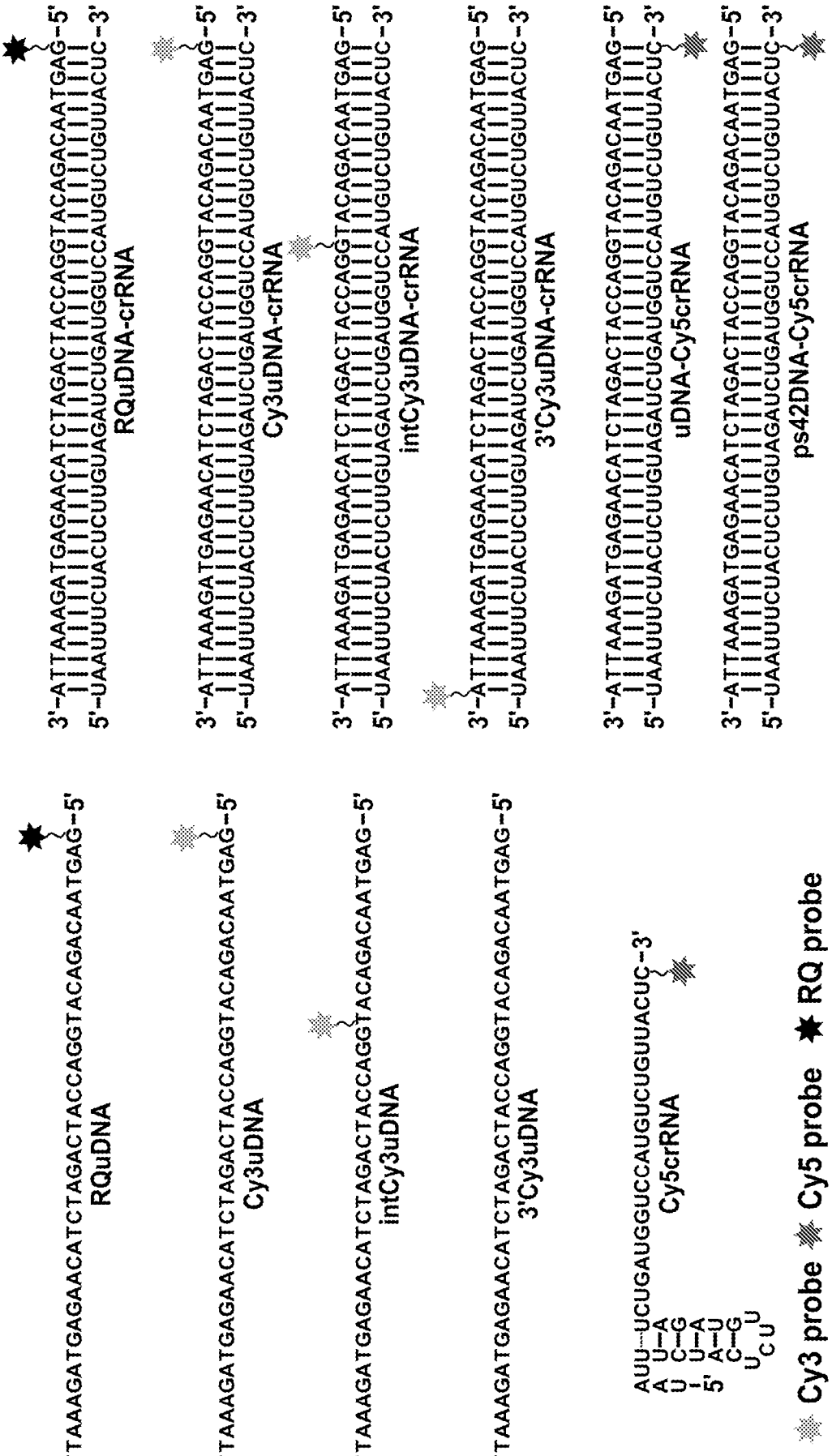

3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
RQuDNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
Cy3uDNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
intCy3uDNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
3'Cy3uDNA
AUU-UCUGAUGGUCCAUGUCUGUUACUC-3'
Cy5crRNA
Cy3 probe
Cy5 probe
RQ probe
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
RQuDNA-crRNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
Cy3uDNA-crRNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
intCy3uDNA-crRNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
3'Cy3uDNA-crRNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
uDNA-Cy5crRNA
3'-ATTAAAGATGAGAACATCTAGACTACCAGGTACAGACAATGAG-5'
5'-UAAUUUCUACUCUUGUAGAUCUGAUGGUCCAUGUCUGUUACUC-3'
ps42DNA-Cy5crRNA

FIG. 5A

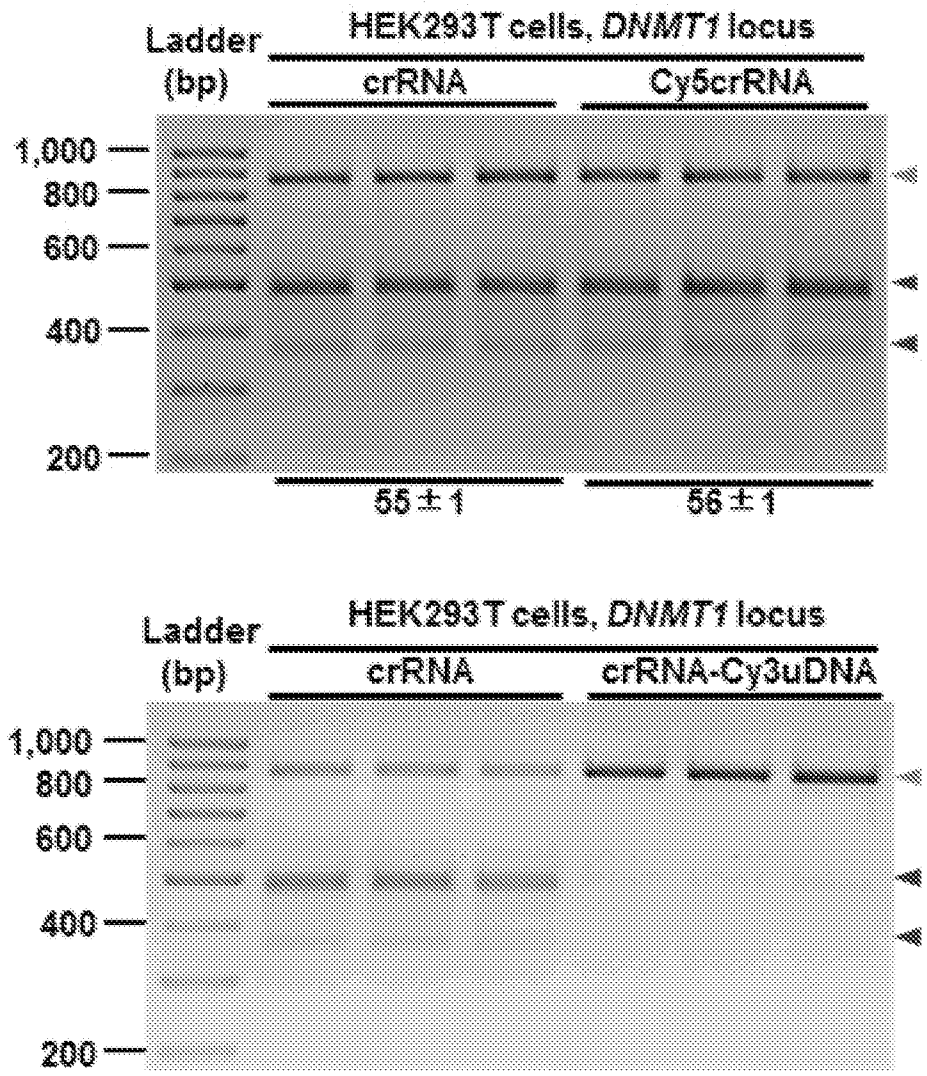

Ladder
(bp)
HEK293T cells, DNMT1 locus
crRNA
Cy5crRNA
1,000
800
600
400
200
55 ± 1
56 ± 1
Ladder
(bp)
HEK293T cells, DNMT1 locus
crRNA
crRNA-Cy3uDNA
1,000
800
600
400
200

FIG. 5B

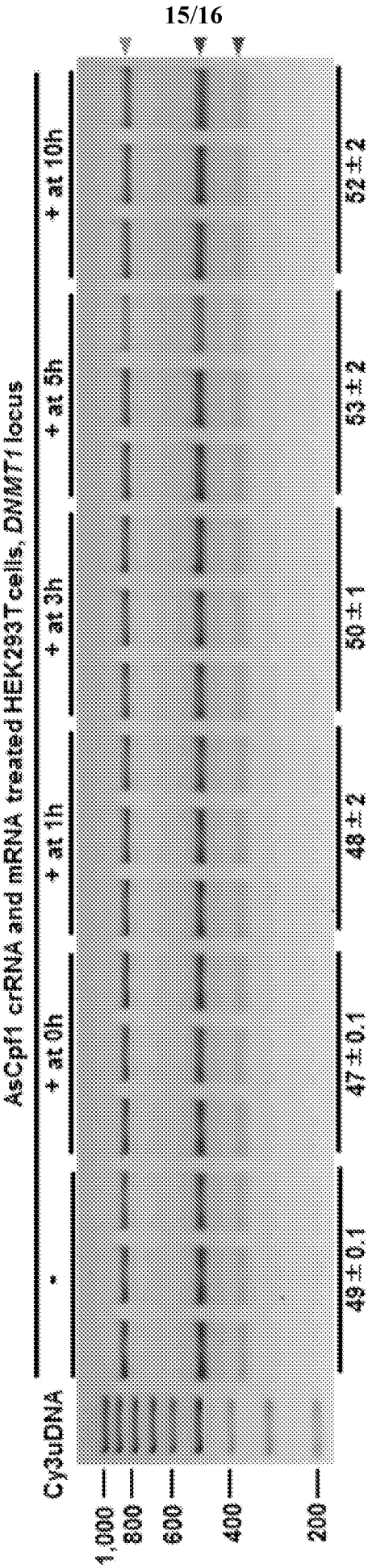

AsCpf1 crRNA and mRNA treated HEK293T cells, DNMT1 locus
Cy3uDNA
1,000
800
600
400
200
-
+ at 0h
+ at 1h
+ at 3h
+ at 5h
+ at 10h
49 ± 0.1
47 ± 0.1
48 ± 2
50 ± 1
53 ± 2
52 ± 2

FIG. 5C

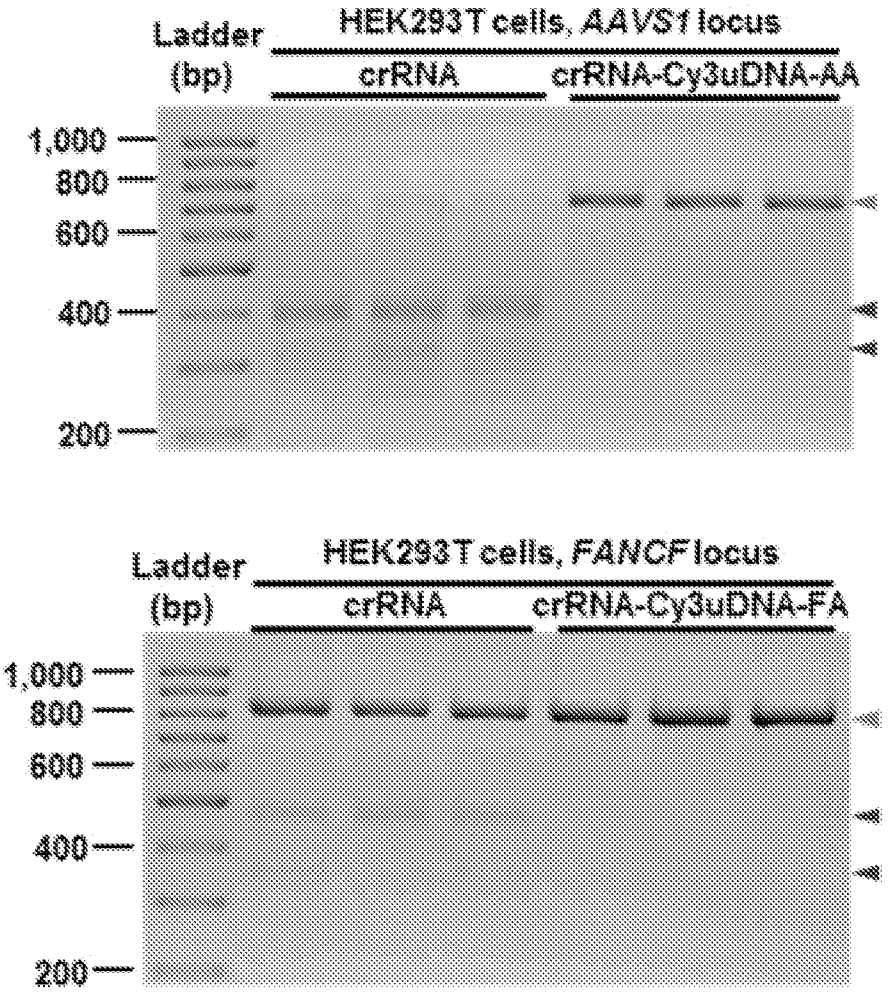

Ladder
(bp)
HEK293T cells, AAVS1 locus
crRNA
crRNA-Cy3uDNA-AA
1,000
800
600
400
200
Ladder
(bp)
HEK293T cells, FANCF locus
crRNA
crRNA-Cy3uDNA-FA
1,000
800
600
400
200

FIG. 5D

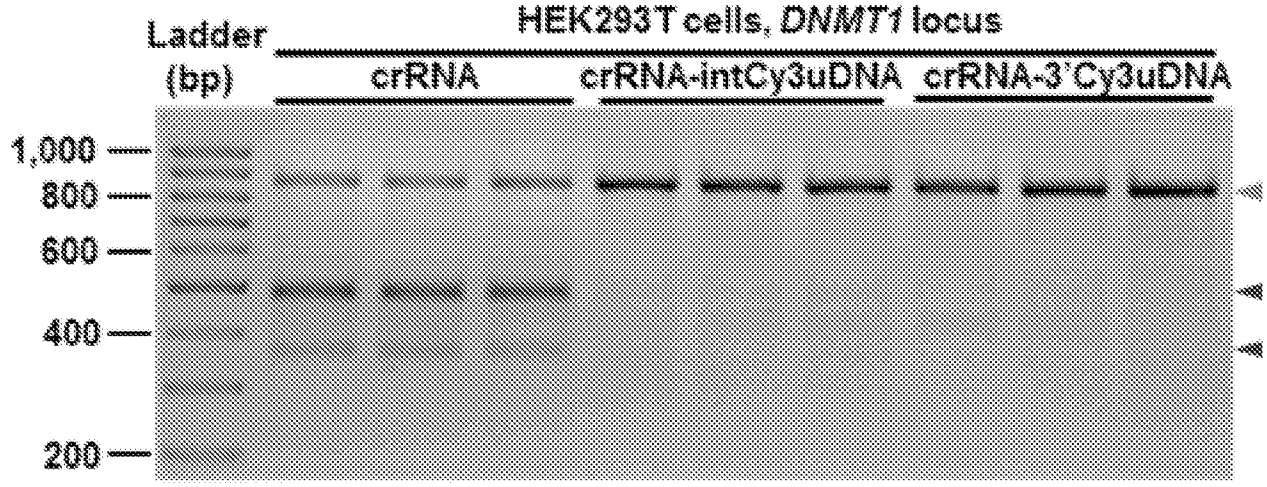

Ladder
(bp)
HEK293T cells, DNMT1 locus
crRNA
crRNA-intCy3uDNA
crRNA-3'Cy3uDNA
1,000
800
600
400
200

FIG. 5E

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2017/041133

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☒ Claims Nos.: 13-16, 25, 26, 35, 36, 41-43, 48-50
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2017/041133

A. CLASSIFICATION OF SUBJECT MATTER

IPC(8) - C12N 9/22; C12N 15/11; C12N 15/90 (2017.01)

CPC - C12N 9/22; C12N 15/1137; C12N 15/902; C12N 2310/20; C12N 2310/31; C12N 2310/32; C12N 2320/51; C12N 2320/53 (2017.08)

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)

See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

USPC - 435/199; 435/455; 435/462; 435/463; 514/44A; 514/44R (keyword delimited)

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X -- Y	RAHDAR et al. "Synthetic CRISPR RNA-Cas9–guided genome editing in human cells," Proceedings of the National Academy of Sciences USA, 16 November 2015 (16.11.2015), Vol. 112, No. 51, Pgs. E7110-E7117. entire document	1-12, 17-22 ---------- 23, 24, 28-32
X -- Y	WO 2016/094867 A1 (THE BROAD INSTITUTE INC. et al) 16 June 2016 (16.06.2016) entire document	27, 33, 34 ---------- 28-32
Y	HUA et al. "Motor neuron cell-nonautonomous rescue of spinal muscular atrophy phenotypes in mild and severe transgenic mouse models," Genes & Development, 01 February 2015 (01.02.2015), Vol. 29, No. 3, Pgs. 288-297. entire document	23, 24
Y	WO 2016/100562 A1 (DANISCO US INC) 23 June 2016 (23.06.2016) entire document	37-40, 44-47
Y	ZHANG et al. "DNase H Activity of Neisseria meningitidis Cas9," Molecular Cell, 15 October 2015 (15.10.2015), Vol. 60, No. 2, Pgs. 242-255. entire document	37-40
Y	US 2015/0232881 A1 (GLUCKSMANN et al) 20 August 2015 (20.08.2015) entire document	44-47
A	GILBERT et al. "CRISPR-Mediated Modular RNA-Guided Regulation of Transcription in Eukaryotes," Cell, 18 July 2013 (18.07.2013), Vol. 154, No. 2, Pgs. 442-451. entire document	1-12, 17-24, 27-34, 37-40, 44-47
P, X	WO 2017/004261 A1 (IONIS PHARMACEUTICALS, INC.) 05 January 2017 (05.01.2017) entire document	1-12, 17-24, 27-34, 37-40, 44-47

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
05 September 2017	25 SEP 2017
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, VA 22313-1450 Facsimile No. 571-273-8300	Authorized officer Blaine R. Copenheaver PCT Helpdesk: 571-272-4300 PCT OSP: 571-272-7774

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2017/041133

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	WO 2016/123230 A1 (PIONEER HI-BRED INTERNATIONAL, INC.) 04 August 2016 (04.08.2016) entire document	1-12, 17-24, 27-34, 37-40, 44-47