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(54) **Titre : NOUVELLES NUCLEASES CRISPR OMNI 115, 124 127, 144-149, 159, 218, 237, 248, 251-253 ET 259**
(54) **Title: NOVEL OMNI 115, 124, 127, 144-149, 159, 218, 237, 248, 251-253 AND 259 CRISPR NUCLEASES**

(57) **Abrégé/Abstract:**
The present invention provides a non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.

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Abstract:

The present invention disclosed herein are compositions that may be utilized for modifying genomic DNA sequences, comprising a non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.

NOVEL OMNI 115, 124, 127, 144-149, 159, 218, 237, 248, 251-253 AND 259 CRISPR NUCLEASES

[0001] This application claims priority of U.S. Provisional Application No. 63/232,723, filed August 13, 2021, the content of which are hereby incorporated by reference.

[0002] Throughout this application, various publications are referenced, including referenced in parenthesis. The disclosures of all publications mentioned in this application in their entireties are hereby incorporated by reference into this application in order to provide additional description of the art to which this invention pertains and of the features in the art which can be employed with this invention.

REFERENCE TO SEQUENCE LISTING

[0003] This application incorporates-by-reference nucleotide sequences which are present in the file named "210812_91769-A-PCT_Sequence_Listing_AWG.xml", which is 575 kilobytes in size, and which was created on August 12, 2022 in the IBM-PC machine format, having an operating system compatibility with MS-Windows, which is contained in the XML file filed August 12, 2022 as part of this application.

FIELD OF THE INVENTION

[0004] The present invention is directed to, *inter alia*, composition and methods for genome editing.

BACKGROUND OF THE INVENTION

[0005] The Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) systems of bacterial and archaeal adaptive immunity show extreme diversity of protein composition and genomic loci architecture. The CRISPR systems have become important tools for research and genome engineering. Nevertheless, many details of CRISPR systems have not been determined and the applicability of CRISPR nucleases may be limited by sequence specificity requirements, expression, or delivery challenges. Different CRISPR nucleases have diverse characteristics such as: size, PAM site, on target activity, specificity, cleavage pattern (e.g. blunt, staggered ends), and prominent pattern of indel formation following cleavage. Different sets of characteristics may be useful for different applications. For example, some CRISPR nucleases may be able to target particular genomic loci that other CRISPR nucleases cannot due to limitations of the PAM site. In

addition, some CRISPR nucleases currently in use exhibit pre-immunity, which may limit *in vivo* applicability. See Charlesworth et al., Nature Medicine (2019) and Wagner et al., Nature Medicine (2019). Accordingly, discovery, engineering, and improvement of novel CRISPR nucleases is of importance.

SUMMARY OF THE INVENTION

[0006] Disclosed herein are compositions and methods that may be utilized for genomic engineering, epigenomic engineering, genome targeting, genome editing of cells, and/or in vitro diagnostics.

[0007] The disclosed compositions may be utilized for modifying genomic DNA sequences. As used herein, genomic DNA refers to linear and/or chromosomal DNA and/or plasmid or other extrachromosomal DNA sequences present in the cell or cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments, the cell of interest is a prokaryotic cell. In some embodiments, the methods produce double-stranded breaks (DSBs) at pre-determined target sites in a genomic DNA sequence, resulting in mutation, insertion, and/or deletion of a DNA sequence at the target site(s) in a genome.

[0008] Accordingly, in some embodiments, the compositions comprise a Clustered Regularly Interspaced Short Palindromic Repeat (CRISPR) nucleases. In some embodiments, the CRISPR nuclease is a CRISPR-associated protein.

OMNI CRISPR Nucleases

[0009] Embodiments of the present invention provide for CRISPR nucleases designated as an "OMNI" nuclease as provided in Table 1.

[0010] This invention provides a method of modifying a nucleotide sequence at a target site in the genome of a mammalian cell comprising introducing into the cell (i) a composition comprising a CRISPR nuclease having at least 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding a CRISPR nuclease which sequence has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 18-51 and (ii) a DNA-targeting RNA molecule, or a

DNA polynucleotide encoding a DNA-targeting RNA molecule, comprising a nucleotide sequence that is complementary to a sequence in the target DNA.

[0011] This invention also provides a non-naturally occurring composition comprising a CRISPR associated system comprising:

a) one or more RNA molecules comprising a guide sequence portion linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence, or one or more nucleotide sequences encoding the one or more RNA molecules; and

b) an CRISPR nuclease comprising an amino acid sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and

wherein the one or more RNA molecules hybridize to the target sequence, wherein the target sequence is adjacent to the 3' end of a complimentary sequence of a Protospacer Adjacent Motif (PAM), and the one or more RNA molecules form a complex with the RNA-guided nuclease.

[0012] This invention also provides a non-naturally occurring composition comprising:

a) a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and

b) one or more RNA molecules, or one or more DNA polynucleotide encoding the one or more RNA molecules, comprising at least one of:

i) a nuclease-binding RNA nucleotide sequence capable of interacting with/binding to the CRISPR nuclease; and

ii) a DNA-targeting RNA nucleotide sequence comprising a sequence complementary to a sequence in a target DNA sequence,

wherein the CRISPR nuclease is capable of complexing with the one or more RNA molecules to form a complex capable of hybridizing with the target DNA sequence.

BRIEF DESCRIPTION OF THE DRAWINGS

[0013] **Figs. 1A-D: The predicted secondary structure of a single guide RNA (sgRNA) (crRNA-tracrRNA) from sgRNA_127, sgRNA_237, and sgRNA_259. Fig. 1A**: A representation of a crRNA–tracrRNA duplex for OMNI-127 is shown with the crRNA and tracrRNA portions of the sgRNA noted. **Fig. 1B**: Example of V1 sgRNA design for OMNI-237. **Fig. 1C**: Example of V2 sgRNA design for OMNI-114. **Fig. 1D:** Example of V1 of sgRNA design for OMNI-259 (Table 2). **Fig. 1E:** Example of V1 of sgRNA design for OMNI-127 (Table 2).

[0014] **Figs. 2-18: *In vitro* TXTL PAM depletion results for OMNI nucleases.** The PAM logo is a schematic representation of the ratio of the depleted site (top panel). Depletion ratio (bottom panel, left) of specific PAM sequences (bottom panel, right) from the PAM plasmid library were calculated following NGS of the TXTL reaction. The calculation for each OMNI is based on a 4N window along the 8bp sequence of the PAM library. The required PAM of the tested OMNI and the level of nuclease activity under the reaction conditions is inferred from the depletion ratio. *In vitro* PAM depletion results for: **Figs. 2-18**: OMNI-115. Fig 3: OMNI-124. Fig 4: OMNI-127. Fig 5: OMNI-144. Fig 6: OMNI-145. Fig 7: OMNI-146. Fig 8: OMNI-147. Fig 9: OMNI-148. Fig 10: OMNI-149. Fig 11: OMNI-159. Fig 12: OMNI-218. Fig 13: OMNI-237. Fig 14: OMNI-248. Fig 15: OMNI-251. Fig 16: OMNI-252. Fig 17: OMNI-253. Fig 18: OMNI-259.

[0015] **Figs 19A-19C: OMNI-127 activity and spacer optimization as part of an RNP complex in U2OS cells.** OMNI-127 nuclease was over-expressed and purified. The purified protein was complexed with synthetic sgRNA to form RNPs. **Fig. 19A**: For *in vitro* assays, decreasing amounts of RNPs (4, 2, 1 and 0.5 pmol) with an ELANE-targeting g135 guide (listed in Table 6) were incubated with 40 ng ELANE DNA target template. Activity was verified by the RNP ability to cleave the linear template. **Figs. 19B-19C**: For *in vivo* assays, (Fig. 19B) RNPs with varying spacer lengths (20-24 nucleotides) of ELANE-targeting g135 and g136 guides were electroporated into U2OS cells and editing levels were measured by next-generation sequencing (NGS) based on indel formation. **Fig. 19C** shows activity assay results for OMNI-127 as part of an RNP complex in U2OS cells: RNPs with ELANE g134,g135 and g136 (22bp spacer length, Table 6) were electroporated into U2OS cell line and editing levels (indels) were measured by NGS.

DETAILED DESCRIPTION

[0016] According to some aspects of the invention, the disclosed compositions comprise a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) nuclease and/or a nucleic acid molecule comprising a sequence encoding the same.

[0017] Table 1 lists novel CRISPR nucleases, as well as substitutions at one or more positions within each nuclease which convert the nuclease to a nickase or catalytically dead nuclease. For example, the catalytic site of any one of the CRISPR nucleases provided herein may be modified such that the nuclease has nickase activity, such that it is capable of performing single-strand DNA cuts. Alternatively, the catalytic site of any one of CRISPR nucleases provided herein may be modified such that the nuclease has no nuclease activity, i.e. a dead nuclease. Throughout the text CRISPR nucleases are referred to, however, any of these nucleases may be modified to have nickase activity (i.e. nucleases which create a single-strand DNA break as opposed to a double-strand break) or to have no nuclease activity (i.e. a catalytically dead nuclease).

[0018] Table 2 provides crRNA, tracrRNA, and single-guide RNA (sgRNA) sequences, and portions of crRNA, tracrRNA, and sgRNA sequences, that are compatible with each listed CRISPR nuclease. Accordingly, a crRNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 as part of a crRNA:tracrRNA complex may comprise any crRNA sequence listed in Table 2. Similarly, a tracrRNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 as part of a crRNA:tracrRNA complex may comprise any tracrRNA sequence listed in Table 2. Also, a single-guide RNA molecule capable of binding and targeting an OMNI nuclease listed in Table 2 may comprise any sequence listed in Table 2.

[0019] For example, a crRNA molecule of OMNI-115 nuclease (SEQ ID NO: 1) may comprise a sequence of any one of SEQ ID NOs: 52--55; a tracrRNA molecule of OMNI-115 nuclease may comprise a sequence of any one of SEQ ID NOs: 56-63; and a sgRNA molecule of OMNI-115 nuclease may comprise a sequence of any one of SEQ ID NOs: 52-64. Other crRNA molecules, tracrRNA molecules, or sgRNA molecules for each OMNI nuclease may be derived from the sequences listed in Table 2 in the same manner.

[0020] Any one of these nucleases can target a desired DNA target sequence via a guide RNA molecule. The nuclease-guide complex will also carry any molecule attached to the complex to the target site. Thus, this disclosure also contemplates fusion proteins comprising CRISPR nucleases

and a DNA modifying domain (e.g., a deaminase, a nuclease, a nickase, a recombinase, a methyltransferase, a methylase, an acetylase, an acetyltransferase, a transcriptional activator, or a transcriptional repressor domain), as well as the use of such fusion proteins in correcting mutations in a genome (e.g., the genome of a human subject) that are associated with disease, or generating mutations in a genome (e.g., the human genome) to decrease or prevent expression of a gene.

[0021] In some embodiments, any of the CRISPR nucleases provided herein may be fused to a protein that has an enzymatic activity. In some embodiments, the enzymatic activity modifies a target DNA. In some embodiments, the enzymatic activity is nuclease activity, methyltransferase activity, demethylase activity, DNA repair activity, DNA damage activity, deamination activity, dismutase activity, alkylation activity, depurination activity, oxidation activity, pyrimidine dimer forming activity, integrase activity, transposase activity, recombinase activity, polymerase activity, ligase activity, helicase activity, photolyase activity or glycosylase activity. In some cases, the enzymatic activity is nuclease activity. In some cases, the nuclease activity introduces a double strand break in the target DNA. In some cases, the enzymatic activity modifies a target polypeptide associated with the target DNA. In some cases, the enzymatic activity is methyltransferase activity, demethylase activity, acetyltransferase activity, deacetylase activity, kinase activity, phosphatase activity, ubiquitin ligase activity, deubiquitinating activity, adenylation activity, deadenylation activity, SUMOylating activity, deSUMOylating activity, ribosylation activity, deribosylation activity, myristoylation activity or demyristoylation activity. In some cases, the target polypeptide is a histone and the enzymatic activity is methyltransferase activity, demethylase activity, acetyltransferase activity, deacetylase activity, kinase activity, phosphatase activity, ubiquitin ligase activity or deubiquitinating activity.

[0022] Thus, any one of the CRISPR nucleases, nickases, or dead-nucleases may be fused (e.g. directly fused or fused via a linker) to another DNA modulating or DNA modifying enzyme, including, but not limited to, base editors such as a deaminase, a reverse transcriptase (e.g. for use in prime editing, see Anzaolone et al. (2019)), an enzyme that modifies the methylation state of DNA (e.g. a methyltransferase), or a modifier of histones (e.g. a histone acetyl transferase). Indeed, the OMNI-50 nucleases, nickases, inactive nucleases described herein may be fused to a DNA modifying enzyme or an effector domain thereof. Examples of DNA modifiers include but are not limited to: a deaminase, a nuclease, a nickase, a recombinase, a methyltransferase, a methylase, an acetylase, an acetyltransferase, a reverse transcriptase, an helicase, an integrase, a ligase, a

transposase, a demethylase, a phosphatase, a transcriptional activator, or a transcriptional repressor. In some embodiments, any of the CRISPR nucleases provided herein are fused to a protein that has an enzymatic activity. In some embodiments, the enzymatic activity modifies a target DNA molecule. the CRISPR nucleases described herein or fusion proteins thereof, may be used to correct or generate one or more mutations in a gene associated with disease, or to increase, correct, decrease or prevent expression of a gene.

[0023] The invention provides a non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 90% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17, or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.

[0024] In some embodiments, the composition further comprises one or more RNA molecules, or a DNA polynucleotide encoding any one of the one or more RNA molecules, wherein the one or more RNA molecules and the CRISPR nuclease do not naturally occur together and the one or more RNA molecules are configured to form a complex with the CRISPR nuclease and/or target the complex to a target site.

[0025] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 52-64.

[0026] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 52-55.

[0027] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 56-63.

[0028] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 52-64.

[0029] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 65-81.

[0030] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 65-68 and 80.

[0031] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 69-77 and 81.

[0032] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 65-81.

[0033] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 82-97.

[0034] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 82-85 and 96.

[0035] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 86-93 and 97.

[0036] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 82-97.

[0037] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 98-114.

[0038] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 98-101 and 114.

[0039] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 102-111.

[0040] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 98-114.

[0041] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 115-127.

[0042] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 115-118.

[0043] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 119-126.

[0044] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 115-127.

[0045] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 128-141.

[0046] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 128-131.

[0047] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 132-140.

[0048] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 128-141.

[0049] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 142-155.

[0050] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 142-145.

[0051] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 146-152 and 155.

[0052] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 142-155.

[0053] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 156-167 and GCUUUAAGC.

[0054] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 156-159.

[0055] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 160-166 and GCUUUAAGC.

[0056] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 156-167 and GCUUUAAGC.

[0057] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 168-176.

[0058] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 168 and 169.

[0059] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 170-175.

[0060] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 168-176.

[0061] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 177-185.

[0062] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177 and 178.

[0063] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 179-184.

[0064] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177-185.

[0065] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 186-202.

[0066] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 186-189 and 201.

[0067] In some embodiments, the composition further comprises a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 190-198 and 202.

[0068] In some embodiments, the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 186-202.

[0069] In some embodiments, the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1.

[0070] In some embodiments, the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1.

[0071] In some embodiments, the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1.

[0072] For example, a nickase may be generated for the OMNI-127 nuclease by inactivating its RuvC domain by substituting an aspartic acid residue (D) in position 9 of the amino acid sequence of OMNI-127 (SEQ ID NO: 3) for another amino acid e.g. alanine (A). Substitution to any other amino acid is permissible for each of the amino acid positions indicated in columns 5-7, unless otherwise indicated in Table 1. Other nickases or catalytically dead nucleases can be generated using the same notation in Table 1.

[0073] In some embodiments, the CRISPR nuclease utilizes a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in columns 2-4 of Table 3.

[0074] The invention also provides a method for modifying a nucleotide sequence at a DNA target site in a cell-free system or the genome of a cell comprising introducing into the cell any one of the compositions described above. In some embodiments, the composition comprises a CRISPR nuclease and a crRNA:tracrRNA complex or a sgRNA molecule.

[0075] In some embodiments, the CRISPR nuclease effects a DNA break in a DNA strand adjacent to a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in columns 2-4 of Table 3, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence. For example, the OMNI-115 nuclease with the appropriate targeting sgRNA or crRNA:tracrRNA complex is capable of forming a DNA break in strand adjacent to a NNRYTT or NNRTTT sequence and in a DNA strand adjacent to a sequence that is complementary to a NNRYTT or NNRTTT sequence. In some embodiments, the DNA strand is within a nucleus of a cell.

[0076] In some embodiments, the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.

[0077] In some embodiments, the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

[0078] In some embodiments, the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

[0079] In some embodiments, the cell is a eukaryotic cell or a prokaryotic cell.

[0080] In some embodiments, the cell is a mammalian cell.

[0081] In some embodiments, the cell is a human cell.

[0082] In some embodiments, the CRISPR nuclease comprises an amino acid sequence having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 89%, 88%, 87%, 86%, 85%, 84%, 83%, or 82% amino acid sequence identity to a CRISPR nuclease as set forth in any of SEQ ID NOs: 1-17. In an embodiment the sequence encoding the CRISPR nuclease has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 18-51.

[0083] According to some aspects of the invention, the disclosed compositions comprise DNA constructs or a vector system comprising nucleotide sequences that encode the CRISPR nuclease or variant CRISPR nuclease. In some embodiments, the nucleotide sequence that encode the CRISPR nuclease or variant CRISPR nuclease is operably linked to a promoter that is operable in the cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments the cell of interest is a mammalian cell. In some embodiments, the nucleic acid sequence encoding the engineered CRISPR nuclease is codon optimized for use in cells from a particular organism. In some embodiments, the nucleic acid sequence encoding the nuclease is codon optimized for *E. coli*. In some embodiments, the nucleic acid sequence encoding the

nuclease is codon optimized for eukaryotic cells. In some embodiments, the nucleic acid sequence encoding the nuclease is codon optimized for mammalian cells.

[0084] In some embodiments, the composition comprises a recombinant nucleic acid, comprising a heterologous promoter operably linked to a polynucleotide encoding a CRISPR enzyme having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90% identity to any of SEQ ID NOs: 1-17. Each possibility represents a separate embodiment.

[0085] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 1 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 18 and 35.

[0086] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 2 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 19 and 36.

[0087] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 3 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 20 and 37.

[0088] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 4 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 21 and 38.

[0089] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 5 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 22 and 39.

[0090] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 6 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 23 and 40.

[0091] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 7 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 24 and 41.

[0092] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 8 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 25 and 42.

[0093] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 9 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 26 and 43.

[0094] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 10 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 27 and 44.

[0095] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 11 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 28 and 45.

[0096] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 12 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 29 and 46.

[0097] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 13 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 30 and 47.

[0098] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 14 or the

sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 31 and 48.

[0099] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 15 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 32 and 49.

[00100] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 16 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 33 and 50.

[00101] In an embodiment of the composition, the CRISPR nuclease has at least 75%, 80%, 85, 90%, 95%, or 97% identity to the amino acid sequence as set forth in SEQ ID NO: 17 or the sequence encoding the CRISPR nuclease has at least a 75%, 80%, 85, 90%, 95%, or 97% sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOs: 34 and 51.

[00102] According to some embodiments, there is provided an engineered or non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease. Each possibility represents a separate embodiment.

In an embodiment, the CRISPR nuclease is engineered or non-naturally occurring. The CRISPR nuclease may also be recombinant. Such CRISPR nucleases are produced using laboratory methods (molecular cloning) to bring together genetic material from multiple sources, creating sequences that would not otherwise be found in biological organisms.

[00103] In an embodiment, the CRISPR nuclease of the invention exhibits increased specificity to a target site compared to a SpCas9 nuclease when complexed with the one or more RNA molecules.

[00104] In an embodiment, the complex of the CRISPR nuclease of the invention and one or more RNA molecules exhibits at least maintained on-target editing activity of the target site and reduced off-target activity compared to SpCas9 nuclease.

[00105] In an embodiment, the CRISPR nuclease further comprises an RNA-binding portion capable of interacting with a DNA-targeting RNA molecule (gRNA) and an activity portion that exhibits site-directed enzymatic activity.

[00106] In an embodiment, the composition further comprises a DNA-targeting RNA molecule or a DNA polynucleotide encoding a DNA-targeting RNA molecule, wherein the DNA-targeting RNA molecule comprises a guide sequence portion, i.e. a nucleotide sequence that is complementary to a sequence in a target region, wherein the DNA-targeting RNA molecule and the CRISPR nuclease do not naturally occur together.

[00107] In an embodiment, the DNA-targeting RNA molecule further comprises a nucleotide sequence that can form a complex with a CRISPR nuclease.

[00108] This invention also provides a non-naturally occurring composition comprising a CRISPR associated system comprising:

a) one or more RNA molecules comprising a guide sequence portion linked to a direct repeat sequence, wherein the guide sequence is capable of hybridizing with a target sequence, or one or more nucleotide sequences encoding the one or more RNA molecules; and

b) a CRISPR nuclease comprising an amino acid sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease;

wherein the one or more RNA molecules hybridize to the target sequence, wherein the target sequence is 3' of a Protospacer Adjacent Motif (PAM), and the one or more RNA molecules form a complex with the RNA-guided nuclease.

[00109] In an embodiment, the composition further comprises an RNA molecule comprising a nucleotide sequence that can form a complex with a CRISPR nuclease (e.g. a tracrRNA molecule) or a DNA polynucleotide comprising a sequence encoding an RNA molecule that can form a complex with the CRISPR nuclease.

[00110] In an embodiment, the composition further comprises a donor template for homology directed repair (HDR).

[00111] In an embodiment, the composition is capable of editing the target region in the genome of a cell.

[00112] According to some embodiments, there is provided a non-naturally occurring composition comprising:

(a) a CRISPR nuclease, or a polynucleotide encoding the CRISPR nuclease, comprising:

an RNA-binding portion; and

an activity portion that exhibits site-directed enzymatic activity, wherein the CRISPR nuclease has at least 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 85%, 80% identity to any of SEQ ID NOs: 1-17; and

(b) one or more RNA molecules or a DNA polynucleotide encoding the one or more RNA molecules comprising:

i) a DNA-targeting RNA sequence, comprising a nucleotide sequence that is complementary to a sequence in a target DNA sequence; and

ii) a protein-binding RNA sequence, capable of interacting with the RNA-binding portion of the CRISPR nuclease,

wherein the DNA targeting RNA sequence and the CRISPR nuclease do not naturally occur together. Each possibility represents a separate embodiment.

[00113] In some embodiments, there is provided a single RNA molecule comprising the DNA-targeting RNA sequence and the protein-binding RNA sequence, wherein the RNA molecule can form a complex with the CRISPR nuclease and serve as the DNA targeting module. In some embodiments, the RNA molecule has a length of up to 1000 bases, 900 bases, 800 bases, 700 bases, 600 bases, 500 bases, 400 bases, 300 bases, 200 bases, 100 bases, 50 bases. Each possibility represents a separate embodiment. In some embodiments, a first RNA molecule comprising the DNA-targeting RNA sequence and a second RNA molecule comprising the protein-binding RNA sequence interact by base pairing or alternatively fused together to form one or more RNA molecules that complex with the CRISPR nuclease and serve as the DNA targeting module.

[00114] This invention also provides a non-naturally occurring composition comprising:

a) a CRISPR nuclease comprising a sequence having at least 95% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease; and

b) one or more RNA molecules, or one or more DNA polynucleotide encoding the one or more RNA molecules, comprising at least one of:

i) a nuclease-binding RNA nucleotide sequence capable of interacting with/binding to the CRISPR nuclease; and

ii) a DNA-targeting RNA nucleotide sequence comprising a sequence complementary to a sequence in a target DNA sequence,

wherein the CRISPR nuclease is capable of complexing with the one or more RNA molecules to form a complex capable of hybridizing with the target DNA sequence.

[00115] In an embodiment, the CRISPR nuclease and the one or more RNA molecules form a CRISPR complex that is capable of binding to the target DNA sequence to effect cleavage of the target DNA sequence.

[00116] In an embodiment, the CRISPR nuclease and at least one of the one or more RNA molecules do not naturally occur together.

[00117] In an embodiment:

a) the CRISPR nuclease comprises an RNA-binding portion and an activity portion that exhibits site-directed enzymatic activity;

b) the DNA-targeting RNA nucleotide sequence comprises a nucleotide sequence that is complementary to a sequence in a target DNA sequence; and

c) the nuclease-binding RNA nucleotide sequence comprises a sequence that interacts with the RNA-binding portion of the CRISPR nuclease.

[00118] In an embodiment, the nuclease-binding RNA nucleotide sequence and the DNA-targeting RNA nucleotide sequence are on a single guide RNA molecule (sgRNA), wherein the sgRNA molecule can form a complex with the CRISPR nuclease and serve as the DNA targeting module.

[00119] In an embodiment, the nuclease-binding RNA nucleotide sequence is on a first RNA molecule and the DNA-targeting RNA nucleotide sequence is on a second RNA molecule, and wherein the first and second RNA molecules interact by base-pairing or are fused together to form a RNA complex or sgRNA that forms a complex with the CRISPR nuclease and serves as a DNA targeting module.

[00120] In an embodiment, the sgRNA has a length of up to 1000 bases, 900 bases, 800 bases, 700 bases, 600 bases, 500 bases, 400 bases, 300 bases, 200 bases, 100 bases, 50 bases.

[00121] In an embodiment, the composition further comprises a donor template for homology directed repair (HDR).

[00122]

[00123] In an embodiment, the CRISPR nuclease is non-naturally occurring.

[00124] In an embodiment, the CRISPR nuclease is engineered and comprises unnatural or synthetic amino acids.

[00125] In an embodiment, the CRISPR nuclease is engineered and comprises one or more of a nuclear localization sequences (NLS), cell penetrating peptide sequences, and/or affinity tags.

[00126] In an embodiment, the CRISPR nuclease comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of a CRISPR complex comprising the CRISPR nuclease in a detectable amount in the nucleus of a eukaryotic cell.

[00127] This invention also provides a method of modifying a nucleotide sequence at a target site in a cell-free system or the genome of a cell comprising introducing into the cell any of the compositions of the invention.

[00128] In an embodiment, the cell is a eukaryotic cell.

[00129] In another embodiment, the cell is a prokaryotic cell.

[00130] In some embodiments, the one or more RNA molecules further comprises an RNA sequence comprising a nucleotide molecule that can form a complex with the RNA nuclease (tracrRNA) or a DNA polynucleotide encoding an RNA molecule comprising a nucleotide sequence that can form a complex with the CRISPR nuclease.

[00131] In an embodiment, the CRISPR nuclease comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the amino-terminus, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near carboxy-terminus, or a combination of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the amino-terminus and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near carboxy-terminus. In an embodiment 1-4 NLSs are fused with the CRISPR nuclease. In an embodiment, an NLS is located within the open-reading frame (ORF) of the CRISPR nuclease.

[00132] Methods of fusing an NLS at or near the amino-terminus, at or near carboxy-terminus, or within the ORF of an expressed protein are well known in the art. As an example, to fuse an NLS to the amino-terminus of a CRISPR nuclease, the nucleic acid sequence of the NLS is placed immediately after the start codon of the CRISPR nuclease on the nucleic acid encoding the NLS-fused CRISPR nuclease. Conversely, to fuse an NLS to the carboxy-terminus of a CRISPR nuclease the nucleic acid sequence of the NLS is placed after the codon encoding the last amino acid of the CRISPR nuclease and before the stop codon.

[00133] Any combination of NLSs, cell penetrating peptide sequences, and/or affinity tags at any position along the ORF of the CRISPR nuclease is contemplated in this invention.

[00134] The amino acid sequences and nucleic acid sequences of the CRISPR nucleases provided herein may include NLS and/or TAGs inserted so as to interrupt the contiguous amino acid or nucleic acid sequences of the CRISPR nucleases.

[00135] In an embodiment, the one or more NLSs are in tandem repeats.

[00136] In an embodiment, the one or more NLSs are considered in proximity to the N- or C-terminus when the nearest amino acid of the NLS is within about 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more amino acids along the polypeptide chain from the N- or C-terminus.

[00137] As discussed, the CRISPR nuclease may be engineered to comprise one or more of a nuclear localization sequences (NLS), cell penetrating peptide sequences, and/or affinity tags.

[00138] In an embodiment, the CRISPR nuclease exhibits increased specificity to a target site compared to the wild-type of the CRISPR nuclease when complexed with the one or more RNA molecules.

[00139] In an embodiment, the complex of the CRISPR nuclease and one or more RNA molecules exhibits at least maintained on-target editing activity of the target site and reduced off-target activity compared to the wild-type of the CRISPR nuclease.

[00140] In an embodiment, the composition further comprises a recombinant nucleic acid molecule comprising a heterologous promoter operably linked to the nucleotide acid molecule comprising the sequence encoding the CRISPR nuclease.

[00141] In an embodiment, the CRISPR nuclease or nucleic acid molecule comprising a sequence encoding the CRISPR nuclease is non-naturally occurring or engineered.

[00142] This invention also provides a non-naturally occurring or engineered composition comprising a vector system comprising the nucleic acid molecule comprising a sequence encoding any of the CRISPR nucleases of the invention.

[00143] This invention also provides use of any of the compositions of the invention for the treatment of a subject afflicted with a disease associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00144] This invention provides a method of modifying a nucleotide sequence at a target site in the genome of a mammalian cell comprising introducing into the cell (i) a composition comprising a CRISPR nuclease having at least 95% identity to an amino acid sequence selected from the group consisting of SEQ ID NOs: 1-17 or a nucleic acid molecule comprising a sequence encoding a CRISPR nuclease which sequence has at least 95% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 18-51 and (ii) a DNA-targeting RNA molecule, or a DNA polynucleotide encoding a DNA-targeting RNA molecule, comprising a nucleotide sequence that is complementary to a sequence in the target DNA.

[00145] In some embodiments, the method is performed ex vivo. In some embodiments, the method is performed in vivo. In some embodiments, some steps of the method are performed ex vivo and some steps are performed in vivo. In some embodiments the mammalian cell is a human cell.

[00146] In an embodiment, the method further comprises introducing into the cell: (iii) an RNA molecule comprising a tracrRNA sequence or a DNA polynucleotide encoding an RNA molecule comprising a tracrRNA sequence.

[00147] In an embodiment, the DNA-targeting RNA molecule comprises a crRNA repeat sequence.

[00148] In an embodiment, the RNA molecule comprising a tracrRNA sequence is able to bind the DNA-targeting RNA molecule.

[00149] In an embodiment, the DNA-targeting RNA molecule and the RNA molecule comprising a tracrRNA sequence interact to form an RNA complex, and the RNA complex is capable of forming an active complex with the CRISPR nuclease.

[00150] In an embodiment, the DNA-targeting RNA molecule and the RNA molecule comprising a nuclease-binding RNA sequence are fused in the form of a single guide RNA molecule that is suitable to form an active complex with the CRISPR nuclease.

[00151] In an embodiment, the guide sequence portion comprises a sequence complementary to a protospacer sequence.

[00152] In an embodiment, the CRISPR nuclease forms a complex with the DNA-targeting RNA molecule and effects a double strand break in a region that is 3' or 5' of a Protospacer Adjacent Motif (PAM).

[00153] In an embodiment of any of the methods described herein, the method is for treating a subject afflicted with a disease associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00154] In an embodiment, the method comprises first selecting a subject afflicted with a disease associated with a genomic mutation and obtaining the cell from the subject.

[00155] This invention also provides a modified cell or cells obtained by any of the methods described herein. In an embodiment these modified cell or cells are capable of giving rise to progeny cells. In an embodiment these modified cell or cells are capable of giving rise to progeny cells after engraftment.

[00156] This invention also provides a composition comprising these modified cells and a pharmaceutically acceptable carrier. Also provided is an *in vitro* or *ex vivo* method of preparing this, comprising mixing the cells with the pharmaceutically acceptable carrier.

DNA-targeting RNA molecules

[00157] The "guide sequence portion" of an RNA molecule refers to a nucleotide sequence that is capable of hybridizing to a specific target DNA sequence, e.g., the guide sequence portion has a nucleotide sequence which is partially or fully complementary to the DNA sequence being targeted along the length of the guide sequence portion. In some embodiments, the guide sequence portion is 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 nucleotides in length, or approximately 17-50, 17-49, 17-48, 17-47, 17-46, 17-45, 17-44, 17-43, 17-42, 17-41, 17-40, 17-39, 17-38, 17-37, 17-36, 17-35, 17-34, 17-33, 17-31, 17-30, 17-29, 17-28, 17-27, 17-26, 17-25, 17-24, 17-22, 17-21, 18-25, 18-24,

18-23, 18-22, 18-21, 19-25, 19-24, 19-23, 19-22, 19-21, 19-20, 20-22, 18-20, 20-21, 21-22, or 17-20 nucleotides in length. The entire length of the guide sequence portion is fully complementary to the DNA sequence being targeted along the length of the guide sequence portion. The guide sequence portion may be part of an RNA molecule that can form a complex with a CRISPR nuclease with the guide sequence portion serving as the DNA targeting portion of the CRISPR complex. When the DNA molecule having the guide sequence portion is present contemporaneously with the CRISPR molecule the RNA molecule is capable of targeting the CRISPR nuclease to the specific target DNA sequence. Each possibility represents a separate embodiment. An RNA molecule can be custom designed to target any desired sequence. Accordingly, a molecule comprising a "guide sequence portion" is a type of targeting molecule. Throughout this application, the terms "guide molecule," "RNA guide molecule," "guide RNA molecule," and "gRNA molecule" are synonymous with a molecule comprising a guide sequence portion, and the term "spacer" is synonymous with a "guide sequence portion.

[00158] In embodiments of the present invention, the CRISPR nuclease has its greatest cleavage activity when used with an RNA molecule comprising a guide sequence portion having 17, 18, 19 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides.

[00159] A single-guide RNA (sgRNA) molecule may be used to direct a CRISPR nuclease to a desired target site. The single-guide RNA comprises a guide sequence portion as well as a scaffold portion. The scaffold portion interacts with a CRISPR nuclease and, together with a guide sequence portion, activates and targets the CRISPR nuclease to a desired target site. A scaffold portion may be further engineered, for example, to have a reduced size.

[00160] According to some aspects of the invention, the disclosed methods comprise a method of modifying a nucleotide sequence at a target site in a cell-free system or the genome of a cell comprising introducing into the cell the composition of any one of the embodiments described herein.

[00161] In some embodiments, the cell is a eukaryotic cell, preferably a mammalian cell or a plant cell.

[00162] According to some aspects of the invention, the disclosed methods comprise a use of any one of the compositions described herein for the treatment of a subject afflicted with a disease

associated with a genomic mutation comprising modifying a nucleotide sequence at a target site in the genome of the subject.

[00163] According to some aspects of the invention, the disclosed methods comprise a method of treating subject having a mutation disorder comprising targeting any one of the compositions described herein to an allele associated with the mutation disorder.

[00164] In some embodiments, the mutation disorder is related to a disease or disorder selected from any of a neoplasia, age-related macular degeneration, schizophrenia, neurological, neurodegenerative, or movement disorder, Fragile X Syndrome, secretase-related disorders, prion-related disorders, ALS, addiction, autism, Alzheimer's Disease, neutropenia, inflammation-related disorders, Parkinson's Disease, blood and coagulation diseases and disorders, beta thalassemia, sickle cell anemia, cell dysregulation and oncology diseases and disorders, inflammation and immune-related diseases and disorders, metabolic, liver, hypercholesteremia, kidney and protein diseases and disorders, muscular and skeletal diseases and disorders, dermatological diseases and disorders, neurological and neuronal diseases and disorders, pulmonary disease and disorders, corneal disease and disorders, retinal diseases and disorders, and ocular diseases and disorders.

Diseases and therapies

[00165] Certain embodiments of the invention target a nuclease to a specific genetic locus associated with a disease or disorder as a form of gene editing, method of treatment, or therapy. For example, to induce editing or knockout of a gene, a novel nuclease disclosed herein may be specifically targeted to a pathogenic mutant allele of the gene using a custom designed guide RNA molecule. The guide RNA molecule is preferably designed by first considering the PAM requirement of the nuclease, which as shown herein is also dependent on the system in which the gene editing is being performed. For example, a guide RNA molecule designed to target an OMNI-115 nuclease to a target site is designed to contain a spacer region complementary to a DNA strand of a DNA double-stranded region that neighbors a OMNI-115 PAM sequence, e.g. "NNRYTT" or "NNRTTT." The guide RNA molecule is further preferably designed to contain a spacer region (i.e. the region of the guide RNA molecule having complementarity to the target allele) of sufficient and preferably optimal length in order to increase specific activity of the nuclease and reduce off-target effects.

[00166] As a non-limiting example, the guide RNA molecule may be designed to target the nuclease to a specific region of a mutant allele, e.g. near the start codon, such that upon DNA damage caused by the nuclease a non-homologous end joining (NHEJ) pathway is induced and leads to silencing of the mutant allele by introduction of frameshift mutations. This approach to guide RNA molecule design is particularly useful for altering the effects of dominant negative mutations and thereby treating a subject. As a separate non-limiting example, the guide RNA molecule may be designed to target a specific pathogenic mutation of a mutated allele, such that upon DNA damage caused by the nuclease a homology directed repair (HDR) pathway is induced and leads to template mediated correction of the mutant allele. This approach to guide RNA molecule design is particularly useful for altering haploinsufficiency effects of a mutated allele and thereby treating a subject.

[00167] Non-limiting examples of specific genes which may be targeted for alteration to treat a disease or disorder are presented herein below. Specific disease-associated genes and mutations that induce a mutation disorder are described in the literature. Such mutations can be used to design a DNA-targeting RNA molecule to target a CRISPR composition to an allele of the disease associated gene, where the CRISPR composition causes DNA damage and induces a DNA repair pathway to alter the allele and thereby treat the mutation disorder.

[00168] Mutations in the ELANE gene are associated with neutropenia. Accordingly, without limitation, embodiments of the invention that target ELANE may be used in methods of treating subjects afflicted with neutropenia.

[00169] CXCR4 is a co-receptor for the human immunodeficiency virus type 1 (HIV-1) infection. Accordingly, without limitation, embodiments of the invention that target CXCR4 may be used in methods of treating subjects afflicted with HIV-1 or conferring resistance to HIV-1 infection in a subject.

[00170] Programmed cell death protein 1 (PD-1) disruption enhances CAR-T cell mediated killing of tumor cells and PD-1 may be a target in other cancer therapies. Accordingly, without limitation, embodiments of the invention that target PD-1 may be used in methods of treating subjects afflicted with cancer. In an embodiment, the treatment is CAR-T cell therapy with T cells that have been modified according to the invention to be PD-1 deficient.

[00171] In addition, BCL11A is a gene that plays a role in the suppression of hemoglobin production. Globin production may be increased to treat diseases such as thalassemia or sickle cell anemia by inhibiting BCL11A. See for example, PCT International Publication No. WO 2017/077394A2; U.S. Publication No. US2011/0182867A1; Humbert et al. Sci. Transl. Med. (2019); and Canver et al. Nature (2015). Accordingly, without limitation, embodiments of the invention that target an enhancer of BCL11A may be used in methods of treating subjects afflicted with beta thalassemia or sickle cell anemia.

[00172] Embodiments of the invention may also be used for targeting any disease-associated gene, for studying, altering, or treating any of the diseases or disorders listed in Table A or Table B below. Indeed, any disease-associated with a genetic locus may be studied, altered, or treated by using the nucleases disclosed herein to target the appropriate disease-associated gene, for example, those listed in U.S. Publication No. 2018/0282762A1 and European Patent No. EP3079726B1.

Table A - Diseases, Disorders and their associated genes

DISEASE / DISORDERS	**GENE(S)**
Neoplasia	PTEN; ATM; ATR; EGFR; ERBB2; ERBB3; ERBB4; Notch1; Notch2; Notch3; Notch4; AKT; AKT2; AKT3; HIF; HIF1a; HIF3a; Met; HRG; Bcl2; PPAR alpha; PPAR gamma; WT1 (Wilms Tumor); FGF Receptor Family members (5 members: 1, 2, 3, 4, 5); CDKN2a; APC; RB (retinoblastoma); MEN1; VHL; BRCA1; BRCA2; AR (Androgen Receptor); TSG101; IGF; IGF Receptor; Igf1 (4 variants); gf2 (3 variants); Igf 1 Receptor; Igf 2 Receptor; Bax; Bcl2; caspases family (9 members: 1, 2, 3, 4, 6, 7, 8, 9, 12); Kras; Apc
Age-related Macular Degeneration	Abcr; Ccl2; Cc2; cp (ceruloplasmin); Timp3; cathepsinD; Vldlr; Ccr2
Schizophrenia	Neuregulin1 (Nrg1); Erb4 (receptor for Neuregulin); Complexin1 (Cplx1); Tph1 Tryptophan hydroxylase; Tph2 Tryptophan hydroxylase 2; Neurexin 1; GSK3; GSK3a; GSK3b
Neurological, Neuro degenerative, and Movement Disorders	5-HTT (S1c6a4); COMT; DRD (Drd1a); SLC6A3; DAOA; DTNBP1; Dao (Dao1)
Trinucleotide Repeat Disorders	HTT (Huntington's Dx); SBMA/SMAX1/AR (Kennedy's Dx); FXN/X25 (Friedrich's Ataxia); ATX3 (Machado-Joseph's Dx); ATXN1 and ATXN2 (spinocerebellar ataxias); DMPK

DISEASE / DISORDERS	GENE(S)
	(myotonic dystrophy); Atrophin-1 and Atn1 (DRPLA Dx); CBP (Creb-BP - global instability); VLDLR (Alzheimer's); Atxn7; Atxn10
Fragile X Syndrome	FMR2; FXR1; FXR2; mGLUR5
Secretase Related Disorders	APH-1 (alpha and beta); Presenilin (Psen1); nicastrin (Ncstn); PEN-2
Others	Nos1; Parp1; Nat1; Nat2
Prion related disorders	Prp
ALS	SOD1; ALS2; STEX; FUS; TARDBP; VEGF (VEGF-a; VEGF-b; VEGF-c)
Addiction	Prkce (alcohol); Drd2; Drd4; ABAT (alcohol); GRIA2; Grm5; Grin1; Htr1b; Grin2a; Drd3; Pdyn; Gria1 (alcohol)
Autism	Mecp2; BZRAP1; MDGA2; Sema5A; Neurexin 1; Fragile X (FMR2 (AFF2); FXR1; FXR2; Mglur5)
Alzheimer's Disease	E1; CHIP; UCH; UBB; Tau; LRP; PICALM; Clusterin; PS1; SORL1; CR1; Vldlr; Uba1; Uba3; CHIP28 (Aqp1, Aquaporin 1); Uchl1; Uchl3; APP
Inflammation	IL-10; IL-1 (IL-1a; IL-1b); IL-13; IL-17 (IL-17a (CTLA8); IL-17b; IL-17c; IL-17d; IL-17f); II-23; Cx3cr1; ptpn22; TNFa; NOD2/CARD15 for IBD; IL-6; IL-12 (IL-12a; IL-12b); CTLA4; Cx3cl1
Parkinson's Disease	x-Synuclein; DJ-1; LRRK2; Parkin; PINK1

Table B - Diseases, Disorders and their associated genes

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
Blood and coagulation diseases and disorders	Anemia (CDAN1, CDA1, RPS19, DBA, PKLR, PK1, NT5C3, UMPH1, PSN1, RHAG, RH50A, NRAMP2, SPTB, ALAS2, ANH1, ASB, ABCB7, ABC7, ASAT); Bare lymphocyte

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	syndrome (TAPBP, TPSN, TAP2, ABCB3, PSF2, RING11, MHC2TA, C2TA, RFX5, RFXAP, RFX5), Bleeding disorders (TBXA2R, P2RX1, P2X1); Factor H and factor H-like 1 (HF1, CFH, HUS); Factor V and factor VIII (MCFD2); Factor VII deficiency (F7); Factor X deficiency (F10); Factor XI deficiency (F11); Factor XII deficiency (F12, HAF); Factor XIIIA deficiency (F13A1, F13A); Factor XIIIB deficiency (F13B); Fanconi anemia (FANCA, FACA, FA1, FA, FAA, FAAP95, FAAP90, FLJ34064, FANCB, FANCC, FACC, BRCA2, FANCD1, FANCD2, FANCD, FACD, FAD, FANCE, FACE, FANCF, XRCC9, FANCG, BRIP1, BACH1, FANCJ, PHF9, FANCL, FANCM, KIAA1596); Hemophagocytic lymphohistiocytosis disorders (PRF1, HPLH2, UNC13D, MUNC13-4, HPLH3, HLH3, FHL3); Hemophilia A (F8, F8C, HEMA); Hemophilia B (F9, HEMB), Hemorrhagic disorders (PI, ATT, F5); Leukocyde deficiencies and disorders (ITGB2, CD18, LCAMB, LAD, EIF2B1, EIF2BA, EIF2B2, EIF2B3, EIF2B5, LVWM, CACH, CLE, EIF2B4); Sickle cell anemia (HBB); Thalassemia (HBA2, HBB, HBD, LCRB, HBA1)
Cell dysregulation and oncology diseases and disorders	B-cell non-Hodgkin lymphoma (BCL7A, BCL7); Leukemia (TAL1, TCL5, SCL, TAL2, FLT3, NBS1, NBS, ZNFN1A1, IK1, LYF1, HOXD4, HOX4B, BCR, CML, PHL, ALL, ARNT, KRAS2, RASK2, GMPS, AF10, ARHGEF12, LARG, KIAA0382, CALM, CLTH, CEBPA, CEBP, CHIC2, BTL, FLT3, KIT, PBT, LPP, NPM1, NUP214, D9S46E, CAN, CAIN, RUNX1, CBFA2, AML1, WHSC1L1, NSD3, FLT3, AF1Q, NPM1, NUMA1, ZNF145, PLZF, PML, MYL, STAT5B, AF10, CALM, CLTH, ARL11, ARLTS1, P2RX7, P2X7, BCR, CML, PHL, ALL, GRAF, NF1, VRNF, WSS, NFNS, PTPN11, PTP2C, SHP2, NS1, BCL2, CCND1, PRAD1, BCL1, TCRA, GATA1, GF1, ERYF1, NFE1, ABL1, NQO1, DIA4, NMOR1, NUP214, D9S46E, CAN, CAIN)
Inflammation and immune related diseases and disorders	AIDS (KIR3DL1, NKAT3, NKB1, AMB11, KIR3DS1, IFNG, CXCL12, SDF1); Autoimmune lymphoproliferative syndrome (TNFRSF6, APT1, FAS, CD95, ALPS1A); Combined immunodeficiency, (IL2RG, SCIDX1, SCIDX, IMD4); HIV-1 (CCL5, SCYA5, D17S136E, TCP228), HIV susceptibility or infection (IL10, CSIF, CMKBR2, CCR2, CMKBR5, CCCKR5 (CCR5)); Immunodeficiencies (CD3E, CD3G, AICDA, AID, HIGM2, TNFRSF5, CD40, UNG, DGU, HIGM4, TNFSF5, CD40LG, HIGM1, IGM, FOXP3, IPEX, AIID, XPID, PIDX,

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	TNFRSF14B, TACI); Inflammation (IL-10, IL-1 (IL-1a, IL-1b), IL-13, IL-17 (IL-17a (CTLA8), IL-17b, IL-17c, IL- 17d, IL-17f), II-23, Cx3cr1, ptpn22, TNFa, NOD2/CARD15 for IBD, IL-6, IL-12 (IL-12a, IL-12b), CTLA4, Cx3cl1); Severe combined immunodeficiencies (SCIDs)(JAK3, JAKL, DCLRE1C, ARTEMIS, SCIDA, RAG1, RAG2, ADA, PTPRC, CD45, LCA, IL7R, CD3D, T3D, IL2RG, SCIDX1, SCIDX, IMD4)
Metabolic, liver, kidney and protein diseases and disorders	Amyloid neuropathy (TTR, PALB); Amyloidosis (APOA1, APP, AAA, CVAP, AD1, GSN, FGA, LYZ, TTR, PALB); Cirrhosis (KRT18, KRT8, CIRH1A, NAIC, TEX292, KIAA1988); Cystic fibrosis (CFTR, ABCC7, CF, MRP7); Glycogen storage diseases (SLC2A2, GLUT2, G6PC, G6PT, G6PT1, GAA, LAMP2, LAMPB, AGL, GDE, GBE1, GYS2, PYGL, PFKM); Hepatic adenoma, 142330 (TCF1, HNF1A, MODY3), Hepatic failure, early onset, and neurologic disorder (SCOD1, SCO1), Hepatic lipase deficiency (LIPC), Hepatoblastoma, cancer and carcinomas (CTNNB1, PDGFRL, PDGRL, PRLTS, AXIN1, AXIN, CTNNB1, TP53, P53, LFS1, IGF2R, MPRI, MET, CASP8, MCH5; Medullary cystic kidney disease (UMOD, HNFJ, FJHN, MCKD2, ADMCKD2); Phenylketonuria (PAH, PKU1, QDPR, DHPR, PTS); Polycystic kidney and hepatic disease (FCYT, PKHD1, ARPKD, PKD1, PKD2, PKD4, PKDTS, PRKCSH, G19P1, PCLD, SEC63)
Muscular / Skeletal diseases and disorders	Becker muscular dystrophy (DMD, BMD, MYF6), Duchenne Muscular Dystrophy (DMD, BMD); Emery-Dreifuss muscular dystrophy (LMNA, LMN1, EMD2, FPLD, CMD1A, HGPS, LGMD1B, LMNA, LMN1, EMD2, FPLD, CMD1A); Facioscapulohumeral muscular dystrophy (FSHMD1A, FSHD1A); Muscular dystrophy (FKRP, MDC1C, LGMD2I, LAMA2, LAMM, LARGE, KIAA0609, MDC1D, FCMD, TTID, MYOT, CAPN3, CANP3, DYSF, LGMD2B, SGCG, LGMD2C, DMDA1, SCG3, SGCA, ADL, DAG2, LGMD2D, DMDA2, SGCB, LGMD2E, SGCD, SGD, LGMD2F, CMD1L, TCAP, LGMD2G, CMD1N, TRIM32, HT2A, LGMD2H, FKRP, MDC1C, LGMD2I, TTN, CMD1G, TMD, LGMD2J, POMT1, CAV3, LGMD1C, SEPN1, SELN, RSMD1, PLEC1, PLTN, EBS1); Osteopetrosis (LRP5, BMND1, LRP7, LR3, OPPG, VBCH2, CLCN7, CLC7, OPTA2, OSTM1, GL, TCIRG1, TIRC7, OC116, OPTB1); Muscular atrophy (VAPB, VAPC, ALS8, SMN1, SMA1, SMA2, SMA3, SMA4, BSCL2,

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
	SPG17, GARS, SMAD1, CMT2D, HEXB, IGHMBP2, SMUBP2, CATF1, SMARD1)
Dermatological diseases and disorders	Albinisim (TYR, OCA2, TYRP1, SLC45A2, LYST), Ectodermal dysplasias (EDAR, EDARADD, WNT10A), Ehlers-Danlos syndrome (COL5A1, COL5A2, COL1A1, COL1A2, COL3A1, TNXB, ADAMTS2, PLOD1, FKBP14), Ichthyosis-associated disorders (FLG, STS, TGM1, ALOXE3/ALOX12B, KRT1, KRT10, ABCA12, KRT2, GJB2, TGM1, ABCA12, CYP4F22, ALOXE3, CERS3, NSHDL, EBP, MBTPS2, GJB2, SPINK5, AGHD5, PHYH, PEX7, ALDH3A2, ERCC2, ERCC3, GFT2H5, GBA), Incontinentia pigmenti (IKBKG, NEMO), Tuberous sclerosis (TSC1, TSC2), Premature aging syndromes (POLR3A, PYCR1, LMNA, POLD1, WRN, DMPK)
Neurological and Neuronal diseases and disorders	ALS (SOD1, ALS2, STEX, FUS, TARDBP, VEGF (VEGF-a, VEGF-b, VEGF-c); Alzheimer disease (APP, AAA, CVAP, AD1, APOE, AD2, PSEN2, AD4, STM2, APBB2, FE65L1, NOS3, PLAU, URK, ACE, DCP1, ACE1, MPO, PACIP1, PAXIP1L, PTIP, A2M, BLMH, BMH, PSEN1, AD3); Autism (Mecp2, BZRAP1, MDGA2, Sema5A, Neurexin 1, GLO1, MECP2, RTT, PPMX, MRX16, MRX79, NLGN3, NLGN4, KIAA1260, AUTSX2); Fragile X Syndrome (FMR2, FXR1, FXR2, mGLUR5); Huntington's disease and disease like disorders (HD, IT15, PRNP, PRIP, JPH3, JP3, HDL2, TBP, SCA17); Parkinson disease (NR4A2, NURR1, NOT, TINUR, SNCAIP, TBP, SCA17, SNCA, NACP, PARK1, PARK4, DJ1, PARK7, LRRK2, PARK8, PINK1, PARK6, UCHL1, PARK5, SNCA, NACP, PARK1, PARK4, PRKN, PARK2, PDJ, DBH, NDUFV2); Rett syndrome (MECP2, RTT, PPMX, MRX16, MRX79, CDKL5, STK9, MECP2, RTT, PPMX, MRX16, MRX79, x-Synuclein, DJ-1); Schizophrenia (Neuregulin1 (Nrg1), Erb4 (receptor for Neuregulin), Complexin1 (Cplx1), Tph1 Tryptophan hydroxylase, Tph2, Tryptophan hydroxylase 2, Neurexin 1, GSK3, GSK3a, GSK3b, 5-HTT (Slc6a4), COMT, DRD (Drd1a), SLC6A3, DAOA, DTNBP1, Dao (Dao1)); Secretase Related Disorders (APH-1 (alpha and beta), Presenilin (Psen1), nicastrin, (Ncstn), PEN-2, Nos1, Parp1, Natl, Nat2); Trinucleotide Repeat Disorders (HTT (Huntington's Dx), SBMA/SMAX1/AR (Kennedy's Dx), FXN/X25 (Friedrich's Ataxia), ATX3 (Machado-Joseph's Dx), ATXN1 and ATXN2 (spinocerebellar ataxias), DMPK (myotonic dystrophy), Atrophin-1 and Atn1 (DRPLA Dx), CBP (Creb-BP - global instability), VLDLR (Alzheimer's), Atxn7, Atxn10)

DISEASE CATEGORY	DISEASE AND ASSOCIATED GENES
Ocular diseases and disorders	Age-related macular degeneration (Abcr, Ccl2, Cc2, cp (ceruloplasmin), Timp3, cathepsinD, Vldlr, Ccr2); Cataract (CRYAA, CRYA1, CRYBB2, CRYB2, PITX3, BFSP2, CP49, CP47, CRYAA, CRYA1, PAX6, AN2, MGDA, CRYBA1, CRYB1, CRYGC, CRYG3, CCL, LIM2, MP19, CRYGD, CRYG4, BFSP2, CP49, CP47, HSF4, CTM, HSF4, CTM, MIP, AQP0, CRYAB, CRYA2, CTPP2, CRYBB1, CRYGD, CRYG4, CRYBB2, CRYB2, CRYGC, CRYG3, CCL, CRYAA, CRYA1, GJA8, CX50, CAE1, GJA3, CX46, CZP3, CAE3, CCM1, CAM, KRIT1); Corneal clouding and dystrophy (APOA1, TGFBI, CSD2, CDGG1, CSD, BIGH3, CDG2, TACSTD2, TROP2, M1S1, VSX1, RINX, PPCD, PPD, KTCN, COL8A2, FECD, PPCD2, PIP5K3, CFD); Cornea plana congenital (KERA, CNA2); Glaucoma (MYOC, TIGR, GLC1A, JOAG, GPOA, OPTN, GLC1E, FIP2, HYPL, NRP, CYP1B1, GLC3A, OPA1, NTG, NPG, CYP1B1, GLC3A); Leber congenital amaurosis (CRB1, RP12, CRX, CORD2, CRD, RPGRIP1, LCA6, CORD9, RPE65, RP20, AIPL1, LCA4, GUCY2D, GUC2D, LCA1, CORD6, RDH12, LCA3); Macular dystrophy (ELOVL4, ADMD, STGD2, STGD3, RDS, RP7, PRPH2, PRPH, AVMD, AOFMD, VMD2)

[00173] Unless otherwise defined, all technical and/or scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of embodiments of the invention, exemplary methods and/or materials are described below. In case of conflict, the patent specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not intended to be necessarily limiting.

[00174] In the discussion unless otherwise stated, adjectives such as "substantially" and "about" modifying a condition or relationship characteristic of a feature or features of an embodiment of the invention, are understood to mean that the condition or characteristic is defined to within tolerances that are acceptable for operation of the embodiment for an application for which it is intended. Unless otherwise indicated, the word "or" in the specification and claims is considered

to be the inclusive "or" rather than the exclusive or, and indicates at least one of and any combination of items it conjoins.

[00175] It should be understood that the terms "a" and "an" as used above and elsewhere herein refer to "one or more" of the enumerated components. It will be clear to one of ordinary skill in the art that the use of the singular includes the plural unless specifically stated otherwise. Therefore, the terms "a," "an" and "at least one" are used interchangeably in this application.

[00176] For purposes of better understanding the present teachings and in no way limiting the scope of the teachings, unless otherwise indicated, all numbers expressing quantities, percentages or proportions, and other numerical values used in the specification and claims, are to be understood as being modified in all instances by the term "about." Accordingly, unless indicated to the contrary, the numerical parameters set forth in the following specification and attached claims are approximations that may vary depending upon the desired properties sought to be obtained. At the very least, each numerical parameter should at least be construed in light of the number of reported significant digits and by applying ordinary rounding techniques.

[00177] It is understood that where a numerical range is recited herein, the present invention contemplates each integer between, and including, the upper and lower limits, unless otherwise stated.

[00178] In the description and claims of the present application, each of the verbs, "comprise," "include" and "have" and conjugates thereof, are used to indicate that the object or objects of the verb are not necessarily a complete listing of components, elements or parts of the subject or subjects of the verb. Other terms as used herein are meant to be defined by their well-known meanings in the art.

[00179] The terms "polynucleotide", "nucleotide", "nucleotide sequence", "nucleic acid" and "oligonucleotide" are used interchangeably. They refer to a polymeric form of nucleotides of any length, either deoxyribonueleotides or ribonucleotides, or analogs thereof. Polynucleotides may have any three-dimensional structure, and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: coding or non-coding regions of a gene or gene fragment, loci (locus) defined from linkage analysis, exons, in Irons, messenger RNA (mRNA), transfer RNA, ribosomal RNA, short interfering RNA (siRNA), short-hairpin RNA (shRNA), micro-RNA (miRNA), ribozymes, cDNA, recombinant polynucleotides, branched

polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers, A polynucleotide may comprise one or more modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The sequence of nucleotides may be interrupted by non-nucleotide components. A polynucleotide may be further modified after polymerization, such as by conjugation with a labeling component.

[00180] The term "nucleotide analog" or "modified nucleotide" refers to a nucleotide that contains one or more chemical modifications (e.g., substitutions), in or on the nitrogenous base of the nucleoside (e.g., cytosine (C), thymine (T) or uracil (U), adenine (A) or guanine (G)), in or on the sugar moiety of the nucleoside (e.g., ribose, deoxyribose, modified ribose, modified deoxyribose, six-membered sugar analog, or open-chain sugar analog), or the phosphate. Each of the RNA sequences described herein may comprise one or more nucleotide analogs.

[00181] As used herein, the following nucleotide identifiers are used to represent a referenced nucleotide base(s):

Nucleotide reference	**Base(s) represented**			
A	A			
C		C		
G			G	
T				T
W	A			T
S		C	G	
M	A	C		
K			G	T
R	A		G	
Y		C		T
B		C	G	T
D	A		G	T
H	A	C		T
V	A	C	G	
N	A	C	G	T

[00182] As used herein, the term "targeting sequence" or "targeting molecule" refers a nucleotide sequence or molecule comprising a nucleotide sequence that is capable of hybridizing to a specific target sequence, e.g., the targeting sequence has a nucleotide sequence which is at least partially complementary to the sequence being targeted along the length of the targeting sequence. The targeting sequence or targeting molecule may be part of a targeting RNA molecule that can form a complex with a CRISPR nuclease with the targeting sequence serving as the targeting portion of the CRISPR complex. When the molecule having the targeting sequence is present contemporaneously with the CRISPR molecule, the RNA molecule is capable of targeting the CRISPR nuclease to the specific target sequence. Each possibility represents a separate embodiment. A targeting RNA molecule can be custom designed to target any desired sequence.

[00183] The term "targets" as used herein, refers to preferential hybridization of a targeting sequence or a targeting molecule to a nucleic acid having a targeted nucleotide sequence. It is understood that the term "targets" encompasses variable hybridization efficiencies, such that there is preferential targeting of the nucleic acid having the targeted nucleotide sequence, but unintentional off-target hybridization in addition to on-target hybridization might also occur. It is understood that where an RNA molecule targets a sequence, a complex of the RNA molecule and a CRISPR nuclease molecule targets the sequence for nuclease activity.

[00184] In the context of targeting a DNA sequence that is present in a plurality of cells, it is understood that the targeting encompasses hybridization of the guide sequence portion of the RNA molecule with the sequence in one or more of the cells, and also encompasses hybridization of the RNA molecule with the target sequence in fewer than all of the cells in the plurality of cells. Accordingly, it is understood that where an RNA molecule targets a sequence in a plurality of cells, a complex of the RNA molecule and a CRISPR nuclease is understood to hybridize with the target sequence in one or more of the cells, and also may hybridize with the target sequence in fewer than all of the cells. Accordingly, it is understood that the complex of the RNA molecule and the CRISPR nuclease introduces a double strand break in relation to hybridization with the target sequence in one or more cells and may also introduce a double strand break in relation to hybridization with the target sequence in fewer than all of the cells. As used herein, the term "modified cells" refers to cells in which a double strand break is affected by a complex of an RNA molecule and the CRISPR nuclease as a result of hybridization with the target sequence, i.e. on-target hybridization.

[00185] As used herein the term "wild type" is a term of the art understood by skilled persons and means the typical form of an organism, strain, gene or characteristic as it occurs in nature as distinguished from mutant or variant forms. Accordingly, as used herein, where a sequence of amino acids or nucleotides refers to a wild type sequence, a variant refers to variant of that sequence, e.g., comprising substitutions, deletions, insertions. In embodiments of the present invention, an engineered CRISPR nuclease is a variant CRISPR nuclease comprising at least one amino acid modification (e.g., substitution, deletion, and/or insertion) compared to the CRISPR nuclease of any of the CRISPR nucleases indicated in Table 1.

[00186] The terms "non-naturally occurring" or "engineered" are used interchangeably and indicate human manipulation. The terms, when referring to nucleic acid molecules or polypeptides may mean that the nucleic acid molecule or the polypeptide is at least substantially free from at least one other component with which they are naturally associated in nature and as found in nature.

[00187] As used herein the term "amino acid" includes natural and/or unnatural or synthetic amino acids, including glycine and both the D or I, optical isomers, and amino acid analogs and peptidomimetics.

[00188] As used herein, “genomic DNA” refers to linear and/or chromosomal DNA and/or to plasmid or other extrachromosomal DNA sequences present in the cell or cells of interest. In some embodiments, the cell of interest is a eukaryotic cell. In some embodiments, the cell of interest is a prokaryotic cell. In some embodiments, the methods produce double-stranded breaks (DSBs) at pre-determined target sites in a genomic DNA sequence, resulting in mutation, insertion, and/or deletion of DNA sequences at the target site(s) in a genome.

[00189] "Eukaryotic" cells include, but are not limited to, fungal cells (such as yeast), plant cells, animal cells, mammalian cells and human cells.

[00190] The term "nuclease" as used herein refers to an enzyme capable of cleaving the phosphodiester bonds between the nucleotide subunits of nucleic acid. A nuclease may be isolated or derived from a natural source. The natural source may be any living organism. Alternatively, a nuclease may be a modified or a synthetic protein which retains the phosphodiester bond cleaving activity.

[00191] The term "PAM" as used herein refers to a nucleotide sequence of a target DNA located in proximity to the targeted DNA sequence and recognized by the CRISPR nuclease. The PAM sequence may differ depending on the nuclease identity.

[00192] The term "mutation disorder" or "mutation disease" as used herein refers to any disorder or disease that is related to dysfunction of a gene caused by a mutation. A dysfunctional gene manifesting as a mutation disorder contains a mutation in at least one of its alleles and is referred to as a "disease-associated gene." The mutation may be in any portion of the disease-associated gene, for example, in a regulatory, coding, or non-coding portion. The mutation may be any class of mutation, such as a substitution, insertion, or deletion. The mutation of the disease-associated gene may manifest as a disorder or disease according to the mechanism of any type of mutation, such as a recessive, dominant negative, gain-of-function, loss-of-function, or a mutation leading to haploinsufficiency of a gene product.

[00193] A skilled artisan will appreciate that embodiments of the present invention disclose RNA molecules capable of complexing with a nuclease, e.g. a CRISPR nuclease, such as to associate with a target genomic DNA sequence of interest next to a protospacer adjacent motif (PAM). The nuclease then mediates cleavage of target DNA to create a double-stranded break within the protospacer.

[00194] In embodiments of the present invention, a CRISPR nuclease and a targeting molecule form a CRISPR complex that binds to a target DNA sequence to effect cleavage of the target DNA sequence. A CRISPR nuclease may form a CRISPR complex comprising the CRISPR nuclease and RNA molecule without a further, separate tracrRNA molecule. Alternatively, CRISPR nucleases may form a CRISPR complex between the CRISPR nuclease, an RNA molecule, and a tracrRNA molecule.

[00195] The term "protein binding sequence" or "nuclease binding sequence" refers to a sequence capable of binding with a CRISPR nuclease to form a CRISPR complex. A skilled artisan will understand that a tracrRNA capable of binding with a CRISPR nuclease to form a CRISPR complex comprises a protein or nuclease binding sequence.

[00196] An "RNA binding portion" of a CRISPR nuclease refers to a portion of the CRISPR nuclease which may bind to an RNA molecule to form a CRISPR complex, e.g. the nuclease binding sequence of a tracrRNA molecule. An "activity portion" or "active portion" of a CRISPR

nuclease refers to a portion of the CRISPR nuclease which effects a double strand break in a DNA molecule, for example when in complex with a DNA-targeting RNA molecule.

[00197] An RNA molecule may comprise a sequence sufficiently complementary to a tracrRNA molecule so as to hybridize to the tracrRNA via basepairing and promote the formation of a CRISPR complex. (See U.S. Patent No. 8,906,616). In embodiments of the present invention, the RNA molecule may further comprise a portion having a tracr mate sequence.

[00198] In embodiments of the present invention, the targeting molecule may further comprise the sequence of a tracrRNA molecule. Such embodiments may be designed as a synthetic fusion of the guide portion of the RNA molecule (gRNA or crRNA) and the trans-activating crRNA (tracrRNA), together forming a single guide RNA (sgRNA). (See Jinek et al., Science (2012)). Embodiments of the present invention may also form CRISPR complexes utilizing a separate tracrRNA molecule and a separate RNA molecule comprising a guide sequence portion. In such embodiments the tracrRNA molecule may hybridize with the RNA molecule via base pairing and may be advantageous in certain applications of the invention described herein.

[00199] In embodiments of the present invention an RNA molecule may comprise a "nexus" region and/or "hairpin" regions which may further define the structure of the RNA molecule. (See Briner et al., Molecular Cell (2014)).

[00200] As used herein, the term "direct repeat sequence" refers to two or more repeats of a specific amino acid sequence of nucleotide sequence.

[00201] As used herein, an RNA sequence or molecule capable of "interacting with" or "binding" with a CRISPR nuclease refers to the RNA sequence or molecules ability to form a CRISPR complex with the CRISPR nuclease.

[00202] As used herein, the term "operably linked" refers to a relationship (i.e. fusion, hybridization) between two sequences or molecules permitting them to function in their intended manner. In embodiments of the present invention, when an RNA molecule is operably linked to a promoter, both the RNA molecule and the promotor are permitted to function in their intended manner.

[00203] As used herein, the term "heterologous promoter" refers to a promoter that does not naturally occur together with the molecule or pathway being promoted.

[00204] As used herein, a sequence or molecule has an X% "sequence identity" to another sequence or molecule if X% of bases or amino acids between the sequences of molecules are the same and in the same relative position. For example, a first nucleotide sequence having at least a 95% sequence identity with a second nucleotide sequence will have at least 95% of bases, in the same relative position, identical with the other sequence.

Nuclear Localization Sequences

[00205] The terms "nuclear localization sequence" and "NLS" are used interchangeably to indicate an amino acid sequence/peptide that directs the transport of a protein with which it is associated from the cytoplasm of a cell across the nuclear envelope barrier. The term "NLS" is intended to encompass not only the nuclear localization sequence of a particular peptide, but also derivatives thereof that are capable of directing translocation of a cytoplasmic polypeptide across the nuclear envelope barrier. NLSs are capable of directing nuclear translocation of a polypeptide when attached to the N-terminus, the C-terminus, or both the N- and C-termini of the polypeptide. In addition, a polypeptide having an NLS coupled by its N- or C-terminus to amino acid side chains located randomly along the amino acid sequence of the polypeptide will be translocated. Typically, an NLS consists of one or more short sequences of positively charged lysines or arginines exposed on the protein surface, but other types of NLS are known. Non- limiting examples of NLSs include an NLS sequence derived from: the SV40 virus large T-antigen, nucleoplasmin, c-myc, the hRNPAl M9 NLS, the IBB domain from importin-alpha, myoma T protein, human p53, mouse c-abl IV, influenza vims NS1, Hepatitis virus delta antigen, mouse Mx1 protein, human poly(ADP-ribose) polymerase, and the steroid hormone receptors (human) glucocorticoid.

Delivery

[00206] The CRISPR nuclease or CRISPR compositions described herein may be delivered as a protein, DNA molecules, RNA molecules, Ribonucleoproteins (RNP), nucleic acid vectors, or any combination thereof. In some embodiments, the RNA molecule comprises a chemical modification. Non-limiting examples of suitable chemical modifications include 2'-0-methyl (M), 2'-0-methyl, 3'phosphorothioate (MS) or 2'-0-methyl, 3'thioPACE (MSP), pseudouridine, and 1-methyl pseudo-uridine. Each possibility represents a separate embodiment of the present invention.

[00207] The CRISPR nucleases and/or polynucleotides encoding same described herein, and optionally additional proteins (e.g., ZFPs, TALENs, transcription factors, restriction enzymes)

and/or nucleotide molecules such as guide RNA may be delivered to a target cell by any suitable means. The target cell may be any type of cell e.g., eukaryotic or prokaryotic, in any environment e.g., isolated or not, maintained in culture, *in vitro, ex vivo, in vivo* or *in planta*.

[00208] In some embodiments, the composition to be delivered includes mRNA of the nuclease and RNA of the guide. In some embodiments, the composition to be delivered includes mRNA of the nuclease, RNA of the guide and a donor template. In some embodiments, the composition to be delivered includes the CRISPR nuclease and guide RNA. In some embodiments, the composition to be delivered includes the CRISPR nuclease, guide RNA and a donor template for gene editing via, for example, homology directed repair. In some embodiments, the composition to be delivered includes mRNA of the nuclease, DNA-targeting RNA and the tracrRNA. In some embodiments, the composition to be delivered includes mRNA of the nuclease, DNA-targeting RNA and the tracrRNA and a donor template. In some embodiments, the composition to be delivered includes the CRISPR nuclease DNA-targeting RNA and the tracrRNA. In some embodiments, the composition to be delivered includes the CRISPR nuclease, DNA-targeting RNA and the tracrRNA and a donor template for gene editing via, for example, homology directed repair.

[00209] Any suitable viral vector system may be used to deliver RNA compositions. Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids and/or CRISPR nuclease in cells (e.g., mammalian cells, plant cells, etc.) and target tissues. Such methods can also be used to administer nucleic acids encoding and/or CRISPR nuclease protein to cells in vitro. In certain embodiments, nucleic acids and/or CRISPR nuclease are administered for in vivo or ex vivo gene therapy uses. Non-viral vector delivery systems include naked nucleic acid, and nucleic acid complexed with a delivery vehicle such as a liposome or poloxamer. For a review of gene therapy procedures, see Anderson, Science (1992); Nabel and Felgner, TIBTECH (1993); Mitani and Caskey, TIBTECH (1993); Dillon, TIBTECH (1993); Miller, Nature (1992); Van Brunt, Biotechnology (1988); Vigne et al., Restorative Neurology and Neuroscience 8:35-36 (1995); Kremer and Perricaudet, British Medical Bulletin (1995); Haddada et al., Current Topics in Microbiology and Immunology (1995); and Yu et al., Gene Therapy 1:13-26 (1994).

[00210] Methods of non-viral delivery of nucleic acids and/or proteins include electroporation, lipofection, microinjection, biolistics, particle gun acceleration, virosomes, liposomes, immunoliposomes, polycation or lipid:nucleic acid conjugates, artificial virions, and agent-enhanced uptake of nucleic acids or can be delivered to plant cells by bacteria or viruses (e.g., Agrobacterium, Rhizobium sp. NGR234, Sinorhizoboiummeliloti, Mesorhizobium loti, tobacco mosaic virus, potato virus X, cauliflower mosaic virus and cassava vein mosaic virus. See, e.g., Chung et al. Trends Plant Sci. (2006). Sonoporation using, e.g., the Sonitron 2000 system (Rich-Mar) can also be used for delivery of nucleic acids. Cationic-lipid mediated delivery of proteins and/or nucleic acids is also contemplated as an in vivo or in vitro delivery method. See Zuris et al., Nat. Biotechnol. (2015), Coelho et al., N. Engl. J. Med. (2013); Judge et al., Mol. Ther. (2006); and Basha et al., Mol. Ther. (2011).

[00211] Non-viral vectors, such as transposon-based systems e.g., recombinant Sleeping Beauty transposon systems or recombinant PiggyBac transposon systems, may also be delivered to a target cell and utilized for transposition of a polynucleotide sequence of a molecule of the composition or a polynucleotide sequence encoding a molecule of the composition in the target cell.

[00212] Additional exemplary nucleic acid delivery systems include those provided by Amaxa® Biosystems (Cologne, Germany), Maxcyte, Inc. (Rockville, Md.), BTX Molecular Delivery Systems (Holliston, Mass.) and Copernicus Therapeutics Inc., (see for example U.S. Patent No. 6,008,336). Lipofection is described in e.g., U.S. Patent No. 5,049,386, U.S. Patent No. 4,946,787; and U.S. Patent No. 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam.TM., Lipofectin.TM. and Lipofectamine.TM. RNAiMAX). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those disclosed in PCT International Publication Nos. WO/1991/017424 and WO/1991/016024. Delivery can be to cells (ex vivo administration) or target tissues (in vivo administration).

[00213] The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science (1995); Blaese et al., Cancer Gene Ther. (1995); Behr et al., Bioconjugate Chem. (1994); Remy et al., Bioconjugate Chem. (1994); Gao and Huang, Gene Therapy (1995); Ahmad and Allen, Cancer Res., (1992); U.S. Patent Nos. 4,186,183; 4,217,344; 4,235,871; 4,261,975; 4,485,054; 4,501,728; 4,774,085; 4,837,028; and 4,946,787).

[00214] Additional methods of delivery include the use of packaging the nucleic acids to be delivered into EnGeneIC delivery vehicles (EDVs). These EDVs are specifically delivered to target tissues using bispecific antibodies where one arm of the antibody has specificity for the target tissue and the other has specificity for the EDV. The antibody brings the EDVs to the target cell surface and then the EDV is brought into the cell by endocytosis. Once in the cell, the contents are released (see MacDiamid et al., Nature Biotechnology (2009)).

[00215] The use of RNA or DNA viral based systems for the delivery of nucleic acids take advantage of highly evolved processes for targeting a virus to specific cells in the body and trafficking the viral payload to the nucleus. Viral vectors can be administered directly to patients (in vivo) or they can be used to treat cells in vitro and the modified cells are administered to patients (ex vivo). Conventional viral based systems for the delivery of nucleic acids include, but are not limited to, recombinant retroviral, lentivirus, adenoviral, adeno-associated, vaccinia and herpes simplex virus vectors for gene transfer. However, an RNA virus is preferred for delivery of the RNA compositions described herein. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues. Nucleic acid of the invention may be delivered by non-integrating lentivirus. Optionally, RNA delivery with Lentivirus is utilized. Optionally the lentivirus includes mRNA of the nuclease, RNA of the guide. Optionally the lentivirus includes mRNA of the nuclease, RNA of the guide and a donor template. Optionally, the lentivirus includes the nuclease protein, guide RNA. Optionally, the lentivirus includes the nuclease protein, guide RNA and/or a donor template for gene editing via, for example, homology directed repair. Optionally the lentivirus includes mRNA of the nuclease, DNA-targeting RNA, and the tracrRNA. Optionally the lentivirus includes mRNA of the nuclease, DNA-targeting RNA, and the tracrRNA, and a donor template. Optionally, the lentivirus includes the nuclease protein, DNA-targeting RNA, and the tracrRNA. Optionally, the lentivirus includes the nuclease protein, DNA-targeting RNA, and the tracrRNA, and a donor template for gene editing via, for example, homology directed repair.

[00216] As mentioned above, the compositions described herein may be delivered to a target cell using a non-integrating lentiviral particle method, e.g. a LentiFlash® system. Such a method may be used to deliver mRNA or other types of RNAs into the target cell, such that delivery of the RNAs to the target cell results in assembly of the compositions described herein inside of the target

cell. See also PCT International Publication Nos. WO2013/014537, WO2014/016690, WO2016185125, WO2017194902, and WO2017194903.

[00217] The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors capable of transducing or infecting non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system depends on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations thereof (see, e.g., Buchscher Panganiban, J. Virol. (1992); Johann et al., J. Virol. (1992); Sommerfelt et al., Virol. (1990); Wilson et al., J. Virol. (1989); Miller et al., J. Virol. (1991); PCT International Publication No. WO/1994/026877A1).

[00218] At least six viral vector approaches are currently available for gene transfer in clinical trials, which utilize approaches that involve complementation of defective vectors by genes inserted into helper cell lines to generate the transducing agent.

[00219] pLASN and MFG-S are examples of retroviral vectors that have been used in clinical trials (Dunbar et al., Blood (1995); Kohn et al., Nat. Med. (1995); Malech et al., PNAS (1997)). PA317/pLASN was the first therapeutic vector used in a gene therapy trial. (Blaese et al., Science (1995)). Transduction efficiencies of 50% or greater have been observed for MFG-S packaged vectors. (Ellem et al., Immunol Immunother. (1997); Dranoff et al., Hum. Gene Ther. (1997).

[00220] Packaging cells are used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, AAV, and psi.2 cells or PA317 cells, which package retrovirus. Viral vectors used in gene therapy are usually generated by a producer cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host (if applicable), other viral sequences being replaced by an expression cassette encoding the protein to be expressed. The missing viral functions are supplied in trans by the packaging cell line. For

example, AAV vectors used in gene therapy typically only possess inverted terminal repeat (ITR) sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences. The cell line is also infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV. Additionally, AAV can be produced at clinical scale using baculovirus systems (see U.S. Patent No. 7,479,554).

[00221] In many gene therapy applications, it is desirable that the gene therapy vector be delivered with a high degree of specificity to a particular tissue type. Accordingly, a viral vector can be modified to have specificity for a given cell type by expressing a ligand as a fusion protein with a viral coat protein on the outer surface of the virus. The ligand is chosen to have affinity for a receptor known to be present on the cell type of interest. For example, Han et al., Proc. Natl. Acad. Sci. USA (1995), reported that Moloney murine leukemia virus can be modified to express human heregulin fused to gp70, and the recombinant virus infects certain human breast cancer cells expressing human epidermal growth factor receptor. This principle can be extended to other virus-target cell pairs, in which the target cell expresses a receptor and the virus expresses a fusion protein comprising a ligand for the cell-surface receptor. For example, filamentous phage can be engineered to display antibody fragments (e.g., FAB or Fv) having specific binding affinity for virtually any chosen cellular receptor. Although the above description applies primarily to viral vectors, the same principles can be applied to non-viral vectors. Such vectors can be engineered to contain specific uptake sequences which favor uptake by specific target cells.

[00222] Gene therapy vectors can be delivered in vivo by administration to an individual patient, typically by systemic administration (e.g., intravenous, intraperitoneal, intramuscular, subdermal, or intracranial infusion) or topical application, as described below. Alternatively, vectors can be delivered to cells ex vivo, such as cells explanted from an individual patient (e.g., lymphocytes, bone marrow aspirates, tissue biopsy) or universal donor hematopoietic stem cells, followed by reimplantation of the cells into a patient, usually after selection for cells which have incorporated the vector. In some embodiments, delivery of mRNA *in vivo* and *ex vivo*, and RNPs delivery may be utilized.

[00223] *Ex vivo* cell transfection for diagnostics, research, or for gene therapy (e.g., via re-infusion of the transfected cells into the host organism) is well known to those of skill in the art. In a preferred embodiment, cells are isolated from the subject organism, transfected with an RNA composition, and re-infused back into the subject organism (e.g., patient). Various cell types suitable for ex vivo transfection are well known to those of skill in the art (see, e.g., Freshney, "Culture of Animal Cells, A Manual of Basic Technique and Specialized Applications (6th edition, 2010)) and the references cited therein for a discussion of how to isolate and culture cells from patients).

[00224] Suitable cells include but not limited to eukaryotic and prokaryotic cells and/or cell lines. Non-limiting examples of such cells or cell lines generated from such cells include COS, CHO (e.g., CHO--S, CHO-K1, CHO-DG44, CHO-DUXB11, CHO-DUKX, CHOK1SV), VERO, MDCK, WI38, V79, B14AF28-G3, BHK, HaK, NSO, SP2/0-Ag14, HeLa, HEK293 (e.g., HEK293-F, HEK293-H, HEK293-T), and perC6 cells, any plant cell (differentiated or undifferentiated) as well as insect cells such as Spodopterafugiperda (Sf), or fungal cells such as Saccharomyces, Pichia and Schizosaccharomyces. In certain embodiments, the cell line is a CHO-K1, MDCK or HEK293 cell line. Additionally, primary cells may be isolated and used ex vivo for reintroduction into the subject to be treated following treatment with the nucleases (e.g. ZFNs or TALENs) or nuclease systems (e.g. CRISPR). Suitable primary cells include peripheral blood mononuclear cells (PBMC), and other blood cell subsets such as, but not limited to, CD4+ T cells or CD8+ T cells. Suitable cells also include stem cells such as, by way of example, embryonic stem cells, induced pluripotent stem cells, hematopoietic stem cells (CD34+), neuronal stem cells and mesenchymal stem cells.

[00225] In one embodiment, stem cells are used in ex vivo procedures for cell transfection and gene therapy. The advantage to using stem cells is that they can be differentiated into other cell types in-vitro or can be introduced into a mammal (such as the donor of the cells) where they will engraft in the bone marrow. Methods for differentiating CD34+ cells in vitro into clinically important immune cell types using cytokines such a GM-CSF, IFN-gamma. and TNF-alpha are known (as a non-limiting example see, Inaba et al., J. Exp. Med. (1992)).

[00226] Stem cells are isolated for transduction and differentiation using known methods. For example, stem cells are isolated from bone marrow cells by panning the bone marrow cells with

antibodies which bind unwanted cells, such as CD4+ and CD8+ (T cells), CD45+(panB cells), GR-1 (granulocytes), and Iad (differentiated antigen presenting cells) (as a non-limiting example see Inaba et al., J. Exp. Med. (1992)). Stem cells that have been modified may also be used in some embodiments.

[00227] Notably, any one of the CRISPR nucleases described herein may be suitable for genome editing in post-mitotic cells or any cell which is not actively dividing, e.g., arrested cells. Examples of post-mitotic cells which may be edited using a CRISPR nuclease of the present invention include, but are not limited to, myocyte, a cardiomyocyte, a hepatocyte, an osteocyte and a neuron.

[00228] Vectors (e.g., retroviruses, liposomes, etc.) containing therapeutic RNA compositions can also be administered directly to an organism for transduction of cells in vivo. Alternatively, naked RNA or mRNA can be administered. Administration is by any of the routes normally used for introducing a molecule into ultimate contact with blood or tissue cells including, but not limited to, injection, infusion, topical application and electroporation. Suitable methods of administering such nucleic acids are available and well known to those of skill in the art, and, although more than one route can be used to administer a particular composition, a particular route can often provide a more immediate and more effective reaction than another route.

[00229] Vectors suitable for introduction of transgenes into immune cells (e.g., T-cells) include non-integrating lentivirus vectors. See, for example, U.S. Patent Publication No. 2009/0117617.

[00230] Pharmaceutically acceptable carriers are determined in part by the particular composition being administered, as well as by the particular method used to administer the composition. Accordingly, there is a wide variety of suitable formulations of pharmaceutical compositions available, as described below (see, e.g., Remington's Pharmaceutical Sciences, 17th ed., 1989).

DNA Repair by Homologous Recombination

[00231] The term "homology-directed repair" or "HDR" refers to a mechanism for repairing DNA damage in cells, for example, during repair of double-stranded and single-stranded breaks in DNA. HDR requires nucleotide sequence homology and uses a "nucleic acid template" (nucleic acid template or donor template used interchangeably herein) to repair the sequence where the double-stranded or single break occurred (e.g., DNA target sequence). This results in the transfer of genetic information from, for example, the nucleic acid template to the DNA target sequence. HDR

may result in alteration of the DNA target sequence (e.g., insertion, deletion, mutation) if the nucleic acid template sequence differs from the DNA target sequence and part or all of the nucleic acid template polynucleotide or oligonucleotide is incorporated into the DNA target sequence. In some embodiments, an entire nucleic acid template polynucleotide, a portion of the nucleic acid template polynucleotide, or a copy of the nucleic acid template is integrated at the site of the DNA target sequence.

[00232] The terms "nucleic acid template" and “donor”, refer to a nucleotide sequence that is inserted or copied into a genome. The nucleic acid template comprises a nucleotide sequence, e.g., of one or more nucleotides, that will be added to or will template a change in the target nucleic acid or may be used to modify the target sequence. A nucleic acid template sequence may be of any length, for example between 2 and 10,000 nucleotides in length (or any integer value there between or there above), preferably between about 100 and 1,000 nucleotides in length (or any integer there between), more preferably between about 200 and 500 nucleotides in length. A nucleic acid template may be a single stranded nucleic acid, a double stranded nucleic acid. In some embodiment, the nucleic acid template comprises a nucleotide sequence, e.g., of one or more nucleotides, that corresponds to wild type sequence of the target nucleic acid, e.g., of the target position. In some embodiment, the nucleic acid template comprises a ribonucleotide sequence, e.g., of one or more ribonucleotides, that corresponds to wild type sequence of the target nucleic acid, e.g., of the target position. In some embodiment, the nucleic acid template comprises modified ribonucleotides.

[00233] Insertion of an exogenous sequence (also called a "donor sequence," donor template” or "donor"), for example, for correction of a mutant gene or for increased expression of a wild-type gene can also be carried out. It will be readily apparent that the donor sequence is typically not identical to the genomic sequence where it is placed. A donor sequence can contain a non-homologous sequence flanked by two regions of homology to allow for efficient HDR at the location of interest. Additionally, donor sequences can comprise a vector molecule containing sequences that are not homologous to the region of interest in cellular chromatin. A donor molecule can contain several, discontinuous regions of homology to cellular chromatin. For example, for targeted insertion of sequences not normally present in a region of interest, said sequences can be present in a donor nucleic acid molecule and flanked by regions of homology to sequence in the region of interest.

[00234] The donor polynucleotide can be DNA or RNA, single-stranded and/or double-stranded and can be introduced into a cell in linear or circular form. See, e.g., U.S. Patent Publication Nos. 2010/0047805; 2011/0281361; 2011/0207221; and 2019/0330620. If introduced in linear form, the ends of the donor sequence can be protected (e.g., from exonucleolytic degradation) by methods known to those of skill in the art. For example, one or more dideoxynucleotide residues are added to the 3' terminus of a linear molecule and/or self- complementary oligonucleotides are ligated to one or both ends. See, for example, Chang and Wilson, Proc. Natl. Acad. Sci. USA (1987); Nehls et al., Science (1996). Additional methods for protecting exogenous polynucleotides from degradation include, but are not limited to, addition of terminal amino group(s) and the use of modified internucleotide linkages such as, for example, phosphorothioates, phosphoramidates, and O-methyl ribose or deoxyribose residues.

[00235] Accordingly, embodiments of the present invention using a donor template for repair may use a DNA or RNA, single-stranded and/or double-stranded donor template that can be introduced into a cell in linear or circular form. In embodiments of the present invention a gene-editing composition comprises: (1) an RNA molecule comprising a guide sequence to affect a double strand break in a gene prior to repair and (2) a donor RNA template for repair, the RNA molecule comprising the guide sequence is a first RNA molecule and the donor RNA template is a second RNA molecule. In some embodiments, the guide RNA molecule and template RNA molecule are connected as part of a single molecule.

[00236] A donor sequence may also be an oligonucleotide and be used for gene correction or targeted alteration of an endogenous sequence. The oligonucleotide may be introduced to the cell on a vector, may be electroporated into the cell, or may be introduced via other methods known in the art. The oligonucleotide can be used to `correct` a mutated sequence in an endogenous gene (e.g., the sickle mutation in beta globin), or may be used to insert sequences with a desired purpose into an endogenous locus.

[00237] A polynucleotide can be introduced into a cell as part of a vector molecule having additional sequences such as, for example, replication origins, promoters and genes encoding antibiotic resistance. Moreover, donor polynucleotides can be introduced as naked nucleic acid, as nucleic acid complexed with an agent such as a liposome or poloxamer, or can be

delivered by recombinant viruses (e.g., adenovirus, AAV, herpesvirus, retrovirus, lentivirus and integrase defective lentivirus (IDLV)).

[00238] The donor is generally inserted so that its expression is driven by the endogenous promoter at the integration site, namely the promoter that drives expression of the endogenous gene into which the donor is inserted. However, it will be apparent that the donor may comprise a promoter and/or enhancer, for example a constitutive promoter or an inducible or tissue specific promoter.

[00239] The donor molecule may be inserted into an endogenous gene such that all, some or none of the endogenous gene is expressed. For example, a transgene as described herein may be inserted into an endogenous locus such that some (N-terminal and/or C-terminal to the transgene) or none of the endogenous sequences are expressed, for example as a fusion with the transgene. In other embodiments, the transgene (e.g., with or without additional coding sequences such as for the endogenous gene) is integrated into any endogenous locus, for example a safe-harbor locus, for example a CCR5 gene, a CXCR4 gene, a PPP1R12c (also known as AAVS1) gene, an albumin gene or a Rosa gene. See, e.g., U.S. Patent Nos. 7,951,925 and 8,110,379; U.S. Publication Nos. 2008/0159996; 20100/0218264; 2010/0291048; 2012/0017290; 2011/0265198; 2013/0137104; 2013/0122591; 2013/0177983 and 2013/0177960 and U.S. Provisional Application No. 61/823,689).

[00240] When endogenous sequences (endogenous or part of the transgene) are expressed with the transgene, the endogenous sequences may be full-length sequences (wild-type or mutant) or partial sequences. Preferably the endogenous sequences are functional. Non-limiting examples of the function of these full length or partial sequences include increasing the serum half-life of the polypeptide expressed by the transgene (e.g., therapeutic gene) and/or acting as a carrier.

[00241] Furthermore, although not required for expression, exogenous sequences may also include transcriptional or translational regulatory sequences, for example, promoters, enhancers, insulators, internal ribosome entry sites, sequences encoding 2A peptides and/or polyadenylation signals.

[00242] In certain embodiments, the donor molecule comprises a sequence selected from the group consisting of a gene encoding a protein (e.g., a coding sequence encoding a protein that is lacking in the cell or in the individual or an alternate version of a gene encoding a protein),

a regulatory sequence and/or a sequence that encodes a structural nucleic acid such as a microRNA or siRNA.

[00243] For the foregoing embodiments, each embodiment disclosed herein is contemplated as being applicable to each of the other disclosed embodiment. For example, it is understood that any of the RNA molecules or compositions of the present invention may be utilized in any of the methods of the present invention.

[00244] As used herein, all headings are simply for organization and are not intended to limit the disclosure in any manner. The content of any individual section may be equally applicable to all sections.

[00245] Additional objects, advantages, and novel features of the present invention will become apparent to one ordinarily skilled in the art upon examination of the following examples, which are not intended to be limiting. Additionally, each of the various embodiments and aspects of the present invention as delineated hereinabove and as claimed in the claims section below finds experimental support in the following examples.

[00246] It is appreciated that certain features of the invention, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the invention, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination or as suitable in any other described embodiment of the invention. Certain features described in the context of various embodiments are not to be considered essential features of those embodiments, unless the embodiment is inoperative without those elements.

[00247] Generally, the nomenclature used herein, and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological and recombinant DNA techniques. Such techniques are thoroughly explained in the literature. See, for example, Sambrook et al., "Molecular Cloning: A laboratory Manual" (1989); Ausubel, R. M. (Ed.), "Current Protocols in Molecular Biology" Volumes I-III (1994); Ausubel et al., "Current Protocols in Molecular Biology", John Wiley and Sons, Baltimore, Maryland (1989); Perbal, "A Practical Guide to Molecular Cloning", John Wiley & Sons, New York (1988); Watson et al., "Recombinant DNA", Scientific American Books, New York; Birren et al. (Eds.), "Genome Analysis: A Laboratory Manual Series", Vols. 1-4, Cold Spring Harbor Laboratory Press, New York (1998);

Methodologies as set forth in U.S. Patent Nos. 4,666,828; 4,683,202; 4,801,531; 5,192,659 and 5,272,057; Cellis, J. E. (Ed.), "Cell Biology: A Laboratory Handbook", Volumes I-III (1994); Freshney, "Culture of Animal Cells - A Manual of Basic Technique" Third Edition, Wiley-Liss, N. Y. (1994); Coligan J. E. (Ed.), "Current Protocols in Immunology" Volumes I-III (1994); Stites et al. (Eds.), "Basic and Clinical Immunology" (8th Edition), Appleton & Lange, Norwalk, CT (1994); Mishell and Shiigi (Eds.), "Strategies for Protein Purification and Characterization - A Laboratory Course Manual" CSHL Press (1996); Clokie and Kropinski (Eds.), "Bacteriophage Methods and Protocols", Volume 1: Isolation, Characterization, and Interactions (2009), all of which are incorporated by reference. Other general references are provided throughout this document.

[00248] Examples are provided below to facilitate a more complete understanding of the invention. The following examples illustrate the exemplary modes of making and practicing the invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only.

EXPERIMENTAL DETAILS

[00250] Examples are provided below to facilitate a more complete understanding of the invention. The following examples illustrate the exemplary modes of making and practicing the invention. However, the scope of the invention is not limited to specific embodiments disclosed in these Examples, which are for purposes of illustration only.

[00251] CRISPR repeat (crRNA), trans-activating RNA (tracrRNA), nuclease polypeptide (OMNI), and protospacer adjacent motif (PAM) sequences were predicted from different metagenomic databases of sequences of environmental samples.

Construction of OMNI nuclease polypeptides

[00252] For construction of novel nuclease polypeptides (OMNIs), the open reading frame of several identified OMNIs were codon optimized for human cell line expression. The ORF was cloned into the bacterial expression plasmid pET9a and into the mammalian expression plasmid pmOMNI (**Table 4**).

Prediction and construction of sgRNA

[00253] For each OMNI the single guide RNA (sgRNA) was predicted by detection of the CRISPR repeat array sequence and a tracrRNA in the respective bacterial genome. The native pre-mature crRNA and tracrRNA sequences were connected *in silico* with a tetra-loop 'gaaa' sequence and the secondary structure elements of the duplex were predicted using an RNA secondary structure prediction tool.

[00254] The predicted secondary structures of the full duplex RNA elements (crRNA-tracrRNA chimera) was used for identification of possible tracrRNA sequences for the design of a sgRNA. Several possible sgRNA scaffolds versions were constructed by shortening the duplex at the upper stem at different locations (sgRNA designs of all OMNIs are listed in **Table 2**). Additionally, to overcome potential transcriptional and structural constraints and to assess the plasticity of the sgRNA scaffold in the human cellular environmental context, small changes in the nucleotide sequence of the possible sgRNA were made in some cases **(Fig. 1, Table 2)**. Finally, up to three versions of possible designed scaffolds were synthesized for each OMNI and connected downstream to a 22-nucleotide universal unique spacer sequence (T2, SEQ ID NO: 268) and

cloned into a bacterial expressing plasmid under an inducible T7 promoter combined with a U6 promoter for mammalian expression (pShuttleGuide, **Table 4**).

T2 – GGAAGAGCAGAGCCTTGGTCTC (SEQ ID NO: 268)

In-vitro Depletion assay by TXTL

[00255] Depletion of PAM sequences *in vitro* was followed as described by Maxwell *et al*, Methods. 2018. Briefly, linear DNA expressing the OMNI nucleases and an sgRNA under T7 promoter were added to a cell-free transcription-translation *in vitro* system (TXTL mix, Arbor Bioscience) together with a linear construct expressing T7 polymerase. RNA expression and protein translation by the TXTL mix result in the formation of a ribonucleoprotein (RNP) complex. Since linear DNA was used, Chi6 DNA sequences were added to the TXTL reaction mix to inhibit the exonuclease activity of RecBCD, thereby protecting the linear DNA from degradation. The sgRNA spacer is designed to target a library of plasmids containing the target protospacer (pbPOS T2 library, **Table 4**) flanked by an 8N randomized set of potential PAM sequences. Depletion of PAM sequences from the library was measured by high-throughput sequencing using PCR to add the necessary adapters and indices to both the cleaved library and to a control library expressing a non-targeting gRNA. Following deep sequencing, the *in vitro* activity was confirmed by the fraction of the depleted sequences having the same PAM sequence relative to their occurrence in the control, indicating functional DNA cleavage by the OMNI nuclease (**Figs. 2-18, Table 3**).

Activity in human cells on endogenous genomic targets

[00256] OMNIs were also assayed for their ability to promote editing on specific genomic locations in human cells. To this end, per each OMNI, the corresponding OMNI-P2A-mCherry expression vector (**Table 4**) was transfected into HeLa cells together with an sgRNA designed to target a specific location in the human genome (pShuttle Guide - **Table 4** and **spacer sequence - Table 5**). At 72 hours, cells were harvested. Half of the harvested cells were used for quantification of transfection efficiency by FACS using mCherry fluorescence as a marker. The other half of the harvested cells were lysed, and their genomic DNA was used to PCR amplify the corresponding putative genomic targets. Amplicons were subjected to next-generation sequencing (NGS) and the resulting sequences were used calculate the percentage of editing events in each target site. Short Insertions or deletions (indels) around the cut site are the typical outcome of repair of DNA ends

following nuclease induced DNA cleavage. The calculation of percent editing was therefore deduced from the fraction of indels containing sequences within each amplicon.

[00257] Genomic activity of each OMNI was assessed using a panel of at least six (6) unique sgRNAs each designed to target a different genomic location. The results of these experiments are summarized in **Table 5**. As can be seen in the table (column 6, "% indels"), several OMNIs exhibit high and significant editing levels in most or some target site tested.

Additional Results For OMNI-127 as Part of an RNP Complex

[00258] **Purification of OMNI-127 protein**: The OMNI-127 construct in pET28a was expressed in BL-21 cells (NEB). Cells were grown in AIM + 0.4% glycerol and expressed at 37°C for 23hr. Cells were lysed using chemical lysis and cleared lysate was purified on Ni-NTA resin. Ni-NTA elution fraction was purified on CEX (SO3 fractogel) resin followed by SEC purification on Superdex® 200 Increase 10/300 GL, AKTA Pure (GE Healthcare Life Sciences). Fractions containing OMNI-127 protein were pooled and concentrated to 25 mg/ml stocks, flash-frozen in liquid nitrogen, and stored at -80 °C.

[00259] **Cleavage activity of OMNI-127 RNP in vitro**: Synthetic sgRNAs of OMNI-127 were synthesized with three 2'-O-methyl 3'-phosphorothioate at the 3' and 5' ends (Agilent).

[00260] Activity assay of OMNI-127 RNP was assayed *in vitro* with ELANE g135 guide (Tables 6, Fig 2A). Briefly, 10 pmol of OMNI-127 nuclease was mixed with 20 pmol of the synthetic guide. After a 10 minute incubation at room-temperature, the RNP complexes were serial diluted to 4, 2, 1, 0.5 pmol and reacted with a 40 ng of linear DNA template prepared by amplification of an ELANE g135 target from extracted genomic DNA. OMNI-127 showed full cleavage of the ELANE template which indicating high cleavage activity (Fig. 19A).

[00261] **Guide optimization of OMNI-127 by editing activity of RNP in U2OS cells:** Spacer length optimization was tested in a mammalian cell context. RNPs was assembled by mixing 100 uM nuclease with 120 uM of synthetic guides of different spacer lengths (20-24 nucleotides, Table 6) and 100 uM Cas9 electroporation enhancer (IDT). After a10 minute incubation at room-temperature, the RNP complexes were mixed with 200,000 pre-washed U2OS cells and electroporated using Lonza SE Cell Line 4D-NucleofectorTM X Kit with DN100, according to the manufacturer's protocol. 72h post-electroporation, cells were lysed and their genomic DNA

content was extracted. The corresponding genomic targets were amplified by PCR. Amplicons were subjected to next-generation sequencing (NGS) and the resulting sequences were then used calculate the percentage of editing events. As can be seen in Fig. 19B and Table 7, OMN1-127 showed high editing level at all spacer lengths.

[00262] **OMNI-127 editing activity as part of an RNP complex in human cells:** Activity of OMNI-127 protein as part of an RNP complex was observed in U2OS cells, (Table 7, Fig 19C) and comparable activity was also observed in HSC-MLP2 cells (Table 8). In the HSC experiment, RNPs were assembled by mixing 100 uM nuclease with 120 uM of synthetic guide (Table 6) and 100 uM Cas9 electroporation enhancer (IDT). After a 10 minute incubation at room-temperature, the RNP complexes were mixed with 250,000 pre-washed HSC-MLP2 cells and electroporated using Lonza P3 Cell Line 4D-NucleofectorTM X Kit with CA137 according to the manufacturer's protocol. At 72h cells were lysed and the genomic DNA targets were amplified by PCR. Amplicons were subjected to NGS and the resulting sequences were then used to calculate the percentage of editing events. OMNI-127 was tested with guides for ELANE- g135 and g136. OMNI-127 showed editing with two ELANE guides (g135, g136).

Table 1 - OMNI CRISPR nuclease sequences

"OMNI" Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
OMNI-115	1	18	35	(D9 or E532 or H755 or D758)	(D611 or H612 or N635)	(D9 or E532 or H755 or D758) and (D611 or H612 or N635)
OMNI-124	2	19	36	(D8 or E502 or H737 or D740)	(D589 or H590 or N613)	(D8 or E502 or H737 or D740) and (D589 or H590 or N613)
OMNI-127	3	20	37	(D9 or E480 or H704 or D707)	(D562 or H563 or N586)	(D9 or E480 or H704 or D707) and (D562 or H563 or N586)
OMNI-144	4	21	38	(D11 or E533 or H768 or D771)	(D618 or H619 or N642)	(D11 or E533 or H768 or D771) and (D618 or H619 or N642)
OMNI-145	5	22	39	(D11 or E531 or H766 or D769)	(D616 or H617 or N640)	(D11 or E531 or H766 or D769) and (D616 or H617 or N640)
OMNI-146	6	23	40	(D11 or E533 or H768 or D771)	(D618 or H619 or N642)	(D11 or E533 or H768 or D771) and (D618 or H619 or N642)
OMNI-147	7	24	41	(D11 or E531 or H766 or D769)	(D616 or H617 or N640)	(D11 or E531 or H766 or D769) and (D616 or

"OMNI" Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
						H617 or N640)
OMNI-148	8	25	42	(D11 or E533 or H765 or D768)	(D618 or H619 or N642)	(D11 or E533 or H765 or D768) and (D618 or H619 or N642)
OMNI-149	9	26	43	(D11 or E531 or H766 or D769)	(D616 or H617 or N640)	(D11 or E531 or H766 or D769) and (D616 or H617 or N640)
OMNI-159	10	27	44	(D8 or E508 or H727 or D730)	(D589 or H590 or N613)	(D8 or E508 or H727 or D730) and (D589 or H590 or N613)
OMNI-218	11	28	45	(D10 or E597 or H856 or D859)	(E683 or H684 or N707)	(D10 or E597 or H856 or D859) and (E683 or H684 or N707)
OMNI-237	12	29	46	(D14 or E778 or H990 or D993)	(D858 or H859 or N882)	(D14 or E778 or H990 or D993) and (D858 or H859 or N882)
OMNI-248	13	30	47	(D9 or E809 or H1033 or D1036)	(D892 or H893 or N916)	(D9 or E809 or H1033 or D1036) and (D892 or H893 or N916)
OMNI-251	14	31	48	(D11 or E846 or H1094 or D1097)	(D939 or H940 or N963)	(D11 or E846 or H1094 or D1097) and (D939 or

"OMNI" Name	SEQ ID NO of OMNI Amino Acid Sequence	SEQ ID NO of DNA sequence encoding OMNI	SEQ ID NO of DNA sequence codon optimized for expression in human cells	Nickase having inactivated RuvC domain	Nickase having inactivated HNH domain	Dead nuclease having inactivated RuvC and HNH domains
						H940 or N963)
OMNI-252	15	32	49	(D11 or E845 or H1093 or D1096)	(D938 or H939 or N962)	(D11 or E845 or H1093 or D1096) and (D938 or H939 or N962)
OMNI-253	16	33	50	(D11 or E846 or H1094 or D1097)	(D939 or H940 or N963)	(D11 or E846 or H1094 or D1097) and (D939 or H940 or N963)
OMNI-259	17	34	51	(D9 or E779 or H989 or D992)	(D857 or H858 or N881)	(D9 or E779 or H989 or D992) and (D857 or H858 or N881)

Table 1. OMNI nuclease sequences: Table 1 lists the OMNI name, its corresponding nuclease protein sequence, its DNA sequence, its human optimized DNA sequence, alternative positions to be substituted to generate a nickase having an inactivated RuvC domain, alternative positions to be substituted to generate a nickase having an inactivated HNH domain, and alternative positions to be substituted to generate a catalytically dead nuclease having inactivated RuvC and HNH domains. Substitution to any other amino acid is permissible for each of the amino acid positions indicated in columns 5-7, except a substitution of aspartic acid (D) to glutamic acid (E) or glutamic acid (E) to aspartic acid (D) in the HNH domain, in order to achieve inactivation.

Table 2 – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-115 with sgRNA 115	OMNI-124 with sgRNA 124
	crRNA (Repeat)	GUUAUAGUUGCCUUUC (SEQ ID NO: 52)	GUUUUAGUACCUGGAGAAA (SEQ ID NO: 65)

		OMNI-115 with sgRNA 115	OMNI-124 with sgRNA 124
crRNA:tracrRNA duplex V1	**Partial crRNA 1**	GUUAUAGUUGCCUUU (SEQ ID NO: 53)	GUUUUAGUACCUGGA (SEQ ID NO: 66)
	Partial crRNA 2	GUUAUAGUUGCC (SEQ ID NO: 54)	GUUUUAGUACCU (SEQ ID NO: 67)
	Partial crRNA 3	GUUAUAGUUG (SEQ ID NO: 55)	GUUUUAGUAC (SEQ ID NO: 68)
	tracrRNA (Antirepeat)	GAAAGGUAACUAUAAU (SEQ ID NO: 56)	UUUCUUCAGACCUACUAAAAU (SEQ ID NO: 69)
	Partial tracrRNA 1	AAAGGUAACUAUAAU (SEQ ID NO: 57)	UUCAGACCUACUAAAAU (SEQ ID NO: 70)
	Partial tracrRNA 2	GGUAACUAUAAU (SEQ ID NO: 58)	AGACCUACUAAAAU (SEQ ID NO: 71)
	Partial tracrRNA 3	UAACUAUAAU (SEQ ID NO: 59)	ACCUACUAAAAU (SEQ ID NO: 72)
tracrRNA sequences	**tracrRNA Portion 1**	AAUCGAGAAUUUCGAGU (SEQ ID NO: 60)	AAGGAUUUAUUCCGAAAGA (SEQ ID NO: 73)
	tracrRNA Portion 1 - partial	Not listed	GGAUUUAUUCC (SEQ ID NO: 74)
	tracrRNA Portion 2	AGGGCUCUAACUUUCGAGU UAUCCCUUAUUUC (SEQ ID NO: 61)	AUUUUUGUAAAUGAAGAAAAUA AGGC (SEQ ID NO: 75)
	tracrRNA Portion 3	AAGCAACUGUUUCAUACAG UUGCUUUUUU (SEQ ID NO: 62)	GAGAAAGGAUGCUGACGGGCAU CCUUUUUU (SEQ ID NO: 76)
	tracrRNA Portion 3 - polyT	AAGCAACUGUUUCAUACAG UUGC (SEQ ID NO: 63)	GAGAAAGGAUGCUGACGGGCAU CC (SEQ ID NO: 77)
sgRNA Versions	**sgRNA V1**	GTTATAGTTGCCTTTCgaaaGA AAGGTAACTATAATAATCGA GAATTTCGAGTAGGGCTCTA ACTTTCGAGTTATCCCTTATT TCAAGCAACTGTTTCATACA GTTGCTTTTTT (SEQ ID NO: 64)	GTTTTAGTACCTGGAGAAAgaaaTT TCTTCAGACCTACTAAAATAAGG ATTTATTCCGAAAGAATTTTTGTA AATGAAGAAAATAAGGCGAGAA AGGATGCTGACGGGCATCCTTTT TT (SEQ ID NO: 78)
	sgRNA V2	Not listed	GTTTAAGTACCTGGAGAAAgaaaT TTCTTCAGACCTACTTAAATAAG GATTTATTCCGAAAGAATTATTG TAAATGAAGAAAATAAGGCGAG AAAGGATGCTGACGGGCATCCTT TTTT (SEQ ID NO: 79)
	sgRNA V2 crRNA (Repeat)	Not listed	GUUUAAGUACCUGGAGAAA (SEQ ID NO: 80)

		OMNI-115 with sgRNA 115	OMNI-124 with sgRNA 124
	sgRNA V2 crRNA (Antirepeat)	Not listed	UUUCUUCAGACCUACUTAAAU (SEQ ID NO: 81)

Table 2 (continued) – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-127 with sgRNA 127	OMNI-144, 145, 146, 147, 148 and 149 with sgRNA 1449
crRNA:tracrRNA duplex V1	**crRNA (Repeat)**	GUUUUGUUACCAUAUGGAU (SEQ ID NO: 82)	GUUUUAGCUCAAUGUUGG (SEQ ID NO: 98)
	Partial crRNA 1	GUUUUGUUACCAUAU (SEQ ID NO: 83)	GUUUUAGCUCAAUGU (SEQ ID NO: 99)
	Partial crRNA 2	GUUUUGUUACCA (SEQ ID NO: 84)	GUUUUAGCUCAA (SEQ ID NO: 100)
	Partial crRNA 3	GUUUUGUUAC (SEQ ID NO: 85)	GUUUUAGCUC (SEQ ID NO: 101)
	tracrRNA (Antirepeat)	AUCUAUAUGACCUAACAAAAC (SEQ ID NO: 86)	CCAACAUGUUCUAAGAU (SEQ ID NO: 102)
	Partial tracrRNA 1	AUAUGACCUAACAAAAC (SEQ ID NO: 87)	ACAUGUUCUAAGAU (SEQ ID NO: 103)
	Partial tracrRNA 2	UGACCUAACAAAAC (SEQ ID NO: 88)	UGUUCUAAGAU (SEQ ID NO: 104)
	Partial tracrRNA 3	ACCUAACAAAAC (SEQ ID NO: 89)	GUUCUAAGAU (SEQ ID NO: 105)
tracrRNA sequences	**tracrRNA Portion 1**	AAGGGUUUAUCCCGGAUUC (SEQ ID NO: 90)	AAGGCAUUAUGGCC (SEQ ID NO: 106)
	tracrRNA Portion 1 - partial	GGGUUUAUCCC (SEQ ID NO: 91)	GGCAUUAUGGCC (SEQ ID NO: 107)
	tracrRNA Portion 2	GGCUCCUUUAUAGGAGCCUUUUUU (SEQ ID NO: 92)	GUGGGGUAUAGCAGUAACCGACA (SEQ ID NO: 108)
	tracrRNA Portion 2 - polyT	GGCUCCUUUAUAGGAGCC (SEQ ID NO: 93)	Not listed
	tracrRNA Portion 3	Not listed	AGCAAUCUGCUCCU (SEQ ID NO: 109)
	tracrRNA Portion 4	Not listed	GAAAGGCUGUAUGAAGAUCUUCUUUAUACAGCCUUUUUU (SEQ ID NO: 110)
	tracrRNA Portion 4 - polyT	Not listed	GAAAGGCUGUAUGAAGAUCUUCUUUAUACAGCC (SEQ ID NO: 111)

		OMNI-127 with sgRNA 127	OMNI-144, 145, 146, 147, 148 and 149 with sgRNA 1449
sgRNA Versions	**sgRNA V1**	GTTTTGTTACCATATGGATgaa aATCTATATGACCTAACAAAA CAAGGGTTTATCCCGGATTC GGCTCCTTTATAGGAGCCTTT TTT (SEQ ID NO: 94)	GTTTTAGCTCAATGTTGGgaaaCCA ACATGTTCTAAGATAAGGCATTA TGGCCGTGGGGTATAGCAGTAAC CGACAAGCAATCTGCTCCTGAAA GGCTGTATGAAGATCTTCTTTAT ACAGCCTTTTTT (SEQ ID NO: 112)
	sgRNA V2	GTTTAGTTACCATATGGATgaa aATCTATATGACCTAACTAAA CAAGGGTTTATCCCGGATTC GGCTCCTTTATAGGAGCCTTT TTT (SEQ ID NO: 95)	GTCTTAGCTCAATGTTGGgaaaCCA ACATGTTCTAAGATAAGGCATTA TGGCCGTGGGGTATAGCAGTAAC CGACAAGCAATCTGCTCCTGAAA GGCTGTATGAAGATCTTCTTTAT ACAGCCTTTTTT (SEQ ID NO: 113)
	sgRNA V2 crRNA (Repeat)	GUUUAGUUACCAUAUGGAU (SEQ ID NO: 96)	GUCUUAGCUCAAUGUUGG (SEQ ID NO: 114)
	sgRNA V2 crRNA (Antirepeat)	AUCUAUAUGACCUAACTAAA C (SEQ ID NO: 97)	Not listed

Table 2 (continued) – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-159 with sgRNA 159	OMNI-218 with sgRNA 218
crRNA:tracrRNA duplex V1	**crRNA (Repeat)**	GUUGUAGUUCCCUAUUUGU (SEQ ID NO: 115)	GUUGUGGUUUGAUGAU (SEQ ID NO: 128)
	Partial crRNA 1	GUUGUAGUUCCCUAU (SEQ ID NO: 116)	GUUGUGGUUUGAUGA (SEQ ID NO: 129)
	Partial crRNA 2	GUUGUAGUUCCC (SEQ ID NO: 117)	GUUGUGGUUUGA (SEQ ID NO: 130)
	Partial crRNA 3	GUUGUAGUUC (SEQ ID NO: 118)	GUUGUGGUUU (SEQ ID NO: 131)
	tracrRNA (Antirepeat)	ACAAUUAGGUUACUAUGAU (SEQ ID NO: 119)	AUCAUCAAAUCACAAU (SEQ ID NO: 132)
	Partial tracrRNA 1	UUAGGUUACUAUGAU (SEQ ID NO: 120)	UCAUCAAAUCACAAU (SEQ ID NO: 133)
	Partial tracrRNA 2	GGUUACUAUGAU (SEQ ID NO: 121)	UCAAAUCACAAU (SEQ ID NO: 134)
	Partial tracrRNA 3	UUACUAUGAU (SEQ ID NO: 122)	AAAUCACAAU (SEQ ID NO: 135)
tracrRNA sequences	**tracrRNA Portion 1**	AAGGUAGUAUACCGC (SEQ ID NO: 123)	AAGGCUAUAUGCC (SEQ ID NO: 136)

		OMNI-159 with sgRNA 159	OMNI-218 with sgRNA 218
	tracrRNA Portion 1 - partial	GGUAGUAUACC (SEQ ID NO: 124)	GGCUAUAUGCC (SEQ ID NO: 137)
	tracrRNA Portion 2	AAAGCUCUAACGCCCCGUCUUUGACGGGGCGUUAUCUUUUUU (SEQ ID NO: 125)	GAAGGAUGAAUUCCUAUC (SEQ ID NO: 138)
	tracrRNA Portion 2 - polyT	AAAGCUCUAACGCCCCGUCUUUGACGGGGCGUUAUC (SEQ ID NO: 126)	Not listed
	tracrRNA Portion 3	Not listed	GCCUCUCUUCUGGAGAGGCUUUUUU (SEQ ID NO: 139)
	tracrRNA Portion 3 - polyT	Not listed	GCCUCUCUUCUGGAGAGGC (SEQ ID NO: 140)
sgRNA Versions	**sgRNA V1**	GTTGTAGTTCCCTATTTGTgaaaACAATTAGGTTACTATGATAAGGTAGTATACCGCAAAGCTCTAACGCCCCGTCTTTGACGGGGCGTTATCTTTTTT (SEQ ID NO: 127)	GTTGTGGTTTGATGATgaaaATCATCAAATCACAATAAGGCTATATGCCGAAGGATGAATTCCTATCGCCTCTCTTCTGGAGAGGCTTTTTT (SEQ ID NO: 141)

Table 2 (continued) – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-237 with sgRNA 237	OMNI-248 with sgRNA 248
crRNA:tracrRNA duplex V1	**crRNA (Repeat)**	GUUUGAGAGUAGUGUAA (SEQ ID NO: 142)	GUUUGAGUGUAAUGUA (SEQ ID NO: 156)
	Partial crRNA 1	GUUUGAGAGUAGUGU (SEQ ID NO: 143)	GUUUGAGUGUAAUGU (SEQ ID NO: 157)
	Partial crRNA 2	GUUUGAGAGUAG (SEQ ID NO: 144)	GUUUGAGUGUAA (SEQ ID NO: 158)
	Partial crRNA 3	GUUUGAGAGU (SEQ ID NO: 145)	GUUUGAGUGU (SEQ ID NO: 159)
	tracrRNA (Antirepeat)	UUACACUACAAGUUCAAAU (SEQ ID NO: 146)	UACAUUACAAAGUUCAAAU (SEQ ID NO: 160)
	Partial tracrRNA 1	ACACUACAAGUUCAAAU (SEQ ID NO: 147)	ACAUUACAAAGUUCAAAU (SEQ ID NO: 161)
	Partial tracrRNA 2	CUACAAGUUCAAAU (SEQ ID NO: 148)	UUACAAAGUUCAAAU (SEQ ID NO: 162)
	Partial tracrRNA 3	ACAAGUUCAAAU (SEQ ID NO: 149)	ACAAAGUUCAAAU (SEQ ID NO: 163)

		OMNI-237 with sgRNA 237	OMNI-248 with sgRNA 248
tracrRNA sequences	**tracrRNA Portion 1**	AAAAAUUUAUUCAAAUCCU UUUGCUGCAUUGUGCAGAA UCU (SEQ ID NO: 150)	AAGCUUUAAGCGAAAUCAUA (SEQ ID NO: 164)
	tracrRNA Portion 1 - partial	Not listed	GCUUUAAGC
	tracrRNA Portion 2	AAAGAUCUGGAAACAGAUC UUUUUUU (SEQ ID NO: 151)	GAGAAGCAGUGCUUCUCAUUUU UUU (SEQ ID NO: 165)
	tracrRNA Portion 2 - polyT	AAAGAUCUGGAAACAGAUC (SEQ ID NO: 152)	GAGAAGCAGUGCUUCUCA (SEQ ID NO: 166)
sgRNA Versions	**sgRNA V1**	GTTTGAGAGTAGTGTAAgaaaT TACACTACAAGTTCAAATAA AAATTTATTCAAATCCTTTTG CTGCATTGTGCAGAATCTAA AGATCTGGAAACAGATCTTT TTTT (SEQ ID NO: 153)	GTTTGAGTGTAATGTAgaaaTACAT TACAAAGTTCAAATAAGCTTTAA GCGAAATCATAGAGAAGCAGTG CTTCTCATTTTTTT (SEQ ID NO: 167)
	sgRNA V2	GTTTGAGAGTAGTGTAAgaaaT TACACTACAAGTTCAAATAA AAATTTATTCAAATCCTTCTG CTGCATTGTGCAGAATCTAA AGATCTGGAAACAGATCTTT TTTT (SEQ ID NO: 154)	Not listed
	sgRNA V2 Modified tracrRNA Portion 1	AAAAAUUUAUUCAAAUCCU UCUGCUGCAUUGUGCAGAA UCU (SEQ ID NO: 155)	Not listed

Table 2 (continued) – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-251 and OMNI-252 with sgRNA 2512	OMNI-253 with sgRNA 253
crRNA:tracrRNA duplex V1	**crRNA (Repeat)**	GUUUGCUAGGUG (SEQ ID NO: 168)	GUUUGCUAGGUG (SEQ ID NO: 177)
	Partial crRNA 3	GUUUGCUAGG (SEQ ID NO: 169)	GUUUGCUAGG (SEQ ID NO: 178)
	tracrRNA (Antirepeat)	CACAGUUGCGUGC (SEQ ID NO: 170)	CACAGCUGCGUGCAAAU (SEQ ID NO: 179)
	Partial tracrRNA 3	CAGUUGCGUGC (SEQ ID NO: 171)	GCUGCGUGCAAAU (SEQ ID NO: 180)
tracrRNA sequences	**tracrRNA Portion 1**	AAAUAAGUCACUUUGUGGC GCAUCCAUG (SEQ ID NO: 172)	AAGUCACUUUGUGGCGUAUCCA UAACU (SEQ ID NO: 181)
	tracrRNA Portion 1 - partial	GUCACUUUGUGGC (SEQ ID NO: 173)	GUCACUUUGUGGC (SEQ ID NO: 182)

		OMNI-251 and OMNI-252 with sgRNA 2512	OMNI-253 with sgRNA 253
	tracrRNA Portion 2	GCUCCAUUGGAACGGAGCAU UUUUU (SEQ ID NO: 174)	CCCCAUUGGAACGGGGCUUUUU U (SEQ ID NO: 183)
	tracrRNA Portion 2 - polyT	GCUCCAUUGGAACGGAGCA (SEQ ID NO: 175)	CCCCAUUGGAACGGGGC (SEQ ID NO: 184)
sgRNA Versions	**sgRNA V1**	GTTTGCTAGGTGgaaaCACAGT TGCGTGCAAATAAGTCACTTT GTGGCGCATCCATGGCTCCA TTGGAACGGAGCATTTTTT (SEQ ID NO: 176)	GTTTGCTAGGTGgaaaCACAGCTG CGTGCAAATAAGTCACTTTGTGG CGTATCCATAACTCCCCATTGGA ACGGGGCTTTTTT (SEQ ID NO: 185)

Table 2 (continued) – OMNI Guide RNA and Scaffold RNA Sequences

		OMNI-259 with sgRNA 259
crRNA:tracrRNA duplex V1	**crRNA (Repeat)**	GUUUUAGUUCUAUGUC (SEQ ID NO: 186)
	Partial crRNA 1	GUUUUAGUUCUAUGU (SEQ ID NO: 187)
	Partial crRNA 2	GUUUUAGUUCUA (SEQ ID NO: 188)
	Partial crRNA 3	GUUUUAGUUC (SEQ ID NO: 189)
	tracrRNA (Antirepeat)	GACAUAGAGAGUUAAAAU (SEQ ID NO: 190)
	Partial tracrRNA 1	ACAUAGAGAGUUAAAAU (SEQ ID NO: 191)
	Partial tracrRNA 2	UAGAGAGUUAAAAU (SEQ ID NO: 192)
	Partial tracrRNA 3	GAGAGUUAAAAU (SEQ ID NO: 193)
tracrRNA sequences	**tracrRNA Portion 1**	AAAGGAUUACCUAAAUA (SEQ ID NO: 194)
	tracrRNA Portion 1 - partial	AGGAUUACCU (SEQ ID NO: 195)
	tracrRNA Portion 2	CUCAUUAUGUGAUGAG (SEQ ID NO: 196)
	tracrRNA Portion 3	AGGCUGCUUAGGCUAGCCUU UUUUUU (SEQ ID NO: 197)

		OMNI-259 with sgRNA 259
	tracrRNA Portion 3 - polyT	AGGCUGCUUAGGCUAGCC (SEQ ID NO: 198)
sgRNA Versions	**sgRNA V1**	GTTTTAGTTCTATGTCgaaaGA CATAGAGAGTTAAAATAAAG GATTACCTAAATACTCATTAT GTGATGAGAGGCTGCTTAGG CTAGCCTTTTTTTT (SEQ ID NO: 199)
	sgRNA V2	GTTCTAGTTCTATGTCgaaaGA CATAGAGAGTTAGAATAAAG GATTACCTAAATACTCATTAT GTGATGAGAGGCTGCTTAGG CTAGCCTTTTTTTT (SEQ ID NO: 200)
	sgRNA V2 crRNA (Repeat)	GUUCUAGUUCUAUGUC (SEQ ID NO: 201)
	sgRNA V2 crRNA (Antirepeat)	GACAUAGAGAGUUAGAAU (SEQ ID NO: 202)

Table 3 – Summary of OMNI Nuclease PAMs

Name	Permissive PAM	PAM Specific 1	Additional Permissive PAM	PAM Specific 2	PAM Specific 3
OMNI-115	NNRYTT	NNRTTT	NNRYTTHN	NNRYTTTN	Not listed
OMNI-124	NNGNRC	Not listed	NNGNDCNN	NNGNRCNN	NNGNRMNN
OMNI-127	NYRRV	Not listed	NYARMNNN	NYAGCNNN	Not listed
OMNI-144	NNRC	NNGC	NNDVNNNN	NNGCCANN	NNRCNNNN
OMNI-145	NNRC	NNGC	NNDVNNNN	NNGCCANN	NNGCCANN
OMNI-146	NNRC	NNGC	NNRCDNNN	NNRCRNCY	NNDCNNNN
OMNI-147	NNRC	NNGC	NNDVNNNN	NNGCCANN	NNRCNNNN
OMNI-148	NNRC	NNGC	NNRCNNNN	NNGCRANN	NNRCNANN
OMNI-149	NNRC	NNGC	NNDCNNNN	NNGCDNHN	NNRCNNCY
OMNI-159	NNNNCH	NNNNCM	NNNNCMAN	NNNNCMAN	NNNNCMNN
OMNI-218	NNGNKC	NGGRKC	NRGNNCRN	SRGGNCRN	NRGGGCRN
OMNI-237	NNVVHY	NNRRHY	NNRVCYNN	NNRACTNN	NNRACYTN
OMNI-248	NRVA	NRMA	NRVANNNN	NAAANNNN	NRAANNNN
OMNI-251	NRNCC	Not listed	NRNCCNNN	NRNCCNNN	Not listed
OMNI-252	NRNCC	Not listed	NRNCCNNN	NRNCCNNN	NRRCCNNN
OMNI-253	NNNCC	Not listed	NNNCCNNN	NRRCCNNN	NNNCYNNN
OMNI-259	NNGAYA	Not listed	NDGHYAHN	NNGAYAHN	NKGWYAHN

Table 4 - Plasmids and Constructs

Plasmid	Purpose	Elements	Example
pET9a	Expressing OMNI polypeptide in the bacterial system	T7 promoter HA Tag-Linker-OMNI ORF (Human optimized) -SV40 NLS-8XHisTag -T7 terminator	pET9a-OMNI-115 (SEQ ID NO:)
pbShuttle Guide T2	Expressing OMNI sgRNA in the bacterial system	U6 promotor - T7promoter - T2 spacer sgRNA scaffold - T7 terminator	pShuttle Guide-T2-OMNI-97 V1 (SEQ ID NO:)
pbPOS T2 library	Bacterial/TXTL depletion assay	T2 protospacer - 8N PAM library - chloramphenicol acetyltransferase	pbPOS T2 library (SEQ ID NO:)
pmOMNI	Expressing OMNI polypeptide in the human cell system	CMV promoter - Kozak - SV40 NLS - OMNI ORF (human optimized) - HA - SV40 NLS - P2A - mCherry - bGH poly(A) signal	pmOMNI-OMNI-127 (SEQ ID NO:)
pET28	Expressing OMNI polypeptide in the bacterial system	T7 promoter HA Tag-Linker-OMNI ORF (Bacterial optimized) -SV40 NLS-8XHisTag -T7 terminator	pET28a-OMNI127

Table 5 - Nuclease activity in endogenous context in mammalian cells

Nuclease	Gene target	Corresponding spacer name	Spacer Sequence	PAM	Max Activity Mean
OMNI-124	B2M	hB2M_s32_22bp_II	AGCGCGAGCACAGCUAAGGCCA (SEQ ID NO: 269)	CGGAGCGA	87.0000
	CXCR4	hCXCR4_s85_22bp_II	CCUCGGUGAUGGAAAUCCACUU (SEQ ID NO: 270)	GTGCACAG	54.0000
	B2M	hB2M_S52_22bp_II	CGUGAGUAAACCUGAAUCUUUG (SEQ ID NO: 271)	GAGTACCT	51.0000

	ELANE	hELANE_g138_22bp_II	GGUGUCAAGCCCCAGAGGCCAC (SEQ ID NO: 272)	AGGGACAG	39.0000
	CXCR4	hCXCR4_S100_22bp_II	UGCCUUGCAUAGGAAGUUCCCA (SEQ ID NO: 273)	AAGTACCA	23.0000
	SARM1	hSARM1_g13_22bp_II	UGCUCAGACACGCGGUGCAGCA(SEQ ID NO: 274)	GGGAGCGG	22.0000
	TRAC	hTRAC_S21_22bp_II	GGCCACUUUCAGGAGGAGGAUU (SEQ ID NO: 275)	CGGAACCC	13.0000
	ELANE	hELANE_g39_22bp_II	CACAGCGGGUGUAGACUCCGAG (SEQ ID NO: 276)	GGGGACGT	13.0000
OMNI-218	ELANE	hELANE_g143_22bp_II	GCCUGUUGCUGCAGUCCGGGCU (SEQ ID NO: 277)	GGGAGCGG	89.0000
	CXCR4	hCXCR4_S25_22bp_II	UGGCAAGAGACCCACACACCGG (SEQ ID NO: 278)	AGGAGCGC	89.0000
	B2M	hB2M_s32_22bp_II	AGCGCGAGCACAGCUAAGGCCA (SEQ ID NO: 279)	CGGAGCGA	71.0000
	TRAC	hTRAC_s128_22bp_II	AGUCUCUCAGCUGGUACACGGC (SEQ ID NO: 280)	AGGGTCAG	65.0000
	TRAC	hTRAC_S22_22bp_II	CAAGAGCAACAGUGCUGUGGCC (SEQ ID NO: 281)	TGGAGCAA	27.0000
	TIGIT	hTIGIT_S24_22bp_II	CAUCAGACAGCUGUGACAGCCA (SEQ ID NO: 282)	TGGAGCTC	22.0000
	CTLA4	hCTLA4_S15_22bp_II	CAAGGACUGAGGGCCAUGGACA (SEQ ID NO: 283)	CGGGACTC	18.0000
	CXCR4	hCXCR4_S103_22bp_II	CUGUUGGCUGCCUUACUACAUU (SEQ ID NO: 284)	GGGATCAG	15.0000
OMNI-237	B2M	hB2M_s12_22bp_II	GUAUGCCUGCCGUGUGAACCAU (SEQ ID NO: 285)	GTGACTTT	18.0000
OMNI-248	CXCR4	hCXCR4_s186_22bp_II	UCCUGGUCAUGGGUUACCAGAA (SEQ ID NO: 286)	GAAACTGA	25.0000
	CXCR4	hCXCR4_s187_22bp_II	AUAAGGCCAACCAUGAUGUGCU (SEQ ID NO: 287)	GAAACTGG	16.0000
	TRAC	hTRAC_S35_22bp_II	GACCCUGCCGUGUACCAGCUGA (SEQ ID NO: 288)	GAGACTCT	14.0000
	B2M	hB2M_S83_22bp_II	AUUCUCUGCUGGAUGACGUGAG (SEQ ID NO: 289)	TAAACCTG	14.0000

OMNI-251	SAMD 9L	hSAMD9L_g13 0alt_22bp_II	GUCCAAAACAGAAC ACCAAAAA (SEQ ID NO: 290)	AATCCAAA	1.0000
OMNI-252	TRAC	hTRAC_S72_22 bp_II	UUCCAGAAGACACC UUCUUCCC (SEQ ID NO: 291)	CAGCCCAG	1.0000
	SAMD 9L	hSAMD9L_g13 0_22bp_II	GUCCAAAACAGAAC ACCAGAAA (SEQ ID NO: 292)	AATCCAAA	1.0000
OMNI-253	CXCR4	hCXCR4_S65_2 2bp_II	AGGGGACUAUGACU CCAUGAAG (SEQ ID NO: 293)	GAACCCTG	4.0000
OMNI-159	GATA2	hGATA2_g71_2 2bp_II	GAUCCAGACUCGGA ACCGGAAG (SEQ ID NO: 294)	ATGTCCAA	91.0000
	CXCR4	hCXCR4_S36_2 2bp_II	GUAAGGCAGCCAAC AGGCGAAG (SEQ ID NO: 295)	AAAGCCAG	87.0000
	ELANE	hELANE_g139a lt_22bp_II	AGUCCCAGCUGCGG GAAUGGGA (SEQ ID NO: 296)	TTCCCAGG	75.0000
	ELANE	hELANE_g133_ 22bp_II	AGUCCGGGCUGGGA GCGGGUGG (SEQ ID NO: 297)	GGAGCAGA	68.0000
	SARM1	hSARM1_g12_2 2bp_II	AGACACGCGGUGCA GCAGGGAG (SEQ ID NO: 298)	CGGTCCAG	63.0000
	ELANE	hELANE_g146_ 22bp_II	UGUUAUGGUCACAG CGGGUGUA (SEQ ID NO: 299)	GACTCCGA	19.0000
	ELANE	hELANE_g48_2 2bp_II	CCCUCGGAGUCUAC ACCCGCUG (SEQ ID NO: 300)	TGACCATA	10.0000
OMNI-127	TRAC	hTRAC_s130_2 2bp_II	GGCCCCUCACCUCA GCUGGACC (SEQ ID NO: 301)	ACAGCCGC	87.0000
OMNI-127	ELANE	hELANE_g136_ 22bp_II	CCACCCGCUCCCAG CCCGGACU (SEQ ID NO: 302)	GCAGCAAC	86.0000
OMNI-127	ELANE	hELANE_g135_ 22bp_II	GCGGGAAAGGGAUU CCCAGGAC (SEQ ID NO: 303)	CCAGCCCC	67.0000
OMNI-127	ELANE	hELANE_g135_ 22bp_II	GCGGGAAAGGGAUU CCCAGGAC (SEQ ID NO: 304)	CCAGCCCC	64.0000
OMNI-127	B2M	hB2M_S38_22b p_II	CUCUUUCUGGCCUG GAGGCUAU (SEQ ID NO: 305)	CCAGCGTG	48.0000
OMNI-127	TRAC	hTRAC_s129_2 2bp_II	GCAUGUGCAAACGC CUUCAACA (SEQ ID NO: 306)	ACAGCATT	43.0000
OMNI-127	CXCR4	hCXCR4_s72_2 2bp_II	GUGGAUUUCCAUCA CCGAGGCC (SEQ ID NO: 307)	CTAGCTTT	41.0000

OMNI-127	CXCR4	hCXCR4_s73_22bp_II	AGGAGGUCGGCCACUGACAGGU (SEQ ID NO: 308)	GCAGCCTG	40.0000
OMNI-127	TRAC	hTRAC_S58_22bp_II	AGAACCCUGACCCUGCCGUGUA (SEQ ID NO: 309)	CCAGCTGA	39.0000
OMNI-127	ELANE	hELANE_g134_22bp_II	GGGUCCUGGGAAUCCCUUUCCC (SEQ ID NO: 310)	GCAGCTGG	23.0000

Table 5. Nuclease activity in endogenous context in mammalian cells: OMNI nucleases were expressed in mammalian cell system (HeLa) by DNA transfection together with an sgRNA expressing plasmid. Cell lysates were used for site specific genomic DNA amplification and NGS. The percentage of indels was measured and analyzed to determine the editing level. Each sgRNA is composed of the tracrRNA (see **Table 2**) and the spacer detailed here. The spacer 3' genomic sequence contains the expected PAM relevant for each OMNI nuclease. Transfection efficiency (% transfection) was measured by flow cytometry of the mCherry signal, as described above. All tests were performed in triplicates. OMNI nuclease only (no guide) transfected cells served as negative a control (data not shown).

Table 6 – OMNI-127 Synthetic sgRNAs targeting ELANE

Site	Spacer length	Spacer sequence	PAM	Scaffold sgRNA12 V2	Full sgRNA
g134_alt	22	SEQ ID NO: 311	GCAGCTGG	SEQ ID NO: 324	SEQ ID NO: 325
g134_ref	22	SEQ ID NO: 312	GCAGCTGG	SEQ ID NO: 324	SEQ ID NO: 326
g135_alt	22	SEQ ID NO: 313	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 327
g135_ref	20	SEQ ID NO: 314	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 328
g135_ref	21	SEQ ID NO: 315	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 329
g135_ref	22	SEQ ID NO: 316	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 330
g135_ref	23	SEQ ID NO: 317	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 331
g135_ref	24	SEQ ID NO: 318	CCAGCCCC	SEQ ID NO: 324	SEQ ID NO: 332
g136	20	SEQ ID NO: 319	GCAGCAAC	SEQ ID NO: 324	SEQ ID NO: 333
g136	21	SEQ ID NO: 320	GCAGCAAC	SEQ ID NO: 324	SEQ ID NO: 334
g136	22	SEQ ID NO: 321	GCAGCAAC	SEQ ID NO: 324	SEQ ID NO: 335
g136	23	SEQ ID NO: 322	GCAGCAAC	SEQ ID NO: 324	SEQ ID NO: 336
g136	24	SEQ ID NO: 323	GCAGCAAC	SEQ ID NO: 324	SEQ ID NO: 337

Table 7 – OMNI-127 RNP activity and spacer optimization in mammalian U2OS cells

Gene	Genomic site	Spacer sequence	PAM	Spacer Length	% indels
ELANE	g134_ref	GGGUCCUGGGAAUCCCUUUCCC (SEQ ID NO: 338)	GCAGCTGG	22	46.0000
	g135_ref	GGGAAAGGGAUUCCCAGGAC (SEQ ID NO: 339)	CCAGCCCC	20	95.0000
	g135_ref	CGGGAAAGGGAUUCCCAGGAC (SEQ ID NO: 340)	CCAGCCCC	21	96.0000
	g135_ref	GCGGGAAAGGGAUUCCCAGGAC (SEQ ID NO: 341)	CCAGCCCC	22	92.0000
	g135_ref	UGCGGGAAAGGGAUUCCCAGGAC (SEQ ID NO: 342)	CCAGCCCC	23	93.0000
	g135_ref	CUGCGGGAAAGGGAUUCCCAGGA C (SEQ ID NO: 343)	CCAGCCCC	24	95.0000
	g136_ref	CCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 344)	GCAGCAAC	20	97.0000
	g136_ref	CCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 345)	GCAGCAAC	21	91.0000
	g136_ref	CCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 346)	GCAGCAAC	22	98.0000
	g136_ref	CCCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 347)	GCAGCAAC	23	97.0000
	g136_ref	CCCCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 348)	GCAGCAAC	24	98.0000

Table 7. OMNI-127 activity and spacer optimization as part of an RNP complex in U2OS cells. OMNI-127 RNP was assembled with synthetic sgRNA (Agilent, **Table 6**) and electroporated into U2OS cells. Gene name, spacer sequences, and spacer lengths are indicated next to the editing level as measured by NGS.

Table 8 – OMNI-127 RNP activity and spacer optimization in mammalian HSC-MLP2 cells

Gene	Genomic Site	Spacer Sequence	PAM	Spacer Length	% indels
ELANE	g135_ref	GCGGGAAAGGGAUUCCCAGGAC (SEQ ID NO: 349)	CCAGCCCC	22	39.0000
	g135_alt	GCGGGAAUGGGAUUCCCAGGAC (SEQ ID NO: 350)	CCAGCCCC	22	49.0000
	g136_ref	CCACCCGCUCCCAGCCCGGACU (SEQ ID NO: 351)	GCAGCAAC	22	71.0000

Table 8. OMNI-127 activity and spacer optimization as an RNP in HSC-MLP2 cells. OMNI-127 RNP was assembled with synthetic sgRNA (Agilent, **Table 6**) and electroporated into HSC-MLP2 cells. Gene name, spacer sequences, and spacer lengths are indicated next to the editing level as was measured by NGS.

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CLAIMS

What is claimed is:

1. A non-naturally occurring composition comprising a CRISPR nuclease comprising a sequence having at least 90% identity to the amino acid sequence selected from the group consisting of SEQ ID NOs: 3, 1, or 2-17, or a nucleic acid molecule comprising a sequence encoding the CRISPR nuclease.

2. The composition of claim 1, further comprising one or more RNA molecules, or a DNA polynucleotide encoding any one of the one or more RNA molecules, wherein the one or more RNA molecules and the CRISPR nuclease do not naturally occur together and the one or more RNA molecules are configured to form a complex with the CRISPR nuclease and/or target the complex to a target site.

3. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 82-97.

4. The composition of claim 3, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 82-85 and 96.

5. The composition of claim 4, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 86-93 and 97.

6. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 3 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 82-97.

7. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 52-64.

8. The composition of claim 7, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 52-55.

9. The composition of claim 8, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 56-63.

10. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 1 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 52-64.

11. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 65-81.

12. The composition of claim 11, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 65-68 and 80.

13. The composition of claim 12, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 69-77 and 81.

14. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 2 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 65-81.

15. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 98-114.

16. The composition of claim 15, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 98-101 and 114.

17. The composition of claim 16, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 102-111.

18. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in any one of SEQ ID NOs: 4-9 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 98-114.

19. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 115-127.

20. The composition of claim 19, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 115-118.

21. The composition of claim 20, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 119-126.

22. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 10 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 115-127.

23. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least

one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 128-141.

24. The composition of claim 23, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 128-131.

25. The composition of claim 24, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 132-140.

26. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 11 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 128-141.

27. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 142-155.

28. The composition of claim 27, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 142-145.

29. The composition of claim 28, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 146-152 and 155.

30. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 12 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 142-155.

31. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least

one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 156-167 and GCUUUAAGC.

32. The composition of claim 31, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 156-159.

33. The composition of claim 32, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 160-166 and GCUUUAAGC.

34. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 13 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 156-167 and GCUUUAAGC.

35. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 168-176.

36. The composition of claim 35, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 168 and 169.

37. The composition of claim 36, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 170-175.

38. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NOs: 14 or 15 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 168-176.

39. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 177-185.

40. The composition of claim 39, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177 and 178.

41. The composition of claim 40, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 179-184.

42. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 16 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 177-185.

43. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17, and at least one RNA molecule comprises a sequence selected from the group consisting of SEQ ID NOs: 186-202.

44. The composition of claim 43, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a CRISPR RNA (crRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 186-189 and 201.

45. The composition of claim 44, further comprising a transactivating CRISPR RNA (tracrRNA) molecule comprising a sequence set forth in the group consisting of SEQ ID NOs: 190-198 and 202.

46. The composition of claim 2, wherein the CRISPR nuclease comprises a sequence having at least 90% identity to the amino acid sequence set forth in SEQ ID NO: 17 and at least one RNA molecule is a single-guide RNA (sgRNA) molecule comprising a guide sequence portion and a sequence selected from the group consisting of SEQ ID NOs: 186-202.

47. The composition of any one of claims 1-46, wherein the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1.

48. The composition of any one of claims 1-46, wherein the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1.

49. The composition of any one of claims 1-46, wherein the CRISPR nuclease is a catalytically dead nuclease having an inactivated RuvC domain and an inactivated HNH domain created by substitutions at the positions provided for the CRISPR nuclease in column 7 of Table 1.

50. The composition of any one of claims 1-49, wherein the CRISPR nuclease utilizes a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in column 2 -4 of Table 3.

51. A method of modifying a nucleotide sequence at a DNA target site in a cell-free system or the genome of a cell comprising introducing into the cell the composition of any one of claims 2-50.

52. The method of claim 51, wherein the CRISPR nuclease effects a DNA break in a DNA strand adjacent to a protospacer adjacent motif (PAM) sequence provided for the CRISPR nuclease in column 2-4 of Table 3, and/or effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.

53. The method of claim 51, wherein the CRISPR nuclease is a nickase having an inactivated RuvC domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 5 of Table 1, and effects a DNA break in a DNA strand adjacent to a sequence that is complementary to the PAM sequence.

54. The method of claim 51, wherein the CRISPR nuclease is a nickase having an inactivated HNH domain created by an amino acid substitution at a position provided for the CRISPR nuclease in column 6 of Table 1, and effects a DNA break in a DNA strand adjacent to the PAM sequence.

55. The method of any one of claims 51-54, wherein the cell is a eukaryotic cell or a prokaryotic cell.

56. The method of claim 55, wherein the cell is a mammalian cell.

57. The method of claim 56, wherein the cell is a human cell.

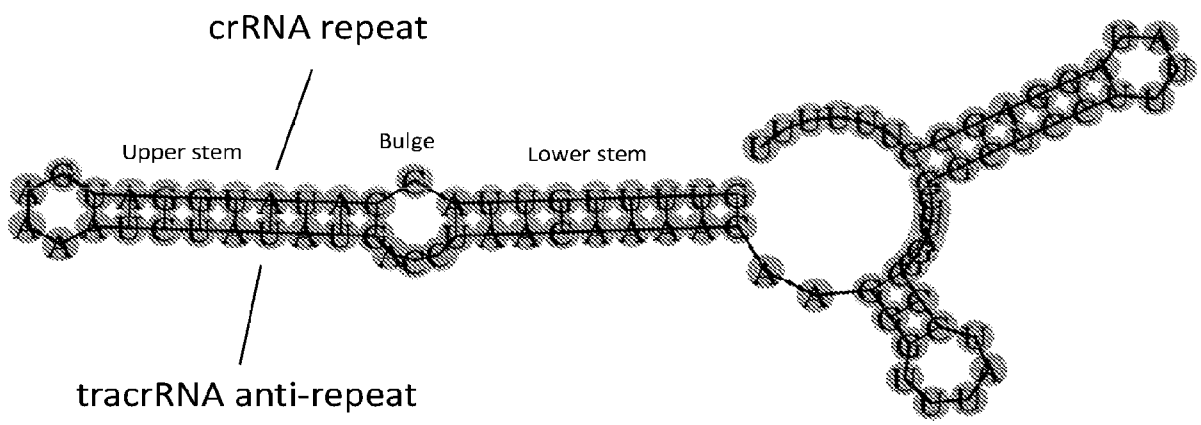

crRNA repeat
Upper stem
Bulge
Lower stem
tracrRNA anti-repeat

Fig. 1A

V1 – 2 hairpins

Fig. 1B

V2 – 2 hairpins

Fig. 1C

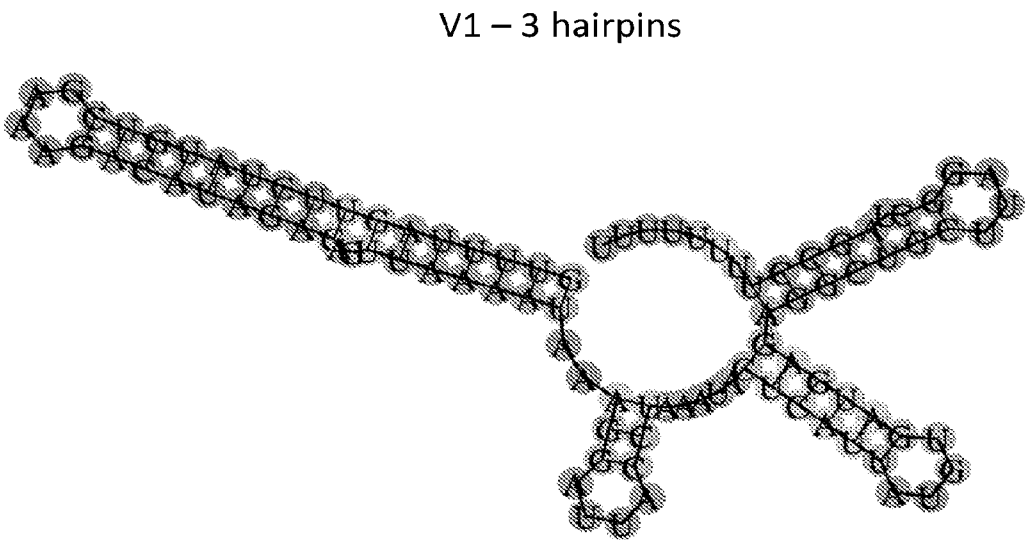
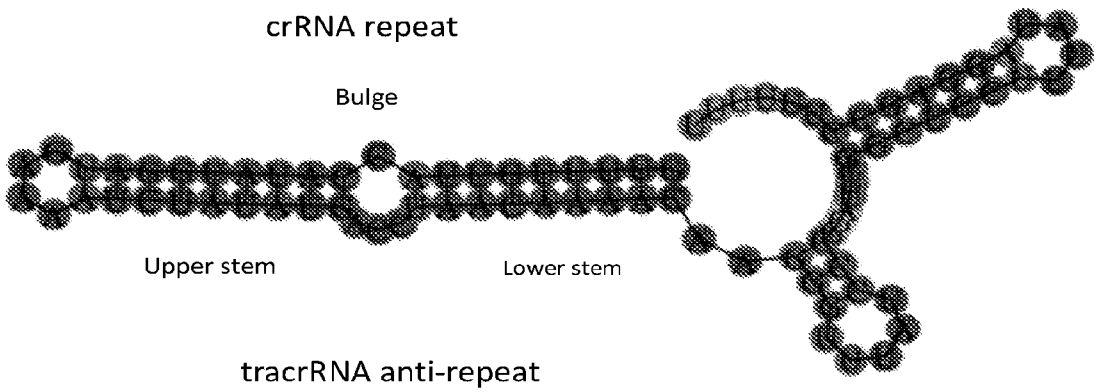
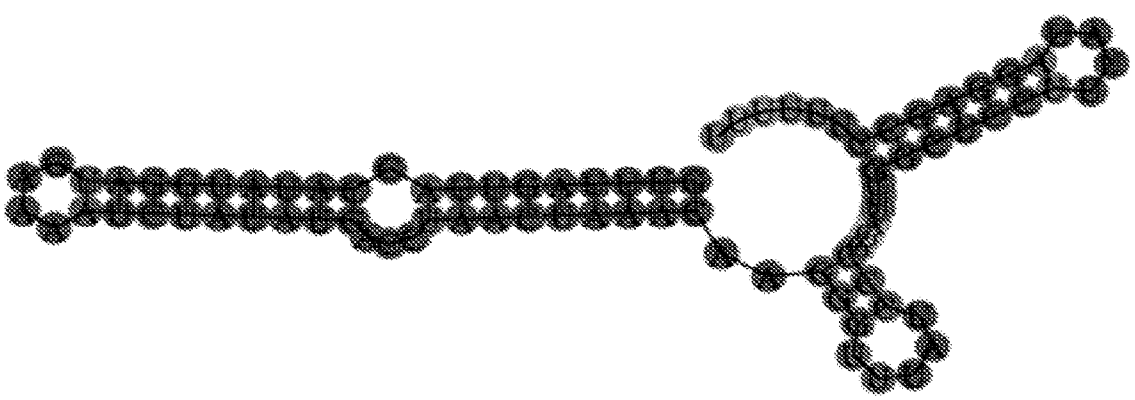


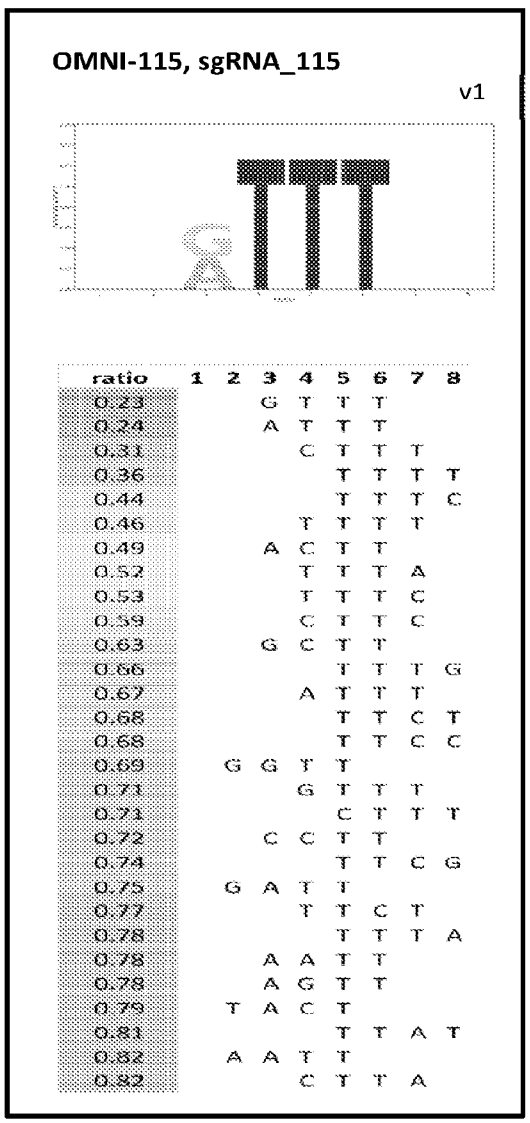
Fig. 1D

V1


crRNA repeat
Bulge
Upper stem
Lower stem
tracrRNA anti-repeat

V2





ratio	1	2	3	4	5	6	7	8
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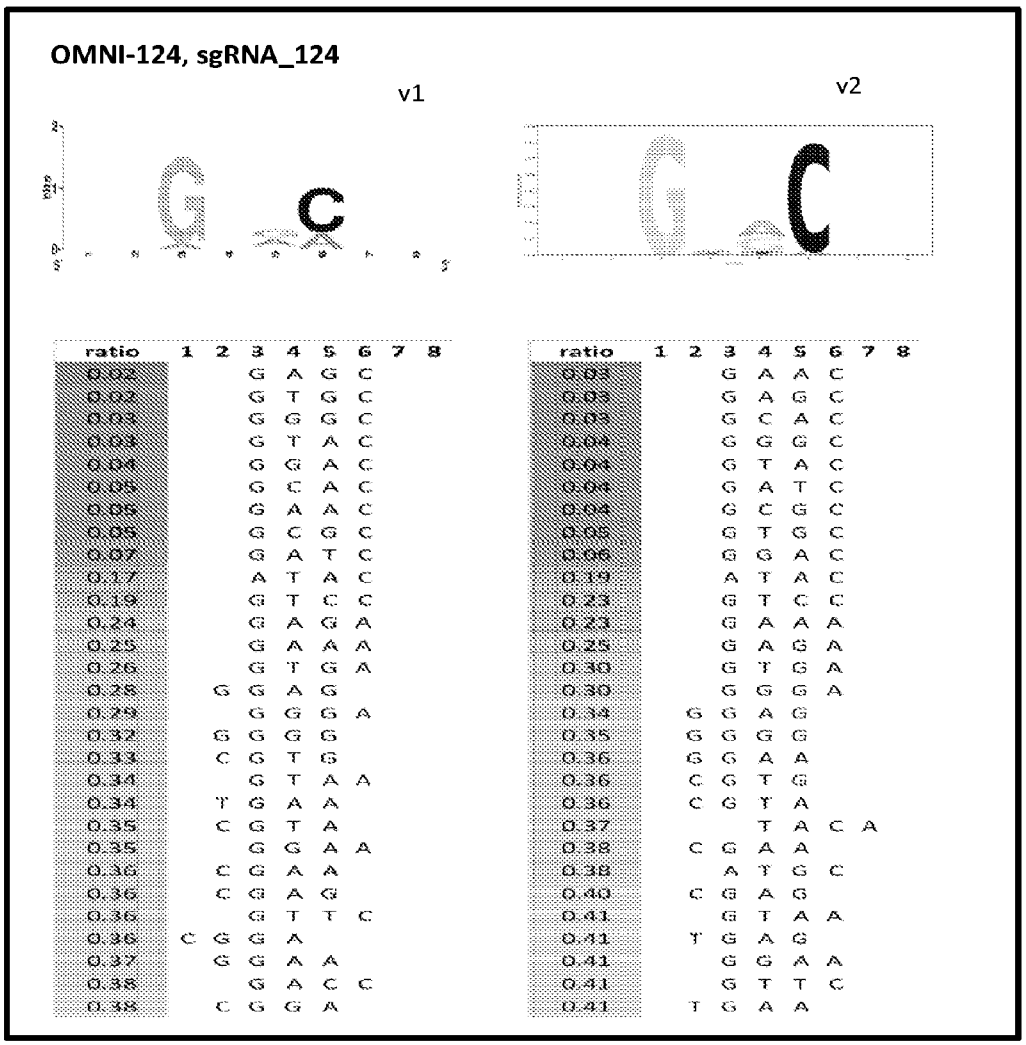
0.24			A	T	T	T		
0.31				C	T	T	T	
0.36					T	T	T	T
0.44					T	T	T	C
0.46				T	T	T	T	
0.49			A	C	T	T		
0.52				T	T	T	A	
0.53				T	T	T	C	
0.59				C	T	T	C	
0.63			G	C	T	T		
0.66					T	T	T	G
0.67				A	T	T	T	
0.68					T	T	C	T
0.68					T	T	C	C
0.69		G	G	T	T			
0.71				G	T	T	T	
0.71					C	T	T	T
0.72			C	C	T	T		
0.74					T	T	C	G
0.75		G	A	T	T			
0.77				T	T	C	T	
0.78					T	T	T	A
0.78			A	A	T	T		
0.78			A	G	T	T		
0.79		T	A	C	T			
0.81					T	T	A	T
0.82		A	A	T	T			
0.82				C	T	T	A	

Fig. 2



ratio	1	2	3	4	5	6	7	8
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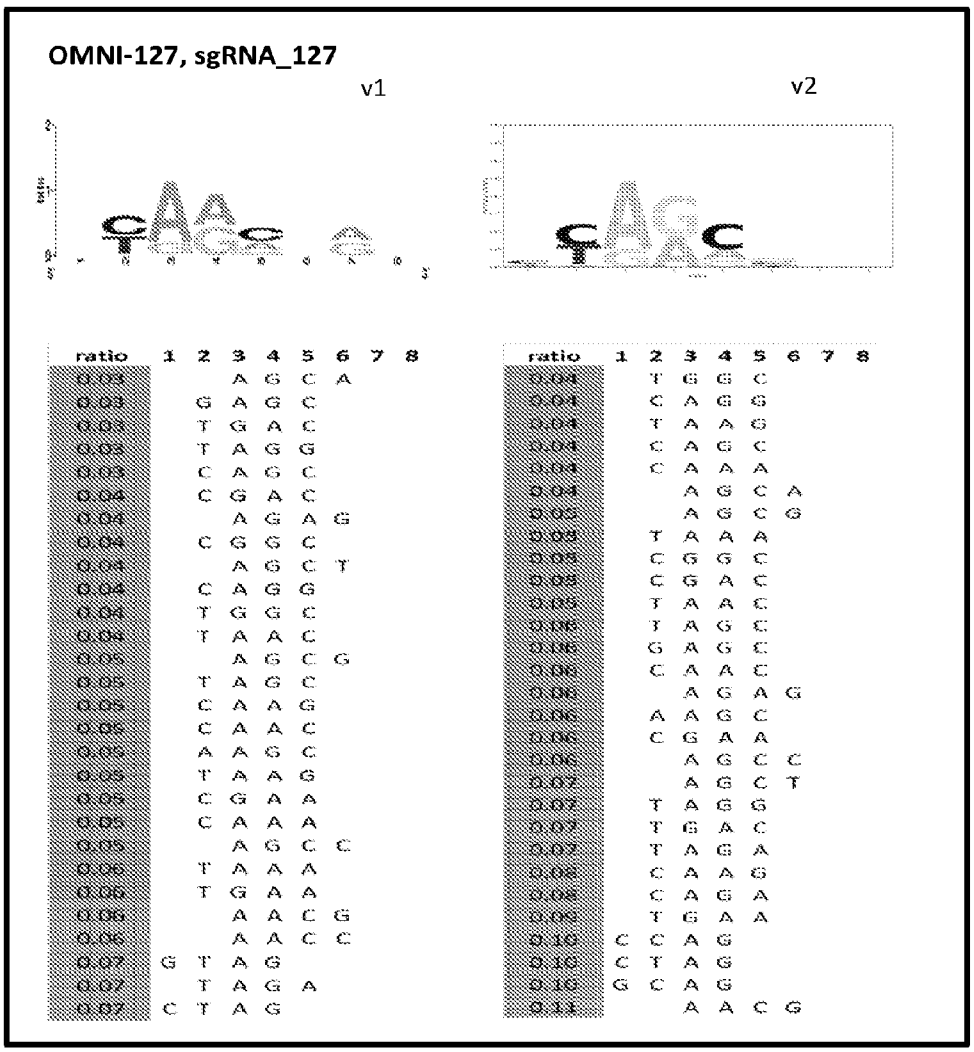
0.02			G	T	G	C		
0.03			G	G	G	C		
0.03			G	T	A	C		
0.04			G	G	A	C		
0.05			G	C	A	C		
0.05			G	A	A	C		
0.06			G	C	G	C		
0.07			G	A	T	C		
0.17			A	T	A	C		
0.19			G	T	C	C		
0.24			G	A	G	A		
0.25			G	A	A	A		
0.26			G	T	G	A		
0.28		G	G	A	G			
0.29			G	G	G	A		
0.32		G	G	G	G			
0.33		C	G	T	G			
0.34			G	T	A	A		
0.34		T	G	A	A			
0.35		C	G	T	A			
0.35			G	G	A	A		
0.36		C	G	A	A			
0.36		C	G	A	G			
0.36			G	T	T	C		
0.36	C	G	G	A				
0.37		G	G	A	A			
0.38			G	A	C	C		
0.38		C	G	G	A			

ratio	1	2	3	4	5	6	7	8
0.03			G	A	A	C		
0.03			G	A	G	C		
0.03			G	C	A	C		
0.04			G	G	G	C		
0.04			G	T	A	C		
0.04			G	A	T	C		
0.04			G	C	G	C		
0.06			G	T	G	C		
0.06			G	G	A	C		
0.19			A	T	A	C		
0.23			G	T	C	C		
0.23			G	A	A	A		
0.25			G	A	G	A		
0.30			G	T	G	A		
0.30			G	G	G	A		
0.34		G	G	A	G			
0.35		G	G	G	G			
0.36		G	G	A	A			
0.36		C	G	T	G			
0.36		C	G	T	A			
0.37				T	A	C	A	
0.38		C	G	A	A			
0.38			A	T	G	C		
0.40		C	G	A	G			
0.41			G	T	A	A		
0.41		T	G	A	G			
0.41			G	G	A	A		
0.41			G	T	T	C		
0.41		T	G	A	A			

Fig. 3


OMNI-127, sgRNA_127
v1
v2
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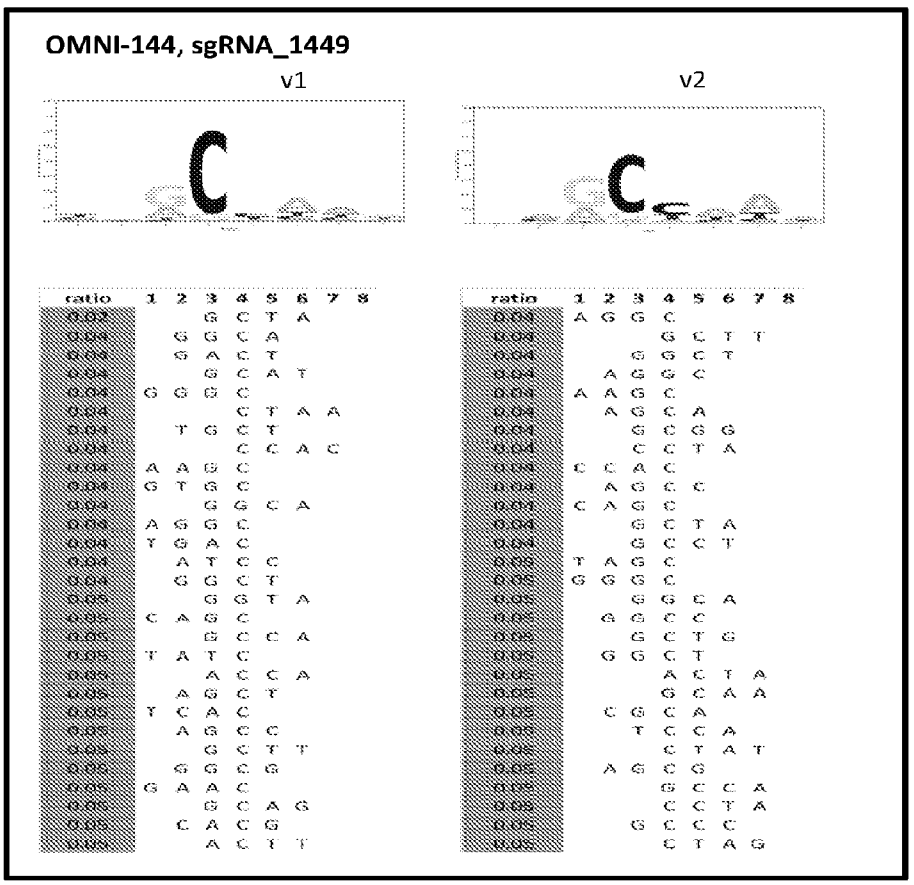
0.03 G A G C
0.03 T G A C
0.03 T A G G
0.03 C A G C
0.04 C G A C
0.04 A G A G
0.04 C G G C
0.04 A G C T
0.04 C A G G
0.04 T G G C
0.04 T A A C
0.05 A G C G
0.05 T A G C
0.05 C A A G
0.05 C A A C
0.05 A A G C
0.05 T A A G
0.05 C G A A
0.05 C A A A
0.05 A G C C
0.06 T A A A
0.06 T G A A
0.06 A A C G
0.06 A A C C
0.07 G T A G
0.07 T A G A
0.07 C T A G
ratio 1 2 3 4 5 6 7 8
0.04 T G G C
0.04 C A G G
0.04 T A A G
0.04 C A G C
0.04 C A A A
0.04 A G C A
0.05 A G C G
0.05 T A A A
0.05 C G G C
0.05 C G A C
0.05 T A A C
0.06 T A G C
0.06 G A G C
0.06 C A A C
0.06 A G A G
0.06 A A G C
0.06 C G A A
0.06 A G C C
0.07 A G C T
0.07 T A G G
0.07 T G A C
0.07 T A G A
0.08 C A A G
0.08 C A G A
0.09 T G A A
0.10 C C A G
0.10 C T A G
0.10 G C A G
0.11 A A C G

Fig. 4


OMNI-144, sgRNA_1449
v1
v2
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0.03 G G C A
0.03 G A C T
0.04 G C A T
0.04 G G G C
0.04 C T A A
0.04 T G C T
0.04 C C A C
0.04 A A G C
0.04 G T G C
0.04 G G C A
0.04 A G G C
0.04 T G A C
0.04 A T C C
0.04 G G C T
0.05 G G T A
0.05 C A G C
0.05 G C C A
0.05 T A T C
0.05 A C C A
0.05 A G C T
0.05 T C A C
0.05 A G C C
0.05 G C T T
0.05 G G C G
0.05 G A A C
0.05 G C A G
0.05 C A C G
0.05 A C T T
ratio 1 2 3 4 5 6 7 8
0.03 A G G C
0.04 G C T T
0.04 G G C T
0.04 A G G C
0.04 A A G C
0.04 A G C A
0.04 G C G G
0.04 C C T A
0.04 C C A C
0.04 A G C C
0.04 C A G C
0.04 G C T A
0.04 G C C T
0.05 T A G C
0.05 G G G C
0.05 G G C A
0.05 G G C C
0.05 G C T G
0.05 G G C T
0.05 A C T A
0.05 G C A A
0.05 C G C A
0.05 T C C A
0.05 C T A T
0.05 A G C G
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0.05 G C C C
0.05 C T A G

Fig. 5

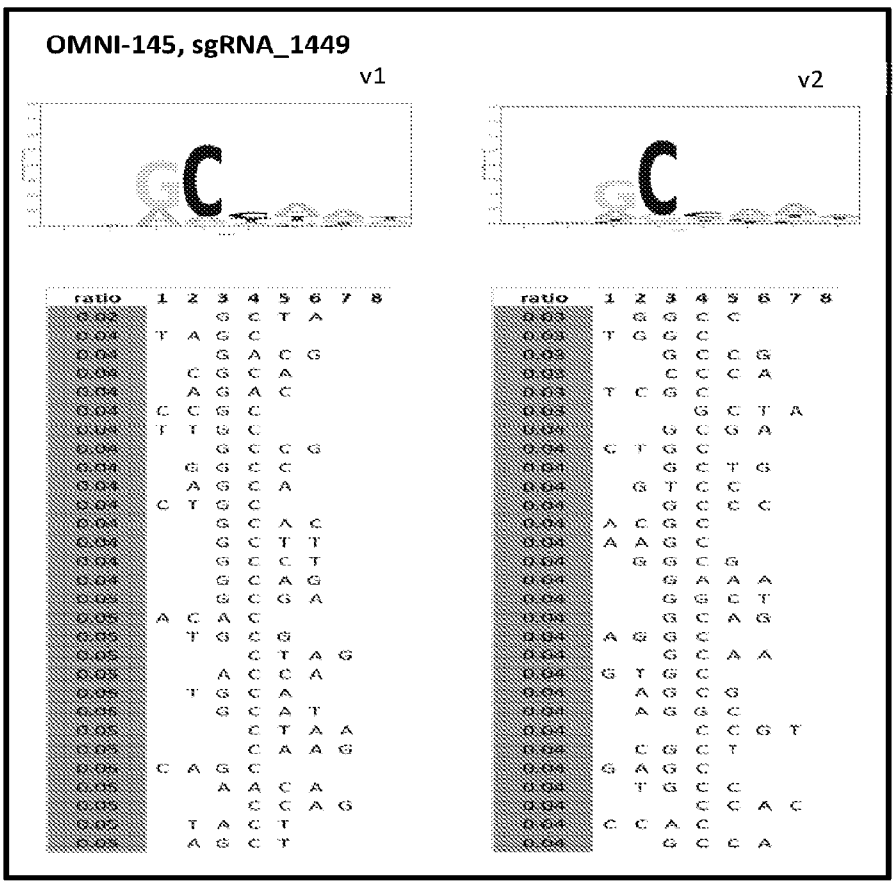
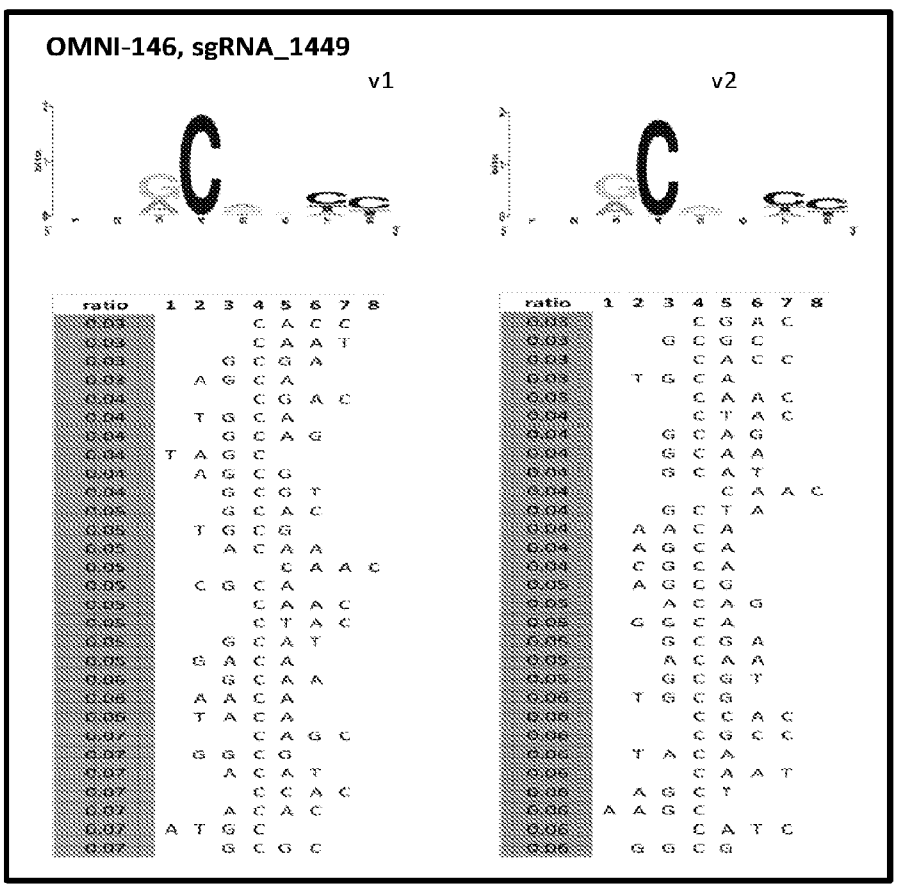


Fig. 6


OMNI-146, sgRNA_1449
v1
v2
ratio 1 2 3 4 5 6 7 8
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0.02 C A A T
0.03 G C G A
0.03 A G C A
0.04 C G A C
0.04 T G C A
0.04 G C A G
0.04 T A G C
0.03 A G C G
0.04 G C G T
0.04 G C A C
0.03 T G C G
0.03 A C A A
0.05 C A A C
0.05 C G C A
0.05 C A A C
0.05 C T A C
0.05 G C A T
0.05 G A C A
0.05 G C A A
0.06 A A C A
0.06 T A C A
0.07 C A G C
0.07 G G C G
0.07 A C A T
0.07 C C A C
0.07 A C A C
0.07 A T G C
0.07 G C G C
ratio 1 2 3 4 5 6 7 8
0.03 C G A C
0.03 G C G C
0.03 C A C C
0.03 T G C A
0.05 C A A C
0.04 C T A C
0.04 G C A G
0.04 G C A A
0.03 G C A T
0.04 C A A C
0.04 G C T A
0.04 A A C A
0.04 A G C A
0.04 C G C A
0.05 A G C G
0.05 A C A G
0.05 G C C A
0.05 G C G A
0.05 A C A A
0.06 G C G T
0.06 T G C G
0.06 C C A C
0.06 C G C C
0.06 T A C A
0.06 C A A T
0.06 A G C T
0.06 A A G C
0.06 C A T C
0.06 G G C G

Fig. 7

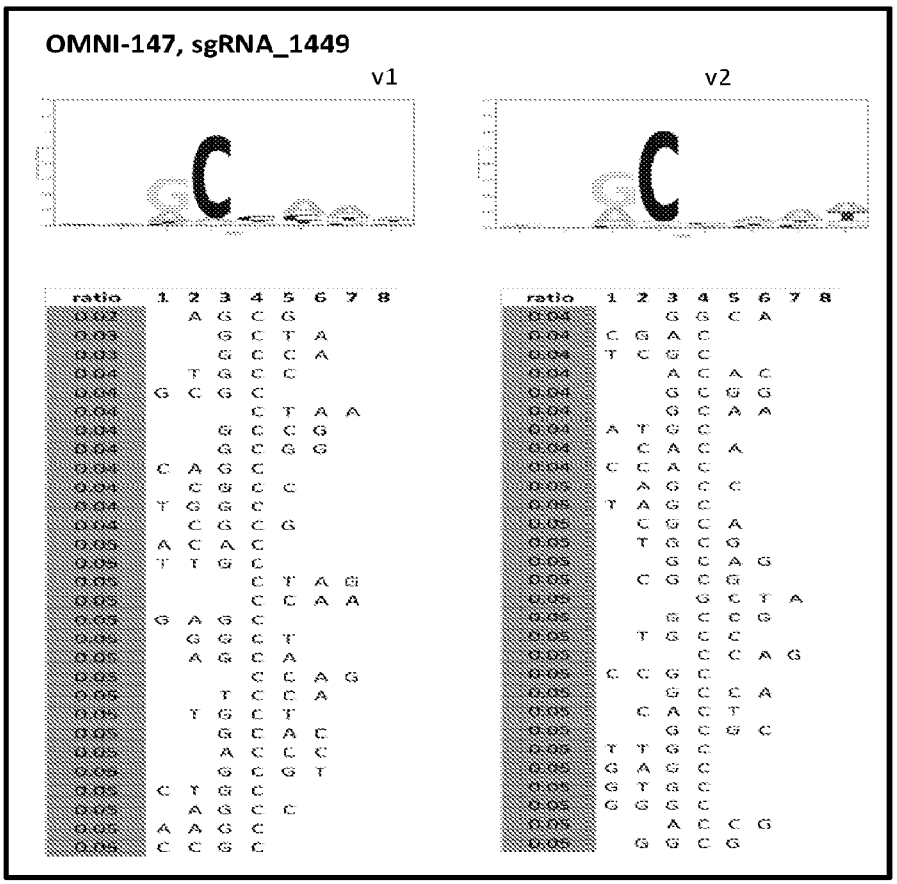
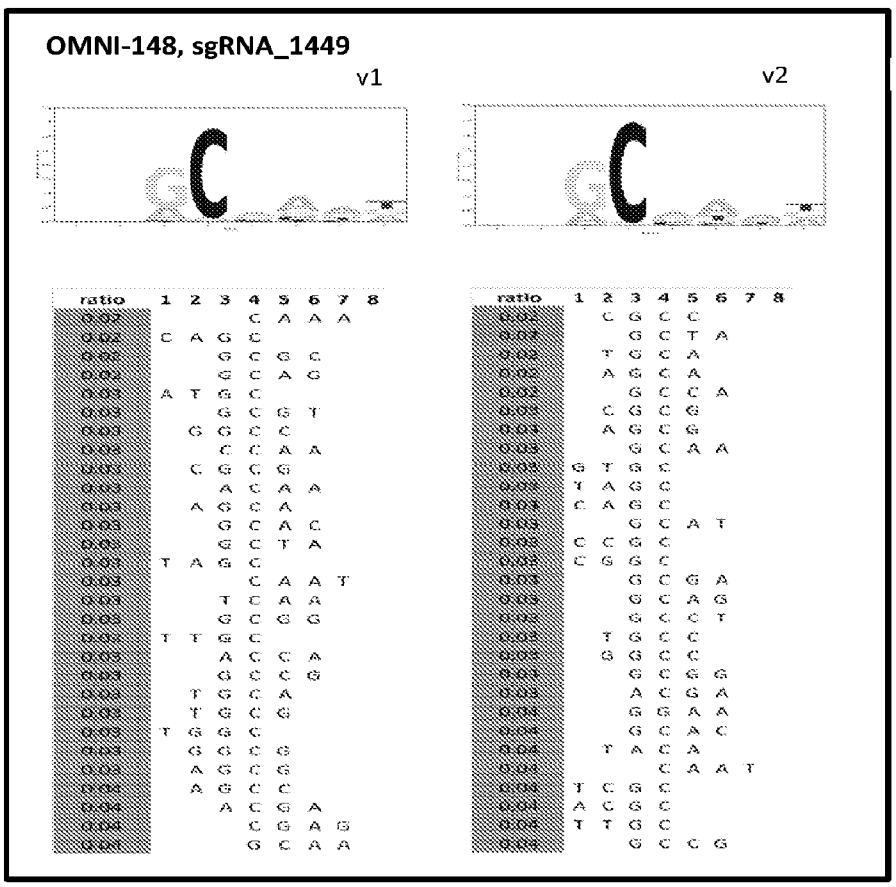


Fig. 8


OMNI-148, sgRNA_1449
v1
v2
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0.02 G C G C
0.02 G C A G
0.03 A T G C
0.03 G C G T
0.03 G G C C
0.03 C C A A
0.03 C G C G
0.03 A C A A
0.03 A G C A
0.03 G C A C
0.03 G C T A
0.03 T A G C
0.03 C A A T
0.03 T C A A
0.03 G C G G
0.03 T T G C
0.03 A C C A
0.03 G C C G
0.03 T G C A
0.03 T G C G
0.03 T G G C
0.03 G C G A
0.03 A G C C
0.03 A G C C
0.04 C A G A
0.04 C G A G
0.04 G C A A
ratio 1 2 3 4 5 6 7 8
0.02 C G C C
0.03 G C T A
0.03 T G C A
0.03 A G C A
0.03 G C C A
0.03 C G C G
0.03 A G C G
0.03 G C A A
0.03 G T G C
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0.03 C A G C
0.03 G C A T
0.03 C C G C
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Fig. 9

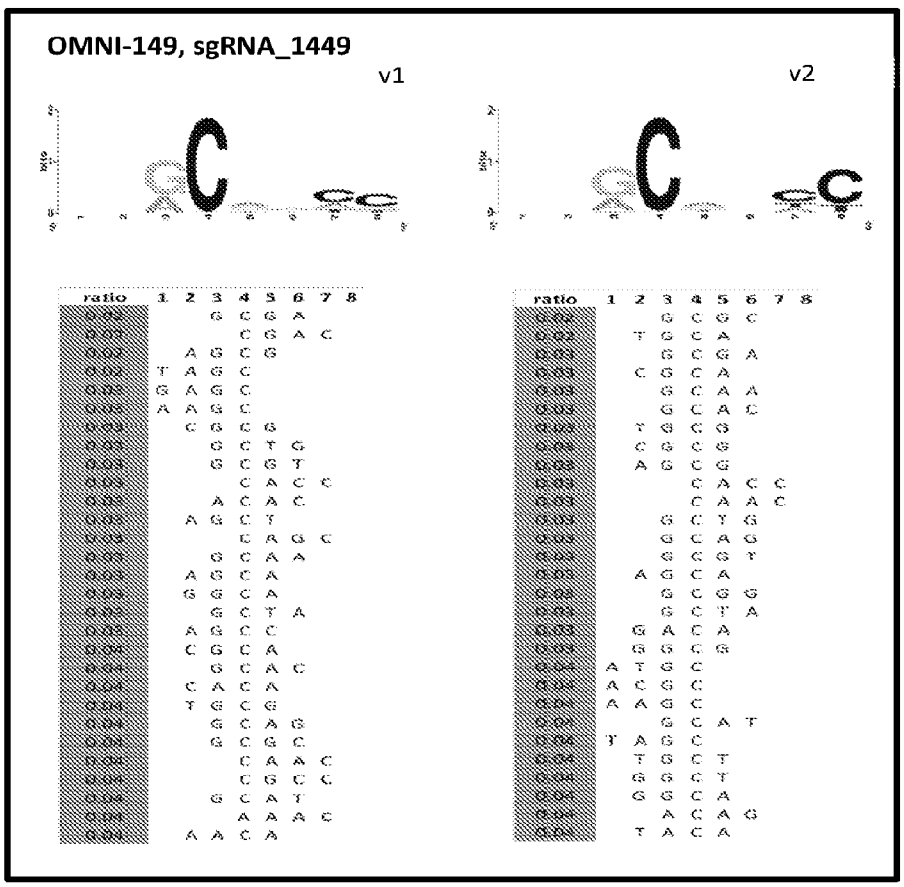
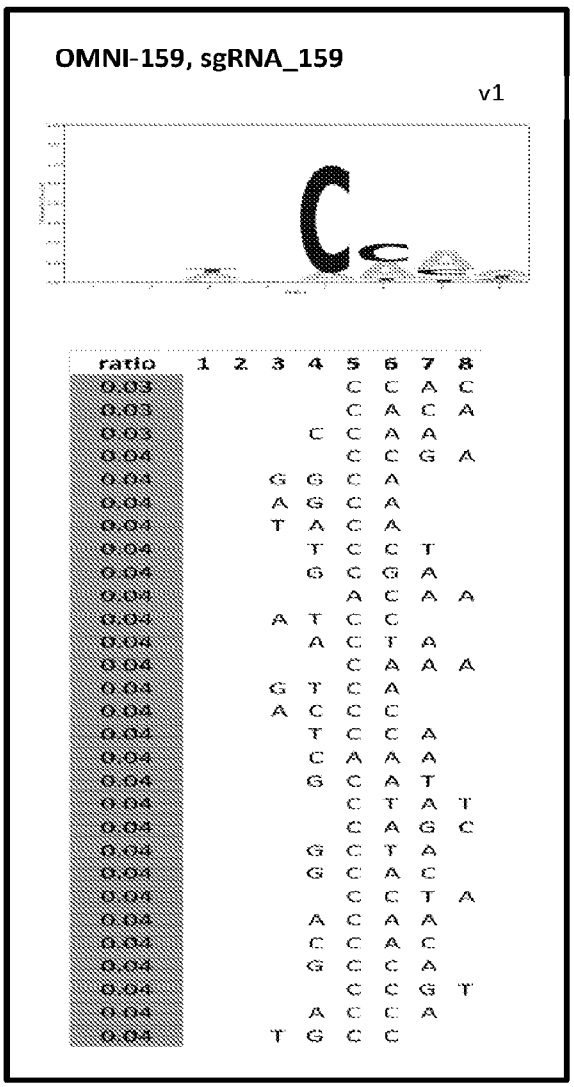


Fig. 10



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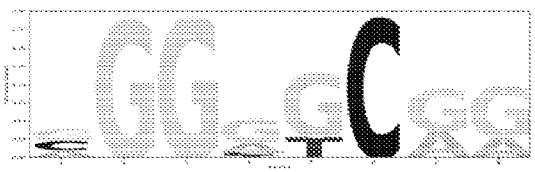
0.03				C	C	A	A	
0.04					C	C	G	A
0.04			G	G	C	A		
0.04			A	G	C	A		
0.04			T	A	C	A		
0.04				T	C	C	T	
0.04				G	C	G	A	
0.04					A	C	A	A
0.04			A	T	C	C		
0.04				A	C	T	A	
0.04					C	A	A	A
0.04			G	T	C	A		
0.04			A	C	C	C		
0.04				T	C	C	A	
0.04				C	A	A	A	
0.04				G	C	A	T	
0.04					C	T	A	T
0.04					C	A	G	C
0.04				G	C	T	A	
0.04				G	C	A	C	
0.04					C	C	T	A
0.04				A	C	A	A	
0.04				C	C	A	C	
0.04				G	C	C	A	
0.04					C	C	G	T
0.04				A	C	C	A	
0.04			T	G	C	C		

Fig. 11

OMNI-218, sgRNA_218

v1



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0.15			G	G	T	C		
0.16			G	G	G	C		
0.18	G	G	G	G				
0.19		G	G	G	G			
0.20		G	G	A	G			
0.20			G	A	G	C		
0.20			G	C	G	C		
0.22	C	G	G	G				
0.25					G	C	G	G
0.27			G	T	G	C		
0.27					G	C	A	G
0.28	A	G	G	G				
0.28				A	G	C	G	
0.29				A	G	C	A	
0.30					G	C	G	A
0.30				G	G	C	A	
0.32				G	T	C	A	
0.33					G	C	A	A
0.34					G	C	A	C
0.34		G	G	G	A			
0.34			G	G	C	C		
0.34	T	G	G	G				
0.35				C	G	C	G	
0.35		A	G	G	T			
0.36				C	G	C	A	
0.37		G	G	T	C			
0.37	C	G	G	A				
0.37		G	G	G	C			

Fig. 12

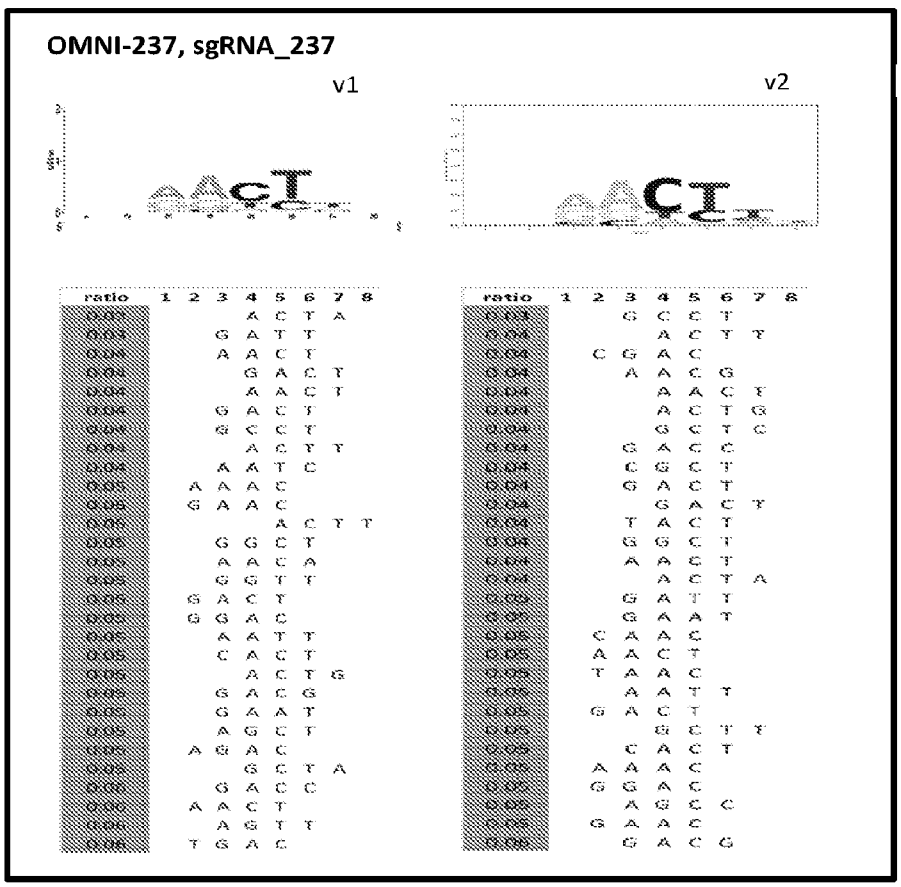
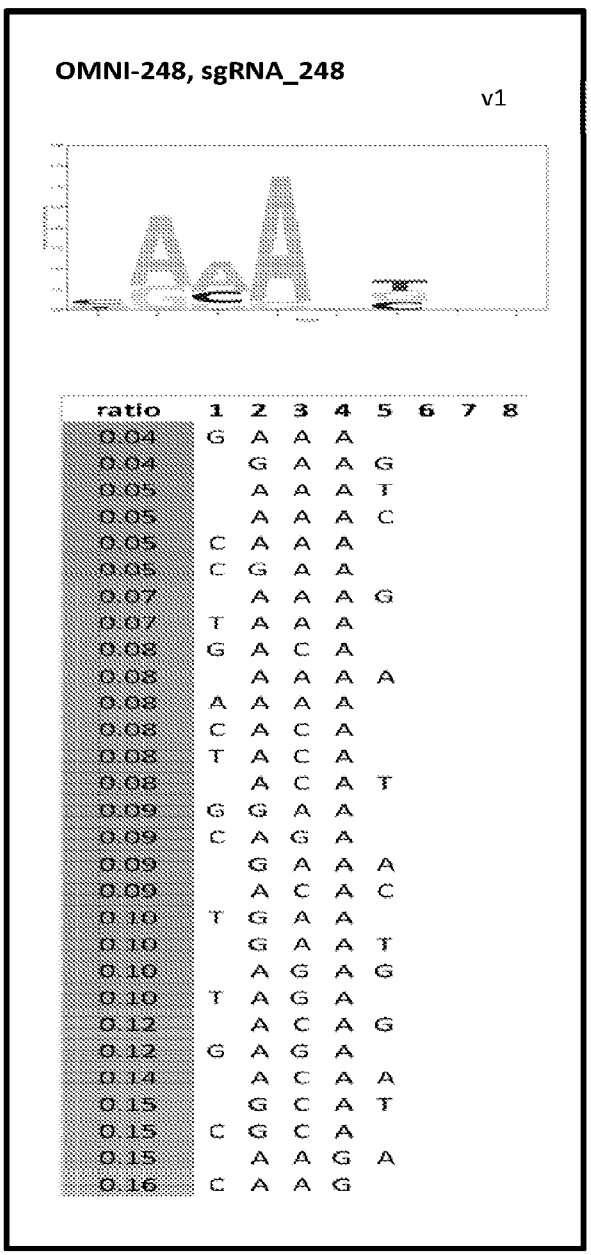


Fig. 13



ratio	1	2	3	4	5	6	7	8
0.04	G	A	A	A				
0.04		G	A	A	G			
0.05		A	A	A	T			
0.05		A	A	A	C			
0.05	C	A	A	A				
0.05	C	G	A	A				
0.07		A	A	A	G			
0.07	T	A	A	A				
0.08	G	A	C	A				
0.08		A	A	A	A			
0.08	A	A	A	A				
0.08	C	A	C	A				
0.08	T	A	C	A				
0.08		A	C	A	T			
0.09	G	G	A	A				
0.09	C	A	G	A				
0.09		G	A	A	A			
0.09		A	C	A	C			
0.10	T	G	A	A				
0.10		G	A	A	T			
0.10		A	G	A	G			
0.10	T	A	G	A				
0.12		A	C	A	G			
0.12	G	A	G	A				
0.14		A	C	A	A			
0.15		G	C	A	T			
0.15	C	G	C	A				
0.15		A	A	G	A			
0.16	C	A	A	G				

Fig. 14

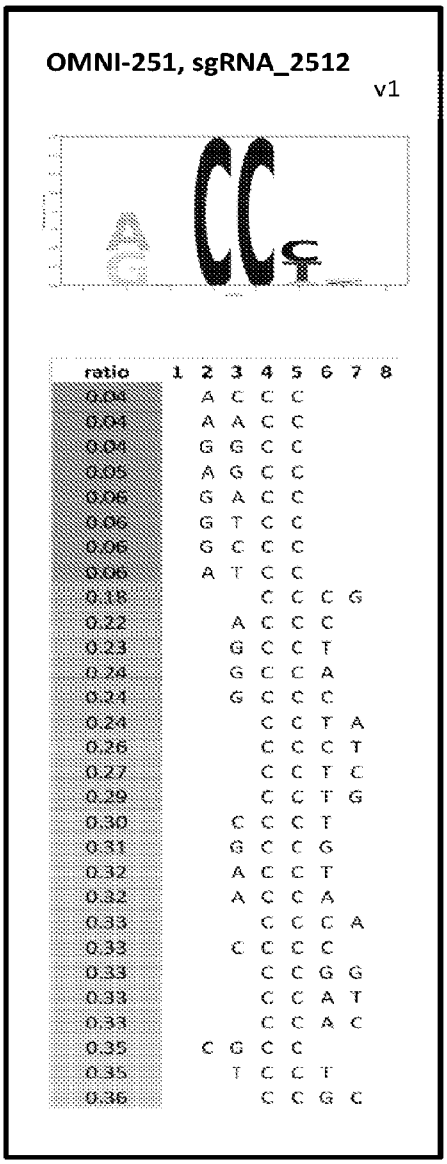
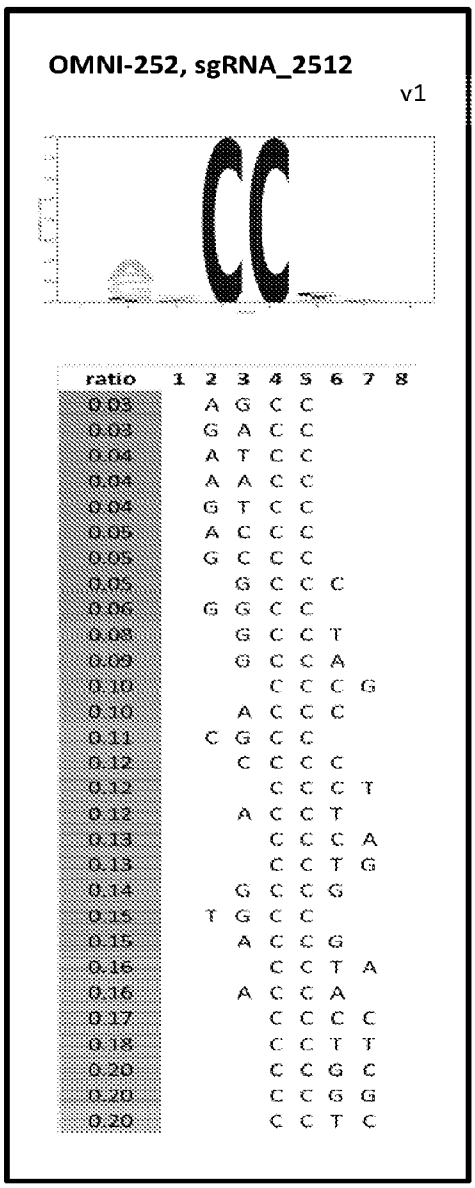
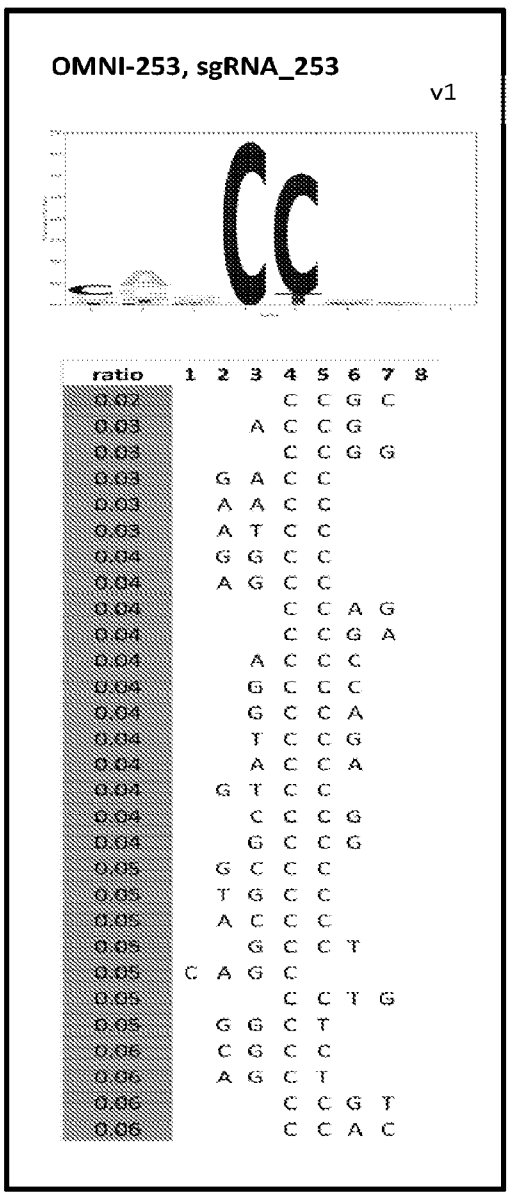

OMNI-251, sgRNA_2512
v1
ratio 1 2 3 4 5 6 7 8
0.04 A C C C
0.04 A A C C
0.04 G G C C
0.05 A G C C
0.06 G A C C
0.06 G T C C
0.06 G C C C
0.06 A T C C
0.18 C C C G
0.22 A C C C
0.23 G C C T
0.24 G C C A
0.24 G C C C
0.24 C C T A
0.26 C C C T
0.27 C C T C
0.29 C C T G
0.30 C C C T
0.31 G C C G
0.32 A C C T
0.32 A C C A
0.33 C C C A
0.33 C C C C
0.33 C C G G
0.33 C C A T
0.33 C C A C
0.35 C G C C
0.35 T C C T
0.36 C C G C

Fig. 15



ratio	1	2	3	4	5	6	7	8
0.03		A	G	C	C			
0.03		G	A	C	C			
0.04		A	T	C	C			
0.04		A	A	C	C			
0.04		G	T	C	C			
0.05		A	C	C	C			
0.05		G	C	C	C			
0.05			G	C	C	C		
0.06		G	G	C	C			
0.08			G	C	C	T		
0.09			G	C	C	A		
0.10				C	C	C	G	
0.10			A	C	C	C		
0.11		C	G	C	C			
0.12			C	C	C	C		
0.12				C	C	C	T	
0.12			A	C	C	T		
0.13				C	C	C	A	
0.13				C	C	T	G	
0.14			G	C	C	G		
0.15		T	G	C	C			
0.15			A	C	C	G		
0.16				C	C	T	A	
0.16			A	C	C	A		
0.17				C	C	C	C	
0.18				C	C	T	T	
0.20				C	C	G	C	
0.20				C	C	G	G	
0.20				C	C	T	C	

Fig. 16



ratio	1	2	3	4	5	6	7	8
0.02				C	C	G	C	
0.03			A	C	C	G		
0.03				C	C	G	G	
0.03		G	A	C	C			
0.03		A	A	C	C			
0.03		A	T	C	C			
0.04		G	G	C	C			
0.04		A	G	C	C			
0.04				C	C	A	G	
0.04				C	C	G	A	
0.04			A	C	C	C		
0.04			G	C	C	C		
0.04			G	C	C	A		
0.04			T	C	C	G		
0.04			A	C	C	A		
0.04		G	T	C	C			
0.04			C	C	C	G		
0.04			G	C	C	G		
0.05		G	C	C	C			
0.05		T	G	C	C			
0.05		A	C	C	C			
0.05			G	C	C	T		
0.05	C	A	G	C				
0.05				C	C	T	G	
0.05		G	G	C	T			
0.06		C	G	C	C			
0.06		A	G	C	T			
0.06				C	C	G	T	
0.06				C	C	A	C	

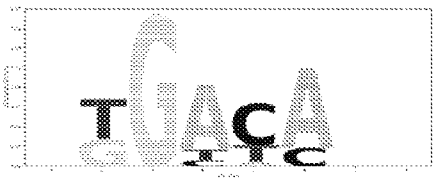
Fig. 17

OMNI-259, sgRNA_259

v1

ratio	1	2	3	4	5	6	7	8
0.04			G	A	T	A		
0.05			G	A	C	A		
0.12		T	G	A	C			
0.14			G	T	A	C		
0.14			G	A	C	C		
0.20		G	G	A	C			
0.20			G	T	C	A		
0.20			G	C	T	A		
0.21			G	A	T	G		
0.21			G	A	T	T		
0.23			G	T	C	C		
0.23		A	G	A	C			
0.25		T	G	A	T			
0.27			G	G	C	A		
0.29			G	C	C	A		
0.30			G	C	T	C		
0.31			G	A	C	G		
0.31			G	G	T	A		
0.33			G	A	C	T		
0.34		T	G	T	C			
0.34			G	T	T	A		
0.35		A	G	A	T			
0.35		G	G	A	T			
0.38		C	G	A	C			
0.39		T	G	C	T			
0.43		C	G	A	T			
0.44	A	T	G	A				
0.45			G	A	A	C		
0.45	C	T	G	A				

v2



ratio	1	2	3	4	5	6	7	8
0.05			G	A	C	A		
0.09			G	A	T	A		
0.15		T	G	A	C			
0.20			G	A	C	C		
0.23			G	C	T	A		
0.25		G	G	A	C			
0.28			G	T	A	C		
0.28			G	T	C	A		
0.32		A	G	A	C			
0.33			G	A	T	G		
0.33			G	C	C	A		
0.33			G	T	C	C		
0.34			G	G	C	A		
0.34		T	G	T	C			
0.35		T	G	A	T			
0.37			G	A	T	T		
0.42			G	A	C	G		
0.43		G	G	A	T			
0.44		T	G	C	T			
0.44			G	A	C	T		
0.44			G	G	T	A		
0.45			G	T	T	A		
0.49		A	G	A	T			
0.50	T	G	G	A				
0.51			G	C	T	C		
0.51		C	G	A	C			
0.51	A	T	G	A				
0.52	G	T	G	A				
0.53		C	G	A	T			
0.55	A	A	G	A				

Fig. 18

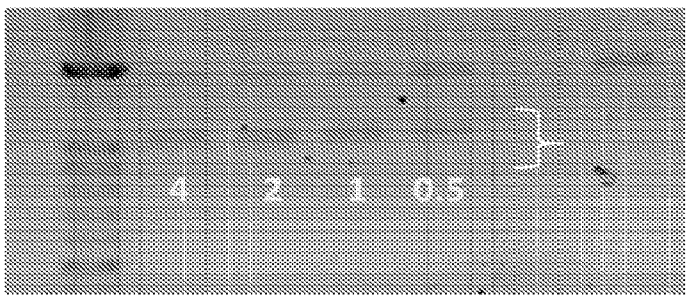


Fig. 19A

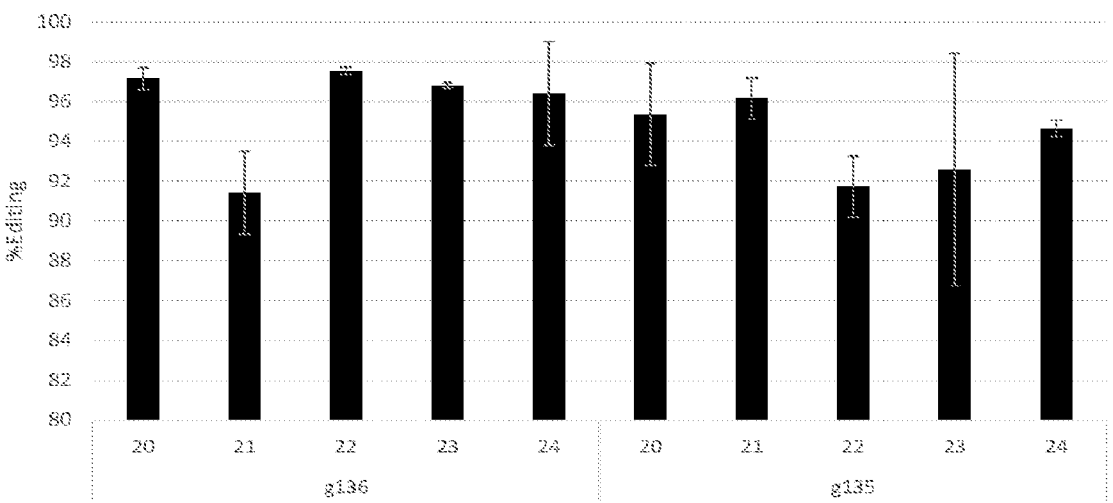


Fig. 19B

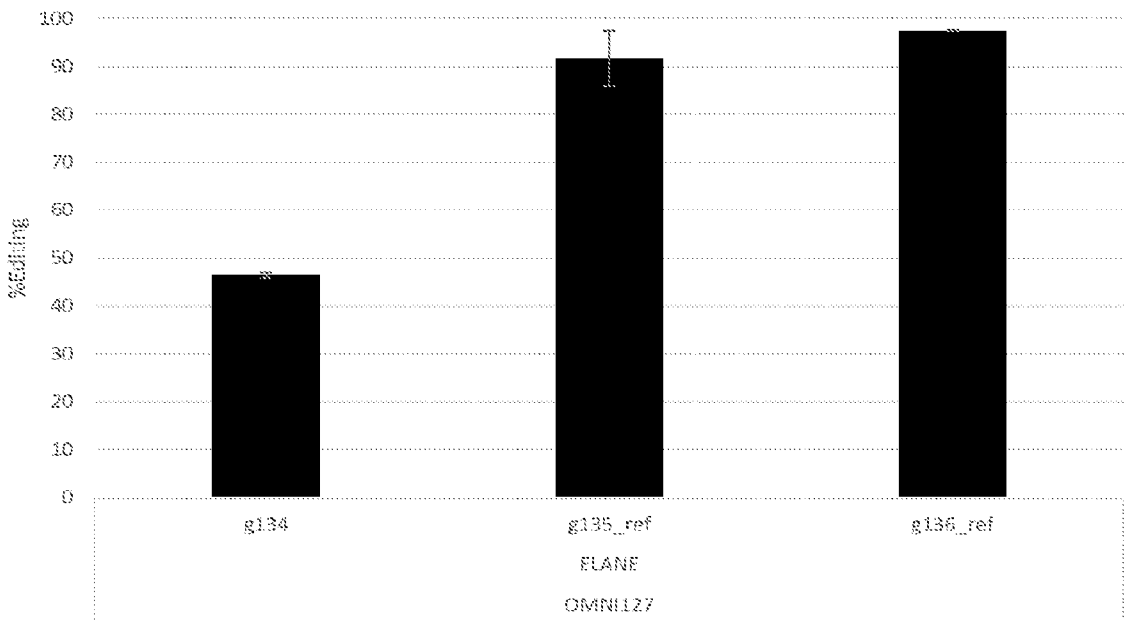

100
90
80
70
60
50
40
30
20
10
0
%Editing
g134
g135_ref
g136_ref
FLANE
OMN1127

Fig. 19C