



(51) International Patent Classification:

C12N 15/10 (2006.01) A61P 7/00 (2006.01)

C12N 9/22 (2006.01) A61P 21/00 (2006.01)

A61P 3/00 (2006.01) A61P 25/28 (2006.01)

(21) International Application Number:

PCT/IB2023/050560

(22) International Filing Date:

23 January 2023 (23.01.2023)

(25) Filing Language:

English

(26) Publication Language:

English

(30) Priority Data:

63/302,271 24 January 2022 (24.01.2022) US

63/386,061 05 December 2022 (05.12.2022) US

(71) Applicant: LIFEEDIT THERAPEUTICS, INC.

[US/US]; 507 Airport Boulevard, Suite 101, Morrisville,
North Carolina 27560 (US).

(72) Inventors: **ARYA, Gunjan H.**; 8544 Rosiere Drive, Cary, North Carolina 27518 (US). **COYLE, Michael**; 407 Elliot Road, Chapel Hill, North Carolina 27514 (US). **CRAWLEY, Alexandra Briner**; 1220 Scott Pl., Cary, North Carolina 27511 (US). **ELICH, Tedd D.**; 5 Alumwood Place, Durham, North Carolina 27705 (US). **PARKER, Joel S.**; 2651 Tosca Trail, Apex, North Carolina 27502 (US).

(74) Agent: **BUCK, B. Logan** et al.; Womble Bond Dickinson (US) LLP, P.O. Box 7037, Atlanta, Georgia 30357-0037 (US).

(81) Designated States (*unless otherwise indicated, for every kind of national protection available*): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CV, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IQ, IR, IS, IT, JM, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS,

(54) Title: RNA-GUIDED NUCLEASES AND ACTIVE FRAGMENTS AND VARIANTS THEREOF AND METHODS OF USE

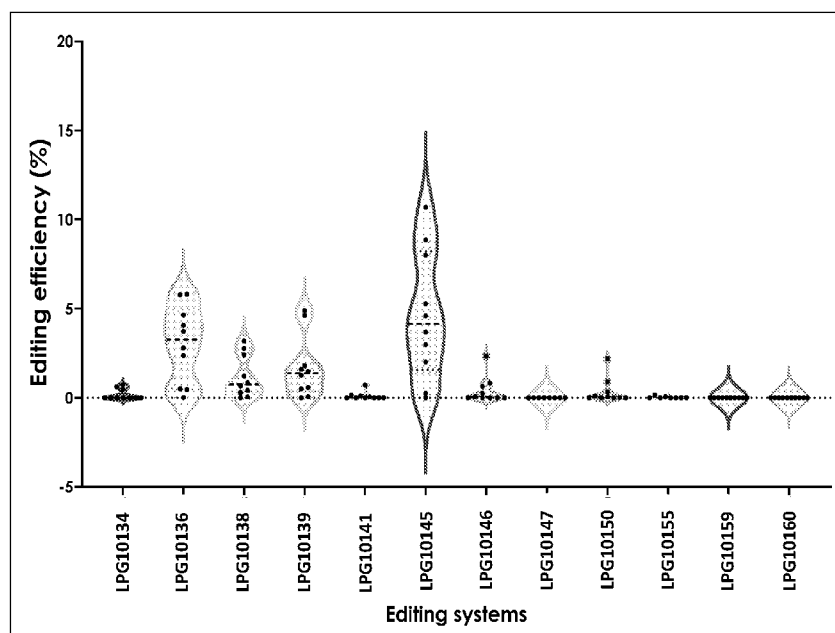


FIGURE 1

(57) **Abstract:** Compositions and methods for binding to a target sequence of interest are provided. The compositions find use in cleaving or modifying a target sequence of interest, visualization of a target sequence of interest, and modifying the expression of a sequence of interest. Compositions comprise RNA-guided nuclease (RGN) polypeptides, CRISPR RNAs, trans-activating CRISPR RNAs, guide RNAs, and nucleic acid molecules encoding the same. Vectors and host cells comprising the nucleic acid molecules are also provided. Further provided are RGN systems for binding a target sequence of interest, wherein the RGN system comprises an RNA-guided nuclease polypeptide and one or more guide RNAs.



RU, RW, SA, SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

- (84) Designated States** (*unless otherwise indicated, for every kind of regional protection available*): ARIPO (BW, CV, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, ME, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

- *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii))*
- *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii))*

Published:

- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
- *with sequence listing part of description (Rule 5.2(a))*
- *in black and white; the international application as filed contained color or greyscale and is available for download from PATENTSCOPE*

RNA-GUIDED NUCLEASES AND ACTIVE FRAGMENTS AND VARIANTS THEREOF AND METHODS OF USE

CROSS-REFERENCE TO RELATED APPLICATION

5 This application claims priority to US Provisional Patent Application Nos. 63/302,271, filed January 24, 2022, and 63/386,061, filed December 5, 2022, each of which is fully incorporated by reference herein.

REFERENCE TO A SEQUENCE LISTING SUBMITTED ELECTRONICALLY AS AN 10 XML FILE

The instant application contains a Sequence Listing which has been submitted in xml format via USPTO Patent Center and is hereby incorporated by reference in its entirety. Said xml copy, created on January 23, 2023, is named L103438_1260WO_Seq_List.xml, and is 905 KB in size.

15 FIELD OF THE INVENTION

The present invention relates to the field of molecular biology and gene editing.

BACKGROUND OF THE INVENTION

20 Targeted genome editing or modification is rapidly becoming an important tool for basic and applied research. Initial methods involved engineering nucleases such as meganucleases, zinc finger fusion proteins or TALENs, requiring the generation of chimeric nucleases with engineered, programmable, sequence-specific DNA-binding domains specific for each particular target sequence. RNA-guided nucleases, such as the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-associated (Cas) proteins of the CRISPR-Cas bacterial system, allow for the targeting of
25 specific sequences by complexing the nucleases with guide RNA that specifically hybridizes with a particular target sequence. Producing target-specific guide RNAs is less costly and more efficient than generating chimeric nucleases for each target sequence. Such RNA-guided nucleases can be used to edit genomes optionally through the introduction of a sequence-specific, double-stranded break that is repaired via error-prone non-homologous end-joining (NHEJ) to introduce a mutation at
30 a specific genomic location. Alternatively, heterologous DNA may be introduced into the genomic site via homology-directed repair. RNA-guided nucleases (RGNs) can also be used for base editing when fused with a deaminase.

BRIEF SUMMARY OF THE INVENTION

35 Compositions and methods for binding a target sequence of interest are provided. The compositions find use in cleaving or modifying a target sequence of interest, detection of a target

sequence of interest, and modifying the expression of a sequence of interest. Compositions comprise RNA-guided nuclease (RGN) polypeptides, CRISPR RNAs (crRNAs), trans-activating CRISPR RNAs (tracrRNAs), guide RNAs (gRNAs), nucleic acid molecules encoding the same, and vectors and host cells comprising the nucleic acid molecules. Also provided are RGN systems for binding a target sequence of interest, wherein the RGN system comprises an RNA-guided nuclease polypeptide and one or more guide RNAs. Thus, methods disclosed herein are drawn to binding a target sequence of interest, and in some embodiments, cleaving or modifying the target sequence of interest. The target sequence of interest can be modified, for example, as a result of non-homologous end joining, homology-directed repair with an introduced donor sequence, or base editing.

In a first aspect, the present disclosure provides a nucleic acid molecule comprising a polynucleotide encoding an RNA-guided nuclease (RGN) polypeptide, wherein the polynucleotide comprises a nucleotide sequence encoding an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; wherein the RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to the target DNA sequence. In some embodiments, the RGN polypeptide comprises an amino acid sequence having 90% sequence identity to SEQ ID NO: 6. In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the polynucleotide encoding an RGN polypeptide is operably linked to a promoter heterologous to the polynucleotide.

In some embodiments of the above aspect, the RGN polypeptide is capable of cleaving the target DNA sequence upon binding.

In some embodiments of the above aspect, the RGN polypeptide is capable of generating a double-stranded break.

In some embodiments of the above aspect, the RGN polypeptide is capable of generating a single-stranded break.

In some embodiments of the above aspect, the RGN polypeptide is nuclease inactive or is a nickase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a prime editing polypeptide. In some embodiments, the prime editing polypeptide comprises a DNA polymerase. In some embodiments, the prime editing polypeptide comprises a reverse transcriptase. In some embodiments of the above aspect, the RGN polypeptide is operably linked to a base-editing polypeptide. In some embodiments, the base-editing polypeptide is a deaminase. In some

embodiments, the deaminase is a cytosine deaminase or an adenine deaminase. In some embodiments, the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448. In some embodiments of the above aspect, the deaminase has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

In some embodiments of the above aspect, the RGN polypeptide comprises one or more nuclear localization signals.

In some embodiments of the above aspect, the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

In some embodiments of the above aspect, the target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

In another aspect, the present disclosure provides a vector comprising a nucleic acid molecule described hereinabove.

In some embodiments of the above aspect, the vector further comprises at least one nucleotide sequence encoding the gRNA capable of hybridizing to the target DNA sequence.

In some embodiments of the above aspect, the guide RNA is selected from the group consisting of: a) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1; b) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2; c) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3; d) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4; e) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5; f) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6; g) a guide RNA comprising a

CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7; h) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8; i) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9; j) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 10; a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and l) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24, and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

In some embodiments of the above aspect, the guide RNA is selected from the group consisting of: a) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1; b) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2; c) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%,

[illegible]

93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 8; i) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9; j) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 10; k) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 11; and l) a guide RNA comprising a CRISPR RNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24, and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12.

In some embodiments of the above aspect, the gRNA is a single guide RNA. In some embodiments, the single guide RNA further comprises an extension comprising an edit template for prime editing.

In some embodiments of the above aspect, the gRNA is a dual-guide RNA.

In another aspect, the present disclosure provides a cell comprising a nucleic acid molecule described hereinabove or a vector described hereinabove. In yet another aspect, the present disclosure provides a method for making an RGN polypeptide comprising culturing a cell described hereinabove under conditions in which the RGN polypeptide is expressed.

5 In another aspect, the present disclosure provides a method for making an RGN polypeptide comprising introducing into a cell a heterologous nucleic acid molecule comprising a nucleotide sequence encoding an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; wherein the RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when
10 bound to a guide RNA (gRNA) capable of hybridizing to the target DNA sequence; and culturing the cell under conditions in which the RGN polypeptide is expressed. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at
15 least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the method further comprises purifying the RGN
20 polypeptide.

In some embodiments of the above aspect, the cell further expresses one or more guide RNAs capable of binding to the RGN polypeptide to form an RGN ribonucleoprotein complex.

In some embodiments of the above aspect, the method further comprises purifying the RGN ribonucleoprotein complex.

25 In still another aspect, the present disclosure provides an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12, and wherein the RGN polypeptide is capable of binding a target DNA sequence of a DNA molecule in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to the target DNA sequence. In some
30 embodiments, the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at
35 least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6. In some embodiments of the above aspect, the RGN polypeptide is an isolated RGN polypeptide.

In some embodiments of the above aspect, the RGN polypeptide is capable of cleaving the target DNA sequence upon binding.

In some embodiments of the above aspect, cleavage by the RGN polypeptide generates a double-stranded break.

5 In some embodiments of the above aspect, cleavage by the RGN polypeptide generates a single-stranded break.

In some embodiments of the above aspect, the RGN polypeptide is nuclease inactive or a nickase.

10 In some embodiments of the above aspect, the RGN polypeptide is operably linked to a prime editing polypeptide. In some embodiments, the prime editing polypeptide comprises a DNA polymerase. In some embodiments, the prime editing polypeptide comprises a reverse transcriptase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a base-editing polypeptide. In some embodiments, the base-editing polypeptide is a deaminase. In some
15 embodiments, the deaminase is a cytosine deaminase or an adenine deaminase. In some
embodiments, the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448. In some embodiments, the deaminase has at least 91%, at least 92%, at
least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%
sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

20 In some embodiments of the above aspect, the target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

In some embodiments of the above aspect, the RGN polypeptide comprises one or more nuclear localization signals.

In another aspect, the present disclosure provides a ribonucleoprotein (RNP) complex comprising a RGN polypeptide described hereinabove and the guide RNA bound to the RGN
25 polypeptide. In some embodiments, the guide RNA is a single guide RNA. In some embodiments, the single guide RNA comprises an extension comprising an edit template for prime editing. In yet another aspect, the present disclosure provides a system for binding a target DNA sequence of a DNA molecule, wherein the system comprises: a) one or more guide RNAs capable of hybridizing to the target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences
30 encoding the one or more guide RNAs (gRNAs); and b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12 or a polynucleotide comprising a nucleotide sequence encoding the RGN polypeptide;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and wherein the one or more guide RNAs are capable of forming a complex with the RGN
35 polypeptide in order to direct the RGN polypeptide to bind to the target DNA sequence of the DNA molecule.

In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, at least one of the nucleotide sequences encoding the one or more guide RNAs and the nucleotide sequence encoding the RGN polypeptide is operably linked to a promoter heterologous to the nucleotide sequence.

In some embodiments of the above aspect, the nucleotide sequences encoding the one or more guide RNAs and the nucleotide sequence encoding the RGN polypeptide are located on one vector.

In still another aspect, the present disclosure provides a system for binding a target DNA sequence of a DNA molecule, wherein the system comprises: a) one or more guide RNAs capable of hybridizing to the target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct the RGN polypeptide to bind to the target DNA sequence of the DNA molecule.

In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, at least one of the nucleotides sequences encoding the one or more guide RNAs is operably linked to a promoter heterologous to the nucleotide sequence.

In some embodiments of the above aspect, the RGN polypeptide and the one or more guide RNAs are not found complexed to one another in nature.

In some embodiments of the above aspect, the target DNA sequence is a eukaryotic target DNA sequence.

In some embodiments of the above aspect, the gRNA is a single guide RNA (sgRNA). In some embodiments, the sgRNA comprises an extension comprising an edit template for prime editing.

In some embodiments of the above aspect, the gRNA is a dual-guide RNA.

In some embodiments of the above aspect, the gRNA is selected from the group consisting of: a) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein the RGN

polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1; b) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2; c) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3; d) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4; e) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5; f) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6; g) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7; h) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8; i) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9; j) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NOs: 10; k) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and l) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12. In some embodiments, the gRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the gRNA is selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1; b) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2; c) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3; d) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 4; e) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 5; f) a gRNA comprising a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%,

[illegible]

least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36, wherein the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12. In some embodiments, the gRNA comprises a CRISPR repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

In some embodiments of the above aspect, the target DNA sequence is within a cell.

In some embodiments of the above aspect, the one or more guide RNAs is capable of hybridizing to the target DNA sequence and the guide RNA is capable of forming a complex with the RGN polypeptide to direct cleavage of the target DNA sequence.

In some embodiments of the above aspect, the cleavage generates a double-stranded break.

In some embodiments of the above aspect, the cleavage generates a single-stranded break.

In some embodiments of the above aspect, the RGN polypeptide is nuclease inactive or is a nickase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a prime editing polypeptide. In some embodiments, the prime editing polypeptide comprises a DNA polymerase. In some embodiments, the prime editing polypeptide comprises a reverse transcriptase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a base-editing polypeptide.

In some embodiments of the above aspect, the base-editing polypeptide is a deaminase. In some embodiments, the deaminase is a cytosine deaminase or an adenine deaminase. In some embodiments, the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448. In some embodiments, the deaminase has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

In some embodiments of the above aspect, the RGN polypeptide comprises one or more nuclear localization signals.

In some embodiments of the above aspect, the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

In some embodiments of the above aspect, the system further comprises one or more donor polynucleotides.

In another aspect, the present disclosure provides a cell comprising a system described hereinabove.

In yet another aspect, the present disclosure provides a pharmaceutical composition comprising a nucleic acid molecule, a vector, a cell, a RGN polypeptide, a RNP complex, or a system described hereinabove, and a pharmaceutically acceptable carrier.

In still another aspect, the present disclosure provides a method for binding a target DNA sequence of a DNA molecule comprising delivering a system described hereinabove to the target DNA sequence or a cell comprising the target DNA sequence.

In some embodiments of the above aspect, the RGN polypeptide or the guide RNA further comprises a detectable label, thereby allowing for detection of the target DNA sequence.

In some embodiments of the above aspect, the guide RNA or the RGN polypeptide further comprises an expression modulator, thereby modulating expression of the target DNA sequence or a gene under transcriptional control by the target DNA sequence.

In another aspect, the present disclosure provides a method for cleaving and/or modifying a target DNA sequence of a DNA molecule comprising delivering a system described hereinabove to the target DNA sequence or a cell comprising the DNA molecule, wherein cleavage or modification of the target DNA sequence occurs.

In some embodiments of the above aspect, the modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

In some embodiments of the above aspect, the modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

In some embodiments of the above aspect, the modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

In another aspect, the present disclosure provides a method for binding a target DNA sequence of a DNA molecule comprising: a) assembling an RNA-guided nuclease (RGN) ribonucleotide complex by combining one or more guide RNAs capable of hybridizing to the target DNA sequence, and an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12 under conditions suitable for formation of the RGN ribonucleotide complex; and b) contacting the target DNA sequence or a cell comprising the target DNA sequence with the assembled RGN ribonucleotide complex; wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing the RGN polypeptide to bind to the target DNA sequence. In some embodiments, the RGN polypeptide has at least 90% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide has at least 91%, at least 92%, at least 93%, at least 94%, at

least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the method is performed *in vitro*, *in vivo*, or *ex vivo*.

5 In some embodiments of the above aspect, the RGN polypeptide or the guide RNA further comprises a detectable label, thereby allowing for detection of the target DNA sequence.

In some embodiments of the above aspect, the guide RNA or the RGN polypeptide further comprises an expression modulator, thereby allowing for the modulation of expression of the target DNA sequence.

10 In some embodiments of the above aspect, the RGN polypeptide is operably linked to a prime editing polypeptide, thereby allowing for the modification of the target DNA sequence. In some embodiments, the prime editing polypeptide comprises a DNA polymerase. In some embodiments, the prime editing polypeptide comprises a reverse transcriptase.

15 In some embodiments of the above aspect, the RGN polypeptide is operably linked to a base-editing polypeptide, thereby allowing for the modification of the target DNA sequence. In some embodiments, the base-editing polypeptide comprises a deaminase. In some embodiments, the deaminase is a cytosine deaminase or an adenine deaminase. In some embodiments of the above aspect, the RGN polypeptide is capable of cleaving the target DNA sequence, thereby allowing for the cleaving and/or modifying of the target DNA sequence.

20 In another aspect, the present disclosure provides a method for cleaving and/or modifying a target DNA sequence of a DNA molecule, comprising contacting the DNA molecule with: a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; and b) one or more guide RNAs capable of targeting the RGN of (a) to the target DNA sequence, wherein the one or more
25 guide RNAs hybridize to the target DNA sequence, thereby directing the RGN polypeptide to bind to the target DNA sequence and cleavage and/or modification of the target DNA sequence occurs. In some embodiments, the RGN polypeptide has at least 90% sequence identity to SEQ ID NO: 6.

In some embodiments of the above aspect, the RGN polypeptide comprises an amino acid sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at
30 least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12. In some embodiments, the RGN polypeptide has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6.

35 In some embodiments of the above aspect, cleavage by the RGN polypeptide generates a double-stranded break.

In some embodiments of the above aspect, cleavage by the RGN polypeptide generates a single-stranded break.

In some embodiments of the above aspect, the RGN polypeptide is nuclease inactive or a nickase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a prime editing polypeptide, thereby allowing for the modification of the target DNA sequence. In some
5 embodiments, the prime editing polypeptide comprises a DNA polymerase. In some embodiments, the prime editing polypeptide comprises a reverse transcriptase.

In some embodiments of the above aspect, the RGN polypeptide is operably linked to a base-editing polypeptide.

In some embodiments of the above aspect, the base-editing polypeptide is a deaminase. In
10 some embodiments, the deaminase is a cytosine deaminase or an adenine deaminase. In some embodiments, the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448. In some embodiments, the deaminase has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

15 In some embodiments of the above aspect, the modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

In some embodiments of the above aspect, the modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

20 In some embodiments of the above aspect, the modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

In some embodiments of the above aspect, the target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

In some embodiments of the above aspect, the target DNA sequence is a eukaryotic target DNA sequence.

25 In some embodiments of the above aspect, the gRNA is a single guide RNA (sgRNA). In some embodiments, the sgRNA comprises an extension comprising an edit template for prime editing.

In some embodiments of the above aspect, the gRNA is a dual-guide RNA.

In some embodiments of the above aspect, the RGN, the guide RNA, and the tracrRNA is selected from the group consisting of: a) an RGN having at least 90% sequence identity to SEQ ID NO: 1, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25; b) an RGN having at least 90% sequence identity to SEQ ID NO: 2, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26; c) an RGN having at least 90% sequence identity to SEQ
30 ID NO: 3, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27; d) an
35 RGN having at least 90% sequence identity to SEQ ID NO: 4, a guide RNA comprising a crRNA

repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28; e) an RGN having at least 90% sequence identity to SEQ ID NO: 5, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29;

5 f) an RGN having at least 90% sequence identity to SEQ ID NO: 6, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30; g) an RGN having at least 90% sequence identity to SEQ ID NO: 7, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ

10 ID NO: 31; h) an RGN having at least 90% sequence identity to SEQ ID NO: 8, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32; i) an RGN having at least 90% sequence identity to SEQ ID NO: 9, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity

15 to SEQ ID NO: 33; j) an RGN having at least 90% sequence identity to SEQ ID NO: 10, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34; k) an RGN having at least 90% sequence identity to SEQ ID NO: 11, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity

20 to SEQ ID NO: 35; and l) an RGN having at least 90% sequence identity to SEQ ID NO: 12, a guide RNA comprising a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36. In some embodiments, the RGN has at least 90% sequence identity to SEQ ID NO: 6, the guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and the tracrRNA has at least 90%

25 sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the RGN, the guide RNA, and the tracrRNA is selected from the group consisting of: a) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1, a guide RNA comprising a crRNA repeat sequence having at least 91%, at

30 least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25; b) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%

35 sequence identity to SEQ ID NO: 2, a guide RNA comprising a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 91%,

[illegible]

99%, or 100% sequence identity to SEQ ID NO: 32; i) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9, a guide RNA comprising a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33; j) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 10, a guide RNA comprising a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34; k) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 11, a guide RNA comprising a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35; and l) an RGN having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12, a guide RNA comprising a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36. In some embodiments, the RGN has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6, the guide RNA comprises a crRNA repeat sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18 and the tracrRNA has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the target DNA sequence is within a cell.

In some embodiments of the above aspect, the method further comprises culturing the cell under conditions in which the RGN polypeptide is expressed and cleaves and modifies the target DNA sequence to produce a DNA molecule comprising a modified target DNA sequence, and selecting a cell comprising the modified target DNA sequence.

In another aspect, the present disclosure provides a cell comprising a modified target DNA sequence according to the method described hereinabove.

In yet another aspect, the present disclosure provides a pharmaceutical composition comprising a cell described hereinabove and a pharmaceutically acceptable carrier.

5 In still another aspect, the present disclosure provides a method of treating a disease, disorder, or condition, comprising administering to a subject in need thereof an effective amount of a pharmaceutical composition described hereinabove.

In some embodiments of the above aspect, the disease is associated with a causal mutation and the effective amount of the pharmaceutical composition corrects or deletes the causal mutation.

10 In some embodiments of the above aspect, the subject is at risk of developing the disease, disorder, or condition.

In another aspect, the present disclosure provides a nucleic acid molecule comprising a CRISPR RNA (crRNA) or a polynucleotide encoding a crRNA, wherein the crRNA comprises a spacer sequence and a CRISPR repeat sequence, wherein the CRISPR repeat sequence comprises a
15 nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 13-24; wherein a guide RNA, comprising the crRNA and a trans-activating CRISPR RNA (tracrRNA) hybridized to the CRISPR repeat sequence of the crRNA, is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of the crRNA when the guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide. In some embodiments, the CRISPR
20 repeat sequence comprises a nucleotide sequence having at least 90% sequence identity to SEQ ID NO: 18.

In some embodiments of the above aspect, the polynucleotide encoding a crRNA is operably linked to a promoter heterologous to the polynucleotide.

In some embodiments of the above aspect, the CRISPR repeat sequence comprises a
25 nucleotide sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 13-24. In some embodiments, the CRISPR repeat sequence comprises a nucleotide sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18.

30 In another aspect, the present disclosure provides a vector comprising a nucleic acid molecule comprising a polynucleotide encoding a crRNA described hereinabove.

In some embodiments of the above aspect, the vector further comprises a polynucleotide encoding the tracrRNA.

In some embodiments of the above aspect, the tracrRNA is selected from the group consisting
35 of: a) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13; b) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein the CRISPR repeat sequence has at least 90%

sequence identity to SEQ ID NO: 14; c) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15; d) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16; e) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17; f) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18; g) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19; h) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20; i) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21; j) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22; k) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23; and l) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24. In some embodiments, the tracrRNA has at least 90% sequence identity to SEQ ID NO: 30 and the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18.

In some embodiments of the above aspect, the tracrRNA is selected from the group consisting of: a) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13; b) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14; c) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15; d) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16; e) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at

least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17; f) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18; g) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 31, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 19; h) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 20; i) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21; j) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22; k) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23; and l) a tracrRNA having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36, wherein the CRISPR repeat sequence has at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24. In some embodiments, the tracrRNA has 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30 and the CRISPR repeat sequence has 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18.

In some embodiments of the above aspect, the vector further comprises a polynucleotide encoding the RGN polypeptide.

In some embodiments of the above aspect, the RGN polypeptide is selected from the group consisting of: a) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 1, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 25; b) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 2, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 14 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 26; c) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 3, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 27; d) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 4, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 28; e) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 5, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 29; f) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 6, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 30; g) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 7, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 31; h) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 8, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 32; i) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 9, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 33; j) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 10, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 34; k) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 11, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 35; and l) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 12, wherein the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24 and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 36. In some embodiments, the RGN polypeptide has at least 90% sequence identity to SEQ ID NO: 6, the CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18, and the tracrRNA has at least 90% sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the RGN polypeptide is selected from the group consisting of: a) a RGN polypeptide having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ

[illegible]

[illegible]

the tracrRNA has 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30.

In another aspect, the present disclosure provides a nucleic acid molecule comprising a trans-activating CRISPR RNA (tracrRNA), or a polynucleotide encoding a tracrRNA comprising a nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 25-36; wherein a guide RNA, comprising the tracrRNA and a crRNA comprising a spacer sequence and a CRISPR repeat sequence, wherein the tracrRNA hybridizes with the CRISPR repeat sequence of the crRNA, is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of the crRNA when the guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide. In some embodiments, the tracrRNA comprises a nucleotide sequence having at least 90% sequence identity to SEQ ID NO: 30.

In some embodiments of the above aspect, the polynucleotide encoding a tracrRNA is operably linked to a promoter heterologous to the polynucleotide.

In some embodiments of the above aspect, the tracrRNA comprises a nucleotide sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 25-36. In some embodiments, the tracrRNA comprises a nucleotide sequence having at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30.

In another aspect, the present disclosure provides a vector comprising a nucleic acid molecule comprising a polynucleotide encoding a tracrRNA described hereinabove.

In yet another aspect, the present disclosure provides a single guide RNA comprising a nucleic acid molecule comprising a crRNA described hereinabove and a nucleic acid molecule comprising a tracrRNA described hereinabove.

In still another aspect, the present disclosure provides a double guide RNA comprising a nucleic acid molecule comprising a crRNA described hereinabove and a nucleic acid molecule comprising a tracrRNA described hereinabove.

In another aspect, the present disclosure provides a cell comprising a nucleic acid molecule, a single guide RNA, a double guide RNA, or a vector described hereinabove.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 provides the editing rates of LPG10134, LPG10136, LPG10138, LPG10139, LPG10141, LPG10145, LPG10146, LPG10147, LPG10150, LPG10155, LPG10159, and LPG10160 on multiple genes. Plasmids comprising expression cassettes for RGNs and guide RNAs were co-transfected into HEK293T cells.

Figure 2 shows that the single-guide RNA (sgRNA) SGN002661, along with the LPG10136 RNA-guided nuclease (RGN), provides for over 75% of editing of the T cell receptor alpha (TRAC) gene as measured by flow cytometry when the RGN and sgRNA are delivered as a ribonucleoprotein (RNP) complex in activated human peripheral blood mononuclear cells (PBMCs). B2M: beta-2-microglobulin.

Figures 3A and 3B demonstrate that increasing concentrations of RNPs improve editing. The figures show the editing efficiency of increasing concentrations of RNPs comprised of LPG10145 and various sgRNAs at a protein:RNA ratio of 1:2 through the measurement of levels of beta-2-microglobulin (B2M) or T cell receptor alpha (TRAC) by flow cytometry in activated human PBMCs. Figure 3B demonstrates dose dependence of increased editing activity with increasing amounts of RNPs comprising sgRNAs with two different spacer lengths (20 or 25 nucleotides).

Figure 4 shows that LPG10145 can edit targets in multiple genes. LPG10145 was delivered as an RNP to T cells through nucleofection. All guides exhibited a coefficient of variation (CV) of less than 50%.

DETAILED DESCRIPTION

Many modifications and other embodiments of the inventions set forth herein will come to mind to one skilled in the art to which these inventions pertain having the benefit of the teachings presented in the foregoing descriptions and the associated drawings. Therefore, it is to be understood that the inventions are not to be limited to the specific embodiments disclosed and that modifications and other embodiments are intended to be included within the scope of the appended embodiments. Although specific terms are employed herein, they are used in a generic and descriptive sense only and not for purposes of limitation.

I. Overview

RNA-guided nucleases (RGNs) allow for the targeted manipulation of specific site(s) within a genome and are useful in the context of gene targeting for therapeutic and research applications. In a variety of organisms, including mammals, RNA-guided nucleases have been used for genome engineering by stimulating non-homologous end joining and homologous recombination, for example. The compositions and methods described herein are useful for creating single- or double-stranded breaks in polynucleotides, modifying polynucleotides, detecting a particular site within a polynucleotide, or modifying the expression of a particular gene.

The RNA-guided nucleases disclosed herein can alter gene expression by modifying a target sequence. In specific embodiments, the RNA-guided nucleases are directed to the target sequence by a guide RNA (gRNA) as part of a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) RNA-guided nuclease system. The RGNs are considered “RNA-guided” because guide RNAs form a complex with the RNA-guided nucleases to direct the RNA-guided nuclease to bind to a

target sequence and in some embodiments, introduce a single-stranded or double-stranded break at the target sequence. After the target sequence has been cleaved, the break can be repaired such that the DNA sequence of the target sequence is modified during the repair process. Thus, provided herein are methods for using the RNA-guided nucleases to modify a target sequence in the DNA of host cells. For example, RNA-guided nucleases can be used to modify a target sequence at a genomic locus of eukaryotic cells or prokaryotic cells.

II. RNA-guided nucleases

Provided herein are RNA-guided nucleases. The term RNA-guided nuclease (RGN) refers to a polypeptide that binds to a particular target nucleotide sequence in a sequence-specific manner and is directed to the target nucleotide sequence by a guide RNA molecule that is complexed with the polypeptide and hybridizes with the target sequence. Although an RNA-guided nuclease can be capable of cleaving the target sequence upon binding, the term RNA-guided nuclease also encompasses nuclease-dead RNA-guided nucleases that are capable of binding to, but not cleaving, a target sequence. Cleavage of a target sequence by an RNA-guided nuclease can result in a single- or double-stranded break. RNA-guided nucleases only capable of cleaving a single strand of a double-stranded nucleic acid molecule are referred to herein as nickases.

The RNA-guided nucleases disclosed herein include the LPG10134, LPG10136, LPG10138, LPG10139, LPG10141, LPG10145, LPG10146, LPG10147, LPG10150, LPG10155, LPG10159, and LPG10160 RNA-guided nucleases, the amino acid sequences of which are set forth, respectively, as SEQ ID NOs: 1-12, and active fragments or variants thereof that retain the ability to bind to a target nucleotide sequence in an RNA-guided sequence-specific manner. In some of these embodiments, the active fragment or variant of the LPG10134, LPG10136, LPG10138, LPG10139, LPG10141, LPG10145, LPG10146, LPG10147, LPG10150, LPG10155, LPG10159, or LPG10160 RGN is capable of cleaving a single- or double-stranded target sequence. In some embodiments, an active variant of the LPG10134, LPG10136, LPG10138, LPG10139, LPG10141, LPG10145, LPG10146, LPG10147, LPG10150, LPG10155, LPG10159, or LPG10160 RGN comprises an amino acid sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to the amino acid sequence set forth as any one of SEQ ID NOs: 1-12. In certain embodiments, an active fragment of the LPG10134, LPG10136, LPG10138, LPG10139, LPG10141, LPG10145, LPG10146, LPG10147, LPG10150, LPG10155, LPG10159, or LPG10160 RGN comprises at least 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more contiguous amino acid residues of the amino acid sequence set forth as any one of SEQ ID NOs: 1-12. RNA-guided nucleases provided herein can comprise at least one nuclease domain (*e.g.*, DNase, RNase domain) and at least one RNA recognition and/or RNA binding domain to interact with guide RNAs. Further domains that can be found in RNA-guided nucleases provided herein include, but are not limited to:

DNA binding domains, helicase domains, protein-protein interaction domains, and dimerization domains. In specific embodiments, the RNA-guided nucleases provided herein can comprise at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to one or more of a DNA binding domain, helicase domain, protein-protein interaction domain, and dimerization domain.

A target nucleotide sequence is bound by an RNA-guided nuclease provided herein and hybridizes with the guide RNA associated with the RNA-guided nuclease. The target sequence can then be subsequently cleaved by the RNA-guided nuclease if the polypeptide possesses nuclease activity. The terms “cleave” or “cleavage” refer to the hydrolysis of at least one phosphodiester bond within the backbone of a target nucleotide sequence that can result in either single-stranded or double-stranded breaks within the target sequence. The presently disclosed RGNs can cleave nucleotides within a polynucleotide, functioning as an endonuclease or can be an exonuclease, removing successive nucleotides from the end (the 5' and/or the 3' end) of a polynucleotide. In other embodiments, the disclosed RGNs can cleave nucleotides of a target sequence within any position of a polynucleotide and thus function as both an endonuclease and exonuclease. The cleavage of a target polynucleotide by the presently disclosed RGNs can result in staggered breaks or blunt ends.

The presently disclosed RNA-guided nucleases can be wild-type sequences derived from bacterial or archaeal species. Alternatively, the RNA-guided nucleases can be variants or fragments of wild-type polypeptides. The wild-type RGN can be modified to alter nuclease activity or alter PAM specificity, for example. In some embodiments, the RNA-guided nuclease is not naturally-occurring.

In certain embodiments, the RNA-guided nuclease functions as a nickase, only cleaving a single strand of the target nucleotide sequence. Such RNA-guided nucleases have a single functioning nuclease domain. In particular embodiments, the nickase is capable of cleaving the positive strand or negative strand. In some of these embodiments, additional nuclease domains have been mutated such that the nuclease activity is reduced or eliminated.

In other embodiments, the RNA-guided nuclease lacks nuclease activity altogether and is referred to herein as nuclease-dead or nuclease inactive. Any method known in the art for introducing mutations into an amino acid sequence, such as PCR-mediated mutagenesis and site-directed mutagenesis, can be used for generating nickases or nuclease-dead RGNs. See, e.g., U.S. Publ. No. 2014/0068797 and U.S. Pat. No. 9,790,490; each of which is incorporated by reference in its entirety. A non-limiting example of a nickase is the LPG10145 D16A nickase, which is set forth herein as SEQ ID NO: 551. Nickases which comprise a mutation in the RuvC domain and have a functional HNH domain are useful in base editing wherein the nickase is fused to a base editing polypeptide such as a deaminase. Another non-limiting example of a nickase is the LPG10145 H611A nickase, which is set forth herein as SEQ ID NO: 552. Nickases which comprise a mutation in the HNH domain and have a functional RuvC domain are useful in prime editing wherein the nickase is fused to a prime editing

polypeptide such as a reverse transcriptase. A non-limiting example of a nuclease dead RGN is the LPG10145 D16A H611A sequence set forth as SEQ ID NO: 553.

RNA-guided nucleases that lack nuclease activity can be used to deliver a fused polypeptide, polynucleotide, or small molecule payload to a particular genomic location. In some of these
5 embodiments, the RGN polypeptide or guide RNA can be fused to a detectable label to allow for detection of a particular sequence. As a non-limiting example, a nuclease-dead RGN can be fused to a detectable label (*e.g.*, fluorescent protein) and targeted to a particular sequence associated with a disease to allow for detection of the disease-associated sequence.

Alternatively, nuclease-dead RGNs can be targeted to particular genomic locations to alter the
10 expression of a desired sequence. In some embodiments, the binding of a nuclease-dead RNA-guided nuclease to a target sequence results in the reduction in expression of the target sequence or a gene under transcriptional control by the target sequence by interfering with the binding of RNA polymerase or transcription factors within the targeted genomic region. In other embodiments, the RGN (*e.g.*, a nuclease-dead RGN) or its complexed guide RNA further comprises an expression
15 modulator that, upon binding to a target sequence, serves to either repress or activate the expression of the target sequence or a gene under transcriptional control by the target sequence. In some of these embodiments, the expression modulator modulates the expression of the target sequence or regulated gene through epigenetic mechanisms.

In other embodiments, the nuclease-dead RGNs or an RGN with nickase activity can be
20 targeted to particular genomic locations to modify the sequence of a target polynucleotide through fusion to a base-editing polypeptide, for example a deaminase polypeptide or active variant or fragment thereof, that directly chemically modifies (*e.g.*, deaminates) a nucleobase, resulting in conversion from one nucleobase to another. The base-editing polypeptide can be fused to the RGN at its N-terminal or C-terminal end. Additionally, the base-editing polypeptide may be fused to the RGN
25 via a peptide linker. A non-limiting example of a deaminase polypeptide that is useful for such compositions and methods includes a cytosine deaminase or an adenine deaminase (such as the adenine deaminase base editor described in Gaudelli *et al.* (2017) *Nature* 551:464-471, U.S. Publ. Nos. 2017/0121693 and 2018/0073012, and International Publ. No. WO 2018/027078, or any of the deaminases disclosed in International Publ. No. WO 2020/139873, U.S. Provisional Appl. Nos.
30 63/077,089 filed September 11, 2020, 63/146,840 filed February 8, 2021, and 63/164,273 filed March 22, 2021, and International Appl. No. PCT/US2021/049853 filed September 10, 2021, each of which is herein incorporated by reference in its entirety). In one embodiment, the deaminase polypeptide that is useful for such compositions and methods is a cytosine deaminase or an adenine deaminase comprising an amino acid sequence selected from any one of SEQ ID NOs: 377-448. In one
35 embodiment, the deaminase polypeptide that is useful for such compositions and methods is a cytosine deaminase or an adenine deaminase having a sequence that is at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%,

93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater identity to any one of the amino acid sequences set forth as SEQ ID NOs: 377-448. In some embodiments, the deaminase polypeptide that is useful for such the presently disclosed compositions and methods is a deaminase disclosed in Table 17 of International Publ. No. WO 2020/139873, which is incorporated herein by reference in its entirety.

Further, it is known in the art that certain fusion proteins between an RGN and a base-editing enzyme (e.g., cytosine deaminase) may also comprise at least one uracil stabilizing polypeptide that increases the mutation rate of a cytidine, deoxycytidine, or cytosine to a thymidine, deoxythymidine, or thymine in a nucleic acid molecule by a deaminase. Non-limiting examples of uracil stabilizing polypeptides include those disclosed in U.S. Provisional Appl. No. 63/052,175, filed July 15, 2020, and International Appl. No. PCT/US2021/041809, filed July 15, 2021 (each of which is herein incorporated by reference in its entirety), including USP2 (SEQ ID NO: 325), and a uracil glycosylase inhibitor (UGI) domain (SEQ ID NO: 315), which may increase base editing efficiency. Therefore, a fusion protein may comprise an RGN described herein or variant thereof, a deaminase, and optionally at least one uracil stabilizing polypeptide, such as UGI or USP2. In certain embodiments, the RGN that is fused to the base-editing polypeptide is a nickase that cleaves the DNA strand that is not acted upon by the base-editing polypeptide (e.g., deaminase).

In some embodiments, an RGN may be fused to a prime editing polypeptide. Prime editing is a versatile and precise genome editing method that directly writes new genetic information into a specified DNA site using a nucleic acid programmable DNA binding protein working in association with a polymerase. The prime editing system uses an RGN that is a nickase, and the system is programmed with a prime editing (PE) guide RNA ("PEgRNA"). The PEgRNA is a guide RNA that both specifies the target sequence and provides the template for polymerization of the replacement strand containing the edit by way of an extension engineered onto the guide RNA (e.g., at the 5' or 3' end, or at an internal portion of the guide RNA). The RGN nickase/prime editing polypeptide fusion is guided to the target sequence by the PEgRNA and nicks the target strand upstream of sequence to be edited and upstream of the PAM, creating a 3' flap on the target strand. The pegRNA includes a primer binding site (PBS) that is complementary to the 3' flap of the target strand. In some embodiments, a PBS is at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 nucleotides in length. In certain embodiments, the pegRNA comprises a PBS that is at least 5 (e.g., at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20) nucleotides in length. In some embodiments, the pegRNA may comprise a PBS that is at least 8 nucleotides in length.

Hybridization of the PBS and 3' flap of the target strand allows polymerization of the replacement strand containing the edit using the extension of the PEgRNA as template. The extension of the PEgRNA can be formed from RNA or DNA. In the case of an RNA extension, the polymerase of the prime editor can be an RNA-dependent DNA polymerase (such as a reverse transcriptase). In the

case of a DNA extension, the polymerase of the prime editor may be a DNA-dependent DNA polymerase.

The replacement strand containing the desired edit (e.g., a single nucleobase substitution) shares the same sequence as the target strand of the target sequence to be edited (with the exception that it includes the desired edit). Through DNA repair and/or replication machinery, the target strand of the target sequence is replaced by the newly synthesized replacement strand containing the desired edit. In some cases, prime editing may be thought of as a “search-and-replace” genome editing technology since the prime editors not only search and locate the desired target sequence to be edited, but at the same time, encode a replacement strand containing a desired edit which is installed in place of the corresponding target strand of the target sequence. Thus, in some embodiments, a guide RNA of the disclosure comprises an extension comprising an edit template for prime editing. In some embodiments, a prime editing polypeptide that can be fused to an RGN includes a DNA polymerase. In certain embodiments, the DNA polymerase is a reverse transcriptase. In certain embodiments, the RGN is a nickase.

RNA-guided nucleases that are fused to a polypeptide or domain can be separated or joined by a linker. The term “linker,” as used herein, refers to a chemical group or a molecule linking two molecules or moieties, e.g., a binding domain and a cleavage domain of a nuclease. In some embodiments, a linker joins a gRNA binding domain of an RNA guided nuclease and a base-editing polypeptide, such as a deaminase. In some embodiments, a linker joins a nuclease-dead RGN and a deaminase. Typically, the linker is positioned between, or flanked by, two groups, molecules, or other moieties and connected to each one via a covalent bond, thus connecting the two. In some embodiments, the linker is an amino acid or a plurality of amino acids (e.g., a peptide or protein). In some embodiments, the linker is an organic molecule, group, polymer, or chemical moiety. In some embodiments, the linker is 5-100 amino acids in length, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 30-35, 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-150, or 150-200 amino acids in length. Longer or shorter linkers are also contemplated.

The presently disclosed RNA-guided nucleases can comprise at least one nuclear localization signal (NLS) to enhance transport of the RGN to the nucleus of a cell. Nuclear localization signals are known in the art and generally comprise a stretch of basic amino acids (see, e.g., Lange *et al.*, *J. Biol. Chem.* (2007) 282:5101-5105). In some embodiments, the RGN comprises 2, 3, 4, 5, 6 or more nuclear localization signals. The nuclear localization signal(s) can be a heterologous NLS. Non-limiting examples of nuclear localization signals useful for the presently disclosed RGNs are the nuclear localization signals of SV40 Large T-antigen, nucleoplasmin, and c-Myc (see, e.g., Ray *et al.* (2015) *Bioconjug Chem* 26(6):1004-7). In particular embodiments, the RGN comprises the NLS sequence set forth as SEQ ID NO: 316 or 317. The RGN can comprise one or more NLS sequences at its N-terminus, C-terminus, or both the N-terminus and C-terminus. For example, the RGN can

comprise two NLS sequences at the N-terminal region and four NLS sequences at the C-terminal region.

Other localization signal sequences known in the art that localize polypeptides to particular subcellular location(s) can also be used to target the RGNs, including, but not limited to, plastid localization sequences, mitochondrial localization sequences, and dual-targeting signal sequences that target to both the plastid and mitochondria (see, e.g., Nassoury and Morse (2005) *Biochim Biophys Acta* 1743:5-19; Kunze and Berger (2015) *Front Physiol* dx.doi.org/10.3389/fphys.2015.00259; Herrmann and Neupert (2003) *IUBMB Life* 55:219-225; Soll (2002) *Curr Opin Plant Biol* 5:529-535; Carrie and Small (2013) *Biochim Biophys Acta* 1833:253-259; Carrie *et al.* (2009) *FEBS J* 276:1187-1195; Silva-Filho (2003) *Curr Opin Plant Biol* 6:589-595; Peeters and Small (2001) *Biochim Biophys Acta* 1541:54-63; Murcha *et al.* (2014) *J Exp Bot* 65:6301-6335; Mackenzie (2005) *Trends Cell Biol* 15:548-554; Glaser *et al.* (1998) *Plant Mol Biol* 38:311-338).

In certain embodiments, the presently disclosed RNA-guided nucleases comprise at least one cell-penetrating domain that facilitates cellular uptake of the RGN. Cell-penetrating domains are known in the art and generally comprise stretches of positively charged amino acid residues (*i.e.*, polycationic cell-penetrating domains), alternating polar amino acid residues and non-polar amino acid residues (*i.e.*, amphipathic cell-penetrating domains), or hydrophobic amino acid residues (*i.e.*, hydrophobic cell-penetrating domains) (see, e.g., Milletti F. (2012) *Drug Discov Today* 17:850-860). A non-limiting example of a cell-penetrating domain is the trans-activating transcriptional activator (TAT) from the human immunodeficiency virus 1.

The nuclear localization signal, plastid localization signal, mitochondrial localization signal, dual-targeting localization signal, and/or cell-penetrating domain can be located at the amino-terminus (N-terminus), the carboxyl-terminus (C-terminus), or in an internal location of the RNA-guided nuclease.

The presently disclosed RGNs can be fused to an effector domain, such as a cleavage domain, a deaminase domain, or an expression modulator domain, either directly or indirectly via a linker peptide. Such a domain can be located at the N-terminus, the C-terminus, or an internal location of the RNA-guided nuclease. In some of these embodiments, the RGN component of the fusion protein is a nuclease-dead RGN or a nickase.

In some embodiments, the RGN fusion protein comprises a cleavage domain, which is any domain that is capable of cleaving a polynucleotide (*i.e.*, RNA, DNA, or RNA/DNA hybrid) and includes, but is not limited to, restriction endonucleases and homing endonucleases, such as Type IIS endonucleases (e.g., *FokI*) (see, e.g., Belfort *et al.* (1997) *Nucleic Acids Res.* 25:3379-3388; Linn *et al.* (eds.) *Nucleases*, Cold Spring Harbor Laboratory Press, 1993).

In other embodiments, the RGN fusion protein comprises a deaminase domain that deaminates a nucleobase, resulting in conversion from one nucleobase to another, and includes, but is not limited to, a cytosine deaminase or an adenine deaminase (see, e.g., Gaudelli *et al.* (2017) *Nature*

551:464-471, U.S. Publ. Nos. 2017/0121693 and 2018/0073012, U.S. Patent No. 9,840,699, and International Publ. No. WO/2018/027078, or any of the deaminases disclosed in International Publ. No. WO 2020/139873, U.S. Provisional Appl. Nos. 63/077,089 filed September 11, 2020, 63/146,840 filed February 8, 2021, and 63/164,273 filed March 22, 2021, and International Appl. No.

5 PCT/US2021/049853 filed September 10, 2021, each of which is herein incorporated by reference in its entirety).

In some embodiments, the effector domain of the RGN fusion protein can be an expression modulator domain, which is a domain that either serves to upregulate or downregulate transcription. The expression modulator domain can be an epigenetic modification domain, a transcriptional
10 repressor domain or a transcriptional activation domain.

In some of these embodiments, the expression modulator of the RGN fusion protein comprises an epigenetic modification domain that covalently modifies DNA or histone proteins to alter histone structure and/or chromosomal structure without altering the DNA sequence, leading to changes in gene expression (*i.e.*, upregulation or downregulation). Non-limiting examples of
15 epigenetic modifications include acetylation or methylation of lysine residues, arginine methylation, serine and threonine phosphorylation, and lysine ubiquitination and sumoylation of histone proteins, and methylation and hydroxymethylation of cytosine residues in DNA. Non-limiting examples of epigenetic modification domains include histone acetyltransferase domains, histone deacetylase domains, histone methyltransferase domains, histone demethylase domains, DNA methyltransferase
20 domains, and DNA demethylase domains.

In other embodiments, the expression modulator of the fusion protein comprises a transcriptional repressor domain, which interacts with transcriptional control elements and/or transcriptional regulatory proteins, such as RNA polymerases and transcription factors, to reduce or terminate transcription of at least one gene. Transcriptional repressor domains are known in the art
25 and include, but are not limited to, Sp1-like repressors, IκB, and Krüppel associated box (KRAB) domains.

In yet other embodiments, the expression modulator of the fusion protein comprises a transcriptional activation domain, which interacts with transcriptional control elements and/or transcriptional regulatory proteins, such as RNA polymerases and transcription factors, to increase or
30 activate transcription of at least one gene. Transcriptional activation domains are known in the art and include, but are not limited to, a herpes simplex virus VP16 activation domain and an NFAT activation domain.

The presently disclosed RGN polypeptides can comprise a detectable label or a purification tag. The detectable label or purification tag can be located at the N-terminus, the C-terminus, or an
35 internal location of the RNA-guided nuclease, either directly or indirectly via a linker peptide. In some of these embodiments, the RGN component of the fusion protein is a nuclease-dead RGN. In other embodiments, the RGN component of the fusion protein is an RGN with nickase activity.

A detectable label is a molecule that can be visualized or otherwise observed. The detectable label may be fused to the RGN as a fusion protein (*e.g.*, fluorescent protein) or may be a small molecule conjugated to the RGN polypeptide that can be detected visually or by other means.

Detectable labels that can be fused to the presently disclosed RGNs as a fusion protein include any detectable protein domain, including but not limited to, a fluorescent protein or a protein domain that can be detected with a specific antibody. Non-limiting examples of fluorescent proteins include green fluorescent proteins (*e.g.*, GFP, EGFP, ZsGreen1) and yellow fluorescent proteins (*e.g.*, YFP, EYFP, ZsYellow1). Non-limiting examples of small molecule detectable labels include radioactive labels, such as ^3H and ^{35}S .

RGN polypeptides can also comprise a purification tag, which is any molecule that can be utilized to isolate a protein or fused protein from a mixture (*e.g.*, biological sample, culture medium). Non-limiting examples of purification tags include biotin, myc, maltose binding protein (MBP), glutathione-S-transferase (GST), and 3X FLAG tag.

III. Guide RNA

The present disclosure provides guide RNAs and polynucleotides encoding the same. The term “guide RNA” refers to a nucleotide sequence having sufficient complementarity with a target nucleotide sequence to hybridize with the target sequence and direct sequence-specific binding of an associated RNA-guided nuclease to the target nucleotide sequence. Thus, an RGN’s respective guide RNA is one or more RNA molecules (generally, one or two), that can bind to the RGN and guide the RGN to bind to a particular target nucleotide sequence, and in those embodiments wherein the RGN has nickase or nuclease activity, also cleave the target nucleotide sequence. In general, a guide RNA comprises a CRISPR RNA (crRNA) and a trans-activating CRISPR RNA (tracrRNA). Native guide RNAs that comprise both a crRNA and a tracrRNA generally comprise two separate RNA molecules that hybridize to each other through the repeat sequence of the crRNA and the anti-repeat sequence of the tracrRNA.

Native direct repeat sequences within a CRISPR array generally range in length from 28 to 37 base pairs, although the length can vary between about 23 bp to about 55 bp. Spacer sequences within a CRISPR array generally range from about 32 to about 38 bp in length, although the length can be between about 21 bp to about 72 bp. Each CRISPR array generally comprises less than 50 units of the CRISPR repeat-spacer sequence. The CRISPRs are transcribed as part of a long transcript termed the primary CRISPR transcript, which comprises much of the CRISPR array. The primary CRISPR transcript is cleaved by Cas proteins to produce crRNAs or in some cases, to produce pre-crRNAs that are further processed by additional Cas proteins into mature crRNAs. Mature crRNAs comprise a spacer sequence and a CRISPR repeat sequence. In some embodiments in which pre-crRNAs are processed into mature (or processed) crRNAs, maturation involves the removal of about one to about six or more 5', 3', or 5' and 3' nucleotides. For the purposes of genome editing or targeting a particular

target nucleotide sequence of interest, these nucleotides that are removed during maturation of the pre-crRNA molecule are not necessary for generating or designing a guide RNA.

A CRISPR RNA (crRNA) comprises a spacer sequence and a CRISPR repeat sequence. The “spacer sequence” is the nucleotide sequence that directly hybridizes with the target nucleotide sequence of interest. The spacer sequence is engineered to be fully or partially complementary with the target sequence of interest. In various embodiments, the spacer sequence can comprise from about 8 nucleotides to about 30 nucleotides, or more. For example, the spacer sequence can be about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, or more nucleotides in length. In some embodiments, the spacer sequence is 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides in length. In some embodiments, the spacer sequence is about 10 to about 26 nucleotides in length, or about 12 to about 30 nucleotides in length. In some embodiments, the spacer sequence is 19-27 nucleotides in length. In certain embodiments, particularly when the RGN has the amino acid sequence set forth as SEQ ID NO: 6 or an active variant or fragment thereof, the spacer sequence is 21-24 nucleotides in length. In particular embodiments, the spacer sequence is about 30 nucleotides in length. In some embodiments, the spacer sequence is 30 nucleotides in length. In some embodiments, the degree of complementarity between a spacer sequence and its corresponding target sequence, when optimally aligned using a suitable alignment algorithm, is between 50% and 99% or more, including but not limited to about or more than about 50%, about 60%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more. In particular embodiments, the degree of complementarity between a spacer sequence and its corresponding target sequence, when optimally aligned using a suitable alignment algorithm, is 50%, 60%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more. In particular embodiments, the spacer sequence is free of secondary structure, which can be predicted using any suitable polynucleotide folding algorithm known in the art, including but not limited to mFold (see, *e.g.*, Zuker and Stiegler (1981) *Nucleic Acids Res.* 9:133-148) and RNAfold (see, *e.g.*, Gruber et al. (2008) *Cell* 106(1):23-24).

The CRISPR RNA repeat sequence comprises a nucleotide sequence that forms a structure, either on its own or in concert with a hybridized tracrRNA, that is recognized by the RGN molecule. In various embodiments, the CRISPR RNA repeat sequence can comprise from about 8 nucleotides to about 30 nucleotides, or more. For example, the CRISPR repeat sequence can be about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, or more nucleotides in length. In particular embodiments, the CRISPR repeat sequence is 8,

9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides in length. In some embodiments, the degree of complementarity between a CRISPR repeat sequence and its corresponding tracrRNA sequence, when optimally aligned using a suitable alignment algorithm, is about or more than about 50%, about 60%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more. In particular embodiments, the degree of complementarity between a CRISPR repeat sequence and its corresponding tracrRNA sequence, when optimally aligned using a suitable alignment algorithm, is 50%, 60%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more.

In particular embodiments, the CRISPR repeat sequence comprises the nucleotide sequence of any one of SEQ ID NOs: 13-24, or an active variant or fragment thereof that when comprised within a guide RNA, is capable of directing the sequence-specific binding of an associated RNA-guided nuclease provided herein to a target sequence of interest. In certain embodiments, an active CRISPR repeat sequence variant of a wild-type sequence comprises a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24. In certain embodiments, an active CRISPR repeat sequence fragment of a wild-type sequence comprises at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22 contiguous nucleotides of any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24.

In certain embodiments, the crRNA is not naturally-occurring. In some of these embodiments, the specific CRISPR repeat sequence is not linked to the engineered spacer sequence in nature and the CRISPR repeat sequence is considered heterologous to the spacer sequence. In certain embodiments, the spacer sequence is an engineered sequence that is not naturally occurring.

A trans-activating CRISPR RNA or tracrRNA molecule comprises a nucleotide sequence comprising a region that has sufficient complementarity to hybridize to a CRISPR repeat sequence of a crRNA, which is referred to herein as the anti-repeat region. In some embodiments, the tracrRNA molecule further comprises a region with secondary structure (*e.g.*, stem-loop) or forms secondary structure upon hybridizing with its corresponding crRNA. In particular embodiments, the region of the tracrRNA that is fully or partially complementary to a CRISPR repeat sequence is at the 5' end of the molecule and the 3' end of the tracrRNA comprises secondary structure. This region of secondary structure generally comprises several hairpin structures, including the nexus hairpin, which is found adjacent to the anti-repeat sequence. The nexus forms the core of the interactions between the guide RNA and the RGN, and is at the intersection between the guide RNA, the RGN, and the target DNA. The nexus hairpin often has a conserved nucleotide sequence in the base of the hairpin stem, with the motif UNANNC (SEQ ID NO: 318) found in many nexus hairpins in tracrRNAs. Interestingly, several of the RGNs of the invention use tracrRNAs that comprise non-canonical sequences in the

base of the hairpin stem of their nexus hairpins, including UNANNA, UNANNG, and CNANNC (SEQ ID NOs: 319, 321, and 322, respectively). There are often terminal hairpins at the 3' end of the tracrRNA that can vary in structure and number, but often comprise a GC-rich Rho-independent transcriptional terminator hairpin followed by a string of U's at the 3' end. See, for example, Briner et al. (2014) *Molecular Cell* 56:333-339, Briner and Barrangou (2016) *Cold Spring Harb Protoc*; doi: 10.1101/pdb.top090902, and U.S. Publication No. 2017/0275648, each of which is herein incorporated by reference in its entirety.

In various embodiments, the anti-repeat region of the tracrRNA that is fully or partially complementary to the CRISPR repeat sequence comprises from about 8 nucleotides to about 30 nucleotides, or more. For example, the region of base pairing between the tracrRNA anti-repeat sequence and the CRISPR repeat sequence can be about 8, about 9, about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 26, about 27, about 28, about 29, about 30, or more nucleotides in length. In particular embodiments, the region of base pairing between the tracrRNA anti-repeat sequence and the CRISPR repeat sequence is 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more nucleotides in length. In some embodiments, the degree of complementarity between a CRISPR repeat sequence and its corresponding tracrRNA anti-repeat sequence, when optimally aligned using a suitable alignment algorithm, is about or more than about 50%, about 60%, about 70%, about 75%, about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or more. In particular embodiments, the degree of complementarity between a CRISPR repeat sequence and its corresponding tracrRNA anti-repeat sequence, when optimally aligned using a suitable alignment algorithm, is 50%, 60%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more.

In various embodiments, the entire tracrRNA can comprise from about 60 nucleotides to more than about 210 nucleotides. For example, the tracrRNA can be about 60, about 65, about 70, about 75, about 80, about 85, about 90, about 95, about 100, about 105, about 110, about 115, about 120, about 125, about 130, about 135, about 140, about 150, about 160, about 170, about 180, about 190, about 200, about 210, or more nucleotides in length. In particular embodiments, the tracrRNA is 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 150, 160, 170, 180, 190, 200, 210 or more nucleotides in length. In particular embodiments, the tracrRNA is about 70 to about 105 nucleotides in length, including about 70, about 71, about 72, about 73, about 74, about 75, about 76, about 77, about 78, about 79, about 80, about 81, about 82, about 83, about 84, about 85, about 86, about 87, about 88, about 89, about 90, about 91, about 92, about 93, about 94, about 95, about 96, about 97, about 98, about 99, about 100, about 101, about 102, about 103, about 104, and about 105 nucleotides in length. In particular embodiments, the tracrRNA is 70 to 105 nucleotides in length,

including 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, and 105 nucleotides in length.

In particular embodiments, the tracrRNA comprises the nucleotide sequence of any one of SEQ ID NOs: 25-36, or an active variant or fragment thereof that when comprised within a guide RNA is capable of directing the sequence-specific binding of an associated RNA-guided nuclease provided herein to a target sequence of interest. In certain embodiments, an active tracrRNA sequence variant of a wild-type sequence comprises a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to any one of the nucleotide sequences set forth as SEQ ID NOs: 25-36. In certain embodiments, an active tracrRNA sequence fragment of a wild-type sequence comprises at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more contiguous nucleotides of any one of the nucleotide sequences set forth as SEQ ID NOs: 25-36.

Two polynucleotide sequences can be considered to be substantially complementary when the two sequences hybridize to each other under stringent conditions. Likewise, an RGN is considered to bind to a particular target sequence within a sequence-specific manner if the guide RNA bound to the RGN binds to the target sequence under stringent conditions. By "stringent conditions" or "stringent hybridization conditions" is intended conditions under which the two polynucleotide sequences will hybridize to each other to a detectably greater degree than to other sequences (*e.g.*, at least 2-fold over background). Stringent conditions are sequence-dependent and will be different in different circumstances. Typically, stringent conditions will be those in which the salt concentration is less than about 1.5 M Na ion, typically about 0.01 to 1.0 M Na ion concentration (or other salts) at pH 7.0 to 8.3, and the temperature is at least about 30°C for short sequences (*e.g.*, 10 to 50 nucleotides) and at least about 60°C for long sequences (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. Exemplary low stringency conditions include hybridization with a buffer solution of 30 to 35% formamide, 1 M NaCl, 1% SDS (sodium dodecyl sulfate) at 37°C, and a wash in 1X to 2X SSC (20X SSC = 3.0 M NaCl/0.3 M trisodium citrate) at 50 to 55°C. Exemplary moderate stringency conditions include hybridization in 40 to 45% formamide, 1.0 M NaCl, 1% SDS at 37°C, and a wash in 0.5X to 1X SSC at 55 to 60°C. Exemplary high stringency conditions include hybridization in 50% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 0.1X SSC at 60 to 65°C. Optionally, wash buffers may comprise about 0.1% to about 1% SDS. Duration of hybridization is generally less than about 24 hours, usually about 4 to about 12 hours. The duration of the wash time will be at least a length of time sufficient to reach equilibrium.

The T_m is the temperature (under defined ionic strength and pH) at which 50% of a complementary target sequence hybridizes to a perfectly matched sequence. For DNA-DNA hybrids, the T_m can be approximated from the equation of Meinkoth and Wahl (1984) *Anal. Biochem.* 138:267-284: $T_m = 81.5^{\circ}\text{C} + 16.6 (\log M) + 0.41 (\%GC) - 0.61 (\% \text{ form}) - 500/L$; where M is the

molarity of monovalent cations, %GC is the percentage of guanosine and cytosine nucleotides in the DNA, % form is the percentage of formamide in the hybridization solution, and L is the length of the hybrid in base pairs. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence and its complement at a defined ionic strength and pH. However, severely stringent conditions can utilize a hybridization and/or wash at 1, 2, 3, or 4°C lower than the thermal melting point (T_m); moderately stringent conditions can utilize a hybridization and/or wash at 6, 7, 8, 9, or 10°C lower than the thermal melting point (T_m); low stringency conditions can utilize a hybridization and/or wash at 11, 12, 13, 14, 15, or 20°C lower than the thermal melting point (T_m). Using the equation, hybridization and wash compositions, and desired T_m, those of ordinary skill will understand that variations in the stringency of hybridization and/or wash solutions are inherently described. An extensive guide to the hybridization of nucleic acids is found in Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Acid Probes*, Part I, Chapter 2 (Elsevier, New York); and Ausubel et al., eds. (1995) *Current Protocols in Molecular Biology*, Chapter 2 (Greene Publishing and Wiley-Interscience, New York). See Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual* (2d ed., Cold Spring Harbor Laboratory Press, Plainview, New York).

The term “sequence specific” can also refer to the binding of a target sequence at a greater frequency than binding to a randomized background sequence.

The guide RNA can be a single guide RNA (sgRNA) or a dual-guide RNA system. A single guide RNA comprises the crRNA and tracrRNA on a single molecule of RNA, whereas a dual-guide RNA system comprises a crRNA and a tracrRNA present on two distinct RNA molecules, hybridized to one another through at least a portion of the CRISPR repeat sequence of the crRNA and at least a portion of the tracrRNA, which may be fully or partially complementary to the CRISPR repeat sequence of the crRNA. In some of those embodiments wherein the guide RNA is a single guide RNA, the crRNA and tracrRNA are separated by a linker nucleotide sequence. In general, the linker nucleotide sequence is one that does not include complementary bases in order to avoid the formation of secondary structure within or comprising nucleotides of the linker nucleotide sequence. In some embodiments, the linker nucleotide sequence between the crRNA and tracrRNA is at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, or more nucleotides in length. In particular embodiments, the linker nucleotide sequence of a single guide RNA is at least 4 nucleotides in length. In certain embodiments, the linker nucleotide sequence is the nucleotide sequence set forth as SEQ ID NO: 323.

The single guide RNA or dual-guide RNA can be synthesized chemically or via *in vitro* transcription. Assays for determining sequence-specific binding between an RGN and a guide RNA are known in the art and include, but are not limited to, *in vitro* binding assays between an expressed RGN and the guide RNA, which can be tagged with a detectable label (e.g., biotin) and used in a pull-down detection assay in which the guide RNA:RGN complex is captured via the detectable label (e.g.,

with streptavidin beads). A control guide RNA with an unrelated sequence or structure to the guide RNA can be used as a negative control for non-specific binding of the RGN to RNA. In certain embodiments, the guide RNA is any one of SEQ ID NOs: 37-48, wherein the spacer sequence can be any sequence and is indicated as a poly-N sequence.

5 In certain embodiments, the guide RNA can be introduced into a target cell, organelle, or embryo as an RNA molecule. The guide RNA can be transcribed *in vitro* or chemically synthesized. In other embodiments, a nucleotide sequence encoding the guide RNA is introduced into the cell, organelle, or embryo. In some of these embodiments, the nucleotide sequence encoding the guide RNA is operably linked to a promoter (*e.g.*, an RNA polymerase III promoter). The promoter can be
10 a native promoter or heterologous to the guide RNA-encoding nucleotide sequence.

In various embodiments, the guide RNA can be introduced into a target cell, organelle, or embryo as a ribonucleoprotein complex, as described herein, wherein the guide RNA is bound to an RNA-guided nuclease polypeptide.

The guide RNA directs an associated RNA-guided nuclease to a particular target nucleotide
15 sequence of interest through hybridization of the guide RNA to the target nucleotide sequence. A target nucleotide sequence can comprise DNA, RNA, or a combination of both and can be single-stranded or double-stranded. A target nucleotide sequence can be genomic DNA (*i.e.*, chromosomal DNA), plasmid DNA, or an RNA molecule (*e.g.*, messenger RNA, ribosomal RNA, transfer RNA, micro RNA, small interfering RNA). The target nucleotide sequence can be bound (and in some
20 embodiments, cleaved) by an RNA-guided nuclease *in vitro* or in a cell. The chromosomal sequence targeted by the RGN can be a nuclear, plastid or mitochondrial chromosomal sequence. In some embodiments, the target nucleotide sequence is unique in the target genome.

The target nucleotide sequence is adjacent to a protospacer adjacent motif (PAM). A protospacer adjacent motif is generally within about 1 to about 10 nucleotides from the target
25 nucleotide sequence, including about 1, about 2, about 3, about 4, about 5, about 6, about 7, about 8, about 9, or about 10 nucleotides from the target nucleotide sequence. In particular embodiments, a PAM is within 1 to 10 nucleotides from the target nucleotide sequence, including 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides from the target nucleotide sequence. When not otherwise noted herein, the given PAM sequence for a presently disclosed RGN is immediately adjacent to the target
30 nucleotide sequence. The PAM can be 5' or 3' of the target sequence. In some embodiments, the PAM is 3' of the target sequence for the presently disclosed RGNs. Generally, the PAM is a consensus sequence of about 3-4 nucleotides, but in particular embodiments it can be 2, 3, 4, 5, 6, 7, 8, 9, or more nucleotides in length. In various embodiments, the PAM sequence recognized by the presently disclosed RGNs comprises the consensus sequence set forth in any one of SEQ ID NOs: 73-
35 84.

In particular embodiments, an RNA-guided nuclease having any one of SEQ ID NOs: 1-12 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as any one of SEQ ID NOs: 73-84. In some embodiments, the RGN binds to a guide sequence comprising a CRISPR repeat sequence set forth in any one of SEQ ID NOs: 13-24, respectively, or an active variant or fragment thereof, and a tracrRNA sequence set forth in any one of SEQ ID NOs: 25-36, respectively, or an active variant or fragment thereof. The RGN systems are described further in Examples 1-3 and Tables 1 and 2 of the present specification.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 1 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 73, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 13 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 25 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 2 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 74, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 14 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 26 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 3 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 75, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 15 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 27 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 4 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 76, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 16 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 28 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 5 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 77, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 17 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 29 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 6 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 78, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 18 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 30 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 7 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 79, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 19 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 31 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 8 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 80, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 20 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 32 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 9 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 81, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 21 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 33 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 10 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 82, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 22 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 34 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 11 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 83, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 23 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 35 or an active variant or fragment thereof.

In some embodiments, an RNA-guided nuclease having SEQ ID NO: 12 or an active variant or fragment thereof binds a target nucleotide sequence adjacent to a PAM sequence set forth as SEQ ID NO: 84, when bound to a guide RNA comprising a CRISPR repeat sequence set forth as SEQ ID NO: 24 or an active variant or fragment thereof and a tracrRNA sequence set forth as SEQ ID NO: 36 or an active variant or fragment thereof.

It is well-known in the art that PAM sequence specificity for a given nuclease enzyme is affected by enzyme concentration (*see, e.g., Karvelis et al. (2015) Genome Biol 16:253*), which may be modified by altering the promoter used to express the RGN, or the amount of ribonucleoprotein complex delivered to the cell, organelle, or embryo.

Upon recognizing its corresponding PAM sequence, the RGN can cleave the target nucleotide sequence at a specific cleavage site. As used herein, a cleavage site is made up of the two particular nucleotides within a target nucleotide sequence between which the nucleotide sequence is cleaved by

an RGN. The cleavage site can comprise the 1st and 2nd, 2nd and 3rd, 3rd and 4th, 4th and 5th, 5th and 6th, 7th and 8th, or 8th and 9th nucleotides from the PAM in either the 5' or 3' direction. In some embodiments, the cleavage site may be over 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides from the PAM in either the 5' or 3' direction. In some embodiments, particularly those wherein the RGN has the amino acid sequence set forth as SEQ ID NO: 6 or an active variant or fragment thereof, the cleavage site of the RGN is between the 3rd and 4th nucleotides 5' of the PAM, generating blunt ends. As RGNs can cleave a target nucleotide sequence resulting in staggered ends, in some embodiments, the cleavage site is defined based on the distance of the two nucleotides from the PAM on the positive (+) strand of the polynucleotide and the distance of the two nucleotides from the PAM on the negative (-) strand of the polynucleotide.

IV. Nucleotides Encoding RNA-guided nucleases, CRISPR RNA, and/or tracrRNA

The present disclosure provides polynucleotides comprising the presently disclosed CRISPR RNAs, tracrRNAs, and/or sgRNAs and polynucleotides comprising a nucleotide sequence encoding the presently disclosed RNA-guided nucleases, CRISPR RNAs, tracrRNAs, and/or sgRNAs. Presently disclosed polynucleotides include those comprising or encoding a CRISPR repeat sequence comprising any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24, or an active variant or fragment thereof that when comprised within a guide RNA is capable of directing the sequence-specific binding of an associated RNA-guided nuclease to a target sequence of interest. Also disclosed are polynucleotides comprising or encoding a tracrRNA comprising any one of the nucleotide sequences set forth as SEQ ID NOs: 25-36, or an active variant or fragment thereof that when comprised within a guide RNA is capable of directing the sequence-specific binding of an associated RNA-guided nuclease to a target sequence of interest. Polynucleotides are also provided that encode an RNA-guided nuclease comprising any one of the amino acid sequences set forth as SEQ ID NOs: 1-12, and active fragments or variants thereof that retain the ability to bind to a target nucleotide sequence in an RNA-guided sequence-specific manner.

The use of the term "polynucleotide" or "nucleic acid molecule" is not intended to limit the present disclosure to polynucleotides comprising DNA. Those of ordinary skill in the art will recognize that polynucleotides can comprise ribonucleotides (RNA) and combinations of ribonucleotides and deoxyribonucleotides. Such deoxyribonucleotides and ribonucleotides include both naturally occurring molecules and synthetic analogues. These include peptide nucleic acids (PNAs), PNA-DNA chimers, locked nucleic acids (LNAs), and phosphothiorate linked sequences. The polynucleotides disclosed herein also encompass all forms of sequences including, but not limited to, single-stranded forms, double-stranded forms, DNA-RNA hybrids, triplex structures, stem-and-loop structures, and the like.

In some embodiments, the polynucleotide encoding a presently disclosed RGN is an mRNA (messenger RNA) molecule. An mRNA refers to any polynucleotide which encodes a polypeptide of

interest and which is capable of being translated to produce the encoded polypeptide of interest *in vitro*, *in vivo*, *in situ*, or *ex vivo*. In embodiments, the basic components of an mRNA molecule include at least a coding region, a 5'UTR, a 3'UTR, a 5' cap and a poly-A tail. In embodiments, an mRNA encoding an RGN useful in the presently disclosed methods and compositions can include one or more structural and/or chemical modifications or alterations which impart useful properties to the polynucleotide. For instance, a useful property of an mRNA includes the lack of a substantial induction of the innate immune response of a cell into which the mRNA is introduced. A "structural" feature or modification is one in which two or more linked nucleotides are inserted, deleted, duplicated, inverted or randomized in an mRNA without significant chemical modification to the nucleotides themselves. Because chemical bonds will necessarily be broken and reformed to effect a structural modification, structural modifications are of a chemical nature and hence are chemical modifications. However, structural modifications will result in a different sequence of nucleotides. Chemical modifications to mRNA can involve inclusion of 5-methylcytosine, N1-methyl-pseudouridine, pseudouridine, 2-thiouridine, 4-thiouridine, 5-methoxyuridine, 2'Fluoroguanosine, 2'Fluorouridine, 5-bromouridine, 5-(2-carbomethoxyvinyl) uridine, 5-[3(1-E-propenylamino)] uridine, α -thiocytidine, N6-methyladenosine, 5-methylcytidine, N4-acetylcytidine, 5-formylcytidine, or combinations thereof, in an mRNA.

The nucleic acid molecules encoding RGNs can be codon optimized for expression in an organism of interest. A "codon-optimized" coding sequence is a polynucleotide coding sequence having its frequency of codon usage designed to mimic the frequency of preferred codon usage or transcription conditions of a particular host cell. Expression in the particular host cell or organism is enhanced as a result of the alteration of one or more codons at the nucleic acid level such that the translated amino acid sequence is not changed. Nucleic acid molecules can be codon optimized, either wholly or in part. Codon tables and other references providing preference information for a wide range of organisms are available in the art (*see, e.g.*, Campbell and Gowri (1990) *Plant Physiol.* 92:1-11 for a discussion of plant-preferred codon usage). Methods are available in the art for synthesizing plant-preferred genes or mammalian (for example human) codon-optimized coding sequences. *See, for example*, U.S. Patent Nos. 5,380,831, and 5,436,391, and Murray *et al.* (1989) *Nucleic Acids Res.* 17:477-498, herein incorporated by reference.

Polynucleotides encoding the RGNs, crRNAs, tracrRNAs, and/or sgRNAs provided herein can be provided in expression cassettes for *in vitro* expression or expression in a cell, organelle, embryo, or organism of interest. The cassette will include 5' and 3' regulatory sequences operably linked to a polynucleotide encoding an RGN, crRNA, tracrRNAs, and/or sgRNAs provided herein that allows for expression of the polynucleotide. The cassette may additionally contain at least one additional gene or genetic element to be cotransformed into the organism. Where additional genes or elements are included, the components are operably linked. The term "operably linked" is intended to mean a functional linkage between two or more elements. For example, an operable linkage between

a promoter and a coding region of interest (*e.g.*, region coding for an RGN, crRNA, tracrRNAs, and/or sgRNAs) is a functional link that allows for expression of the coding region of interest. Operably linked elements may be contiguous or non-contiguous. When used to refer to the joining of two protein coding regions, by operably linked is intended that the coding regions are in the same reading frame. Alternatively, the additional gene(s) or element(s) can be provided on multiple expression cassettes. For example, the nucleotide sequence encoding a presently disclosed RGN can be present on one expression cassette, whereas the nucleotide sequence encoding a crRNA, tracrRNA, or complete guide RNA can be on a separate expression cassette. Such an expression cassette is provided with a plurality of restriction sites and/or recombination sites for insertion of the polynucleotides to be under the transcriptional regulation of the regulatory regions. The expression cassette may additionally contain a selectable marker gene.

The expression cassette will include in the 5'-3' direction of transcription, a transcriptional (and, in some embodiments, translational) initiation region (*i.e.*, a promoter), an RGN-, crRNA-, tracrRNA-and/or sgRNA- encoding polynucleotide of the invention, and a transcriptional (and in some embodiments, translational) termination region (*i.e.*, termination region) functional in the organism of interest. The promoters of the invention are capable of directing or driving expression of a coding sequence in a host cell. The regulatory regions (*e.g.*, promoters, transcriptional regulatory regions, and translational termination regions) may be endogenous or heterologous to the host cell or to each other. As used herein, "heterologous" in reference to a sequence is a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human intervention. As used herein, a chimeric gene comprises a coding sequence operably linked to a transcription initiation region that is heterologous to the coding sequence.

Convenient termination regions are available from the Ti-plasmid of *A. tumefaciens*, such as the octopine synthase and nopaline synthase termination regions. See also Guerineau *et al.* (1991) *Mol. Gen. Genet.* 262:141-144; Proudfoot (1991) *Cell* 64:671-674; Sanfacon *et al.* (1991) *Genes Dev.* 5:141-149; Mogen *et al.* (1990) *Plant Cell* 2:1261-1272; Munroe *et al.* (1990) *Gene* 91:151-158; Ballas *et al.* (1989) *Nucleic Acids Res.* 17:7891-7903; and Joshi *et al.* (1987) *Nucleic Acids Res.* 15:9627-9639.

Additional regulatory signals include, but are not limited to, transcriptional initiation start sites, operators, activators, enhancers, other regulatory elements, ribosomal binding sites, an initiation codon, termination signals, and the like. See, for example, U.S. Pat. Nos. 5,039,523 and 4,853,331; EPO 0480762A2; Sambrook *et al.* (1992) *Molecular Cloning: A Laboratory Manual*, ed. Maniatis *et al.* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.), hereinafter "Sambrook 11"; Davis *et al.*, eds. (1980) *Advanced Bacterial Genetics* (Cold Spring Harbor Laboratory Press), Cold Spring Harbor, N.Y., and the references cited therein.

In preparing the expression cassette, the various DNA fragments may be manipulated, so as to provide for the DNA sequences in the proper orientation and, as appropriate, in the proper reading frame. Toward this end, adapters or linkers may be employed to join the DNA fragments or other manipulations may be involved to provide for convenient restriction sites, removal of superfluous DNA, removal of restriction sites, or the like. For this purpose, *in vitro* mutagenesis, primer repair, restriction, annealing, resubstitutions, *e.g.*, transitions and transversions, may be involved.

A number of promoters can be used in the practice of the invention. The promoters can be selected based on the desired outcome. The nucleic acids can be combined with constitutive, inducible, growth stage-specific, cell type-specific, tissue-preferred, tissue-specific, or other promoters for expression in the organism of interest. See, for example, promoters set forth in WO 99/43838 and in US Patent Nos: 8,575,425; 7,790,846; 8,147,856; 8,586,832; 7,772,369; 7,534,939; 6,072,050; 5,659,026; 5,608,149; 5,608,144; 5,604,121; 5,569,597; 5,466,785; 5,399,680; 5,268,463; 5,608,142; and 6,177,611; herein incorporated by reference.

For expression in plants, constitutive promoters also include CaMV 35S promoter (Odell *et al.* (1985) *Nature* 313:810-812); rice actin (McElroy *et al.* (1990) *Plant Cell* 2:163-171); ubiquitin (Christensen *et al.* (1989) *Plant Mol. Biol.* 12:619-632 and Christensen *et al.* (1992) *Plant Mol. Biol.* 18:675-689); pEMU (Last *et al.* (1991) *Theor. Appl. Genet.* 81:581-588); and MAS (Velten *et al.* (1984) *EMBO J.* 3:2723-2730).

Examples of inducible promoters are the Adh1 promoter which is inducible by hypoxia or cold stress, the Hsp70 promoter which is inducible by heat stress, the PPKK promoter and the pepcarboxylase promoter which are both inducible by light. Also useful are promoters which are chemically inducible, such as the In2-2 promoter which is safener induced (U.S. Pat. No. 5,364,780), the Axig1 promoter which is auxin induced and tapetum specific but also active in callus (PCT US01/22169), the steroid-responsive promoters (see, for example, the ERE promoter which is estrogen induced, and the glucocorticoid-inducible promoter in Schena *et al.* (1991) *Proc. Natl. Acad. Sci. USA* 88:10421-10425 and McNellis *et al.* (1998) *Plant J.* 14(2):247-257) and tetracycline-inducible and tetracycline-repressible promoters (see, for example, Gatz *et al.* (1991) *Mol. Gen. Genet.* 227:229-237, and U.S. Pat. Nos. 5,814,618 and 5,789,156), herein incorporated by reference.

Tissue-specific or tissue-preferred promoters can be utilized to target expression of an expression construct within a particular tissue. In certain embodiments, the tissue-specific or tissue-preferred promoters are active in plant tissue. Examples of promoters under developmental control in plants include promoters that initiate transcription preferentially in certain tissues, such as leaves, roots, fruit, seeds, or flowers. A "tissue specific" promoter is a promoter that initiates transcription only in certain tissues. Unlike constitutive expression of genes, tissue-specific expression is the result of several interacting levels of gene regulation. As such, promoters from homologous or closely related plant species can be preferable to use to achieve efficient and reliable expression of transgenes in particular tissues. In some embodiments, the expression comprises a tissue-preferred promoter. A

"tissue preferred" promoter is a promoter that initiates transcription preferentially, but not necessarily entirely or solely in certain tissues.

In some embodiments, the nucleic acid molecules encoding an RGN, crRNA, and/or tracrRNA comprise a cell type-specific promoter. A "cell type specific" promoter is a promoter that primarily drives expression in certain cell types in one or more organs. Some examples of plant cells in which cell type specific promoters functional in plants may be primarily active include, for example, BETL cells, vascular cells in roots, leaves, stalk cells, and stem cells. The nucleic acid molecules can also include cell type preferred promoters. A "cell type preferred" promoter is a promoter that primarily drives expression mostly, but not necessarily entirely or solely in certain cell types in one or more organs. Some examples of plant cells in which cell type preferred promoters functional in plants may be preferentially active include, for example, BETL cells, vascular cells in roots, leaves, stalk cells, and stem cells.

The nucleic acid sequences encoding the RGNs, crRNAs, tracrRNAs, and/or sgRNAs can be operably linked to a promoter sequence that is recognized by a phage RNA polymerase for example, for *in vitro* mRNA synthesis. In such embodiments, the *in vitro*-transcribed RNA can be purified for use in the methods described herein. For example, the promoter sequence can be a T7, T3, or SP6 promoter sequence or a variation of a T7, T3, or SP6 promoter sequence. In such embodiments, the expressed protein and/or RNAs can be purified for use in the methods of genome modification described herein.

In certain embodiments, the polynucleotide encoding the RGN, crRNA, tracrRNA, and/or sgRNA also can be linked to a polyadenylation signal (*e.g.*, SV40 polyA signal and other signals functional in plants) and/or at least one transcriptional termination sequence. Additionally, the sequence encoding the RGN also can be linked to sequence(s) encoding at least one nuclear localization signal, at least one cell-penetrating domain, and/or at least one signal peptide capable of trafficking proteins to particular subcellular locations, as described elsewhere herein.

The polynucleotide encoding the RGN, crRNA, tracrRNA, and/or sgRNA can be present in a vector or multiple vectors. A "vector" refers to a polynucleotide composition for transferring, delivering, or introducing a nucleic acid into a host cell. Suitable vectors include plasmid vectors, phagemids, cosmids, artificial/mini-chromosomes, transposons, and viral vectors (*e.g.*, lentiviral vectors, adeno-associated viral vectors, baculoviral vector). The vector can comprise additional expression control sequences (*e.g.*, enhancer sequences, Kozak sequences, polyadenylation sequences, transcriptional termination sequences), selectable marker sequences (*e.g.*, antibiotic resistance genes), origins of replication, and the like. Additional information can be found in "Current Protocols in Molecular Biology" Ausubel *et al.*, John Wiley & Sons, New York, 2003 or "Molecular Cloning: A Laboratory Manual" Sambrook & Russell, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., 3rd edition, 2001.

The vector can also comprise a selectable marker gene for the selection of transformed cells. Selectable marker genes are utilized for the selection of transformed cells or tissues. Marker genes include genes encoding antibiotic resistance, such as those encoding neomycin phosphotransferase II (NEO) and hygromycin phosphotransferase (HPT), as well as genes conferring resistance to herbicidal compounds, such as glufosinate ammonium, bromoxynil, imidazolinones, and 2,4-dichlorophenoxyacetate (2,4-D).

In some embodiments, the expression cassette or vector comprising the sequence encoding the RGN polypeptide can further comprise a sequence encoding a crRNA and/or a tracrRNA, or the crRNA and tracrRNA combined to create a sgRNA. The sequence(s) encoding the crRNA and/or tracrRNA can be operably linked to at least one transcriptional control sequence for expression of the crRNA and/or tracrRNA in the organism or host cell of interest. For example, the polynucleotide encoding the crRNA and/or tracrRNA can be operably linked to a promoter sequence that is recognized by RNA polymerase III (Pol III). Examples of suitable Pol III promoters include, but are not limited to, mammalian U6, U3, H1, and 7SL RNA promoters and rice U6 and U3 promoters, such as the human U6 promoter set forth as SEQ ID NO: 329, as well as the promoters disclosed in U.S. Provisional Appl. No. 63/209,660, filed June 11, 2021, which is herein incorporated by reference in its entirety, including those set forth herein as SEQ ID NOs: 449-458.

As indicated, expression constructs comprising nucleotide sequences encoding the RGNs, crRNA, tracrRNA, and/or sgRNA can be used to transform organisms of interest. Methods for transformation involve introducing a nucleotide construct into an organism of interest. By "introducing" is intended to introduce the nucleotide construct to the host cell in such a manner that the construct gains access to the interior of the host cell. The methods of the invention do not require a particular method for introducing a nucleotide construct to a host organism, only that the nucleotide construct gains access to the interior of at least one cell of the host organism. The host cell can be a eukaryotic or prokaryotic cell. In particular embodiments, the eukaryotic host cell is a plant cell, a mammalian cell, an avian cell, or an insect cell. In some embodiments, the eukaryotic cell that comprises or expresses a presently disclosed RGN or that has been modified by a presently disclosed RGN is a human cell. In some embodiments, the eukaryotic cell that comprises or expresses a presently disclosed RGN or that has been modified by a presently disclosed RGN is a cell of hematopoietic origin, such as an immune cell (i.e., a cell of the innate or adaptive immune system) including but not limited to a B cell, a T cell, a natural killer (NK) cell, a pluripotent stem cell, an induced pluripotent stem cell, a chimeric antigen receptor T (CAR-T) cell, a monocyte, a macrophage, and a dendritic cell. In some embodiments, the eukaryotic cell that comprises or expresses a presently disclosed RGN or that has been modified by a presently disclosed RGN is an ocular cell, muscle cell (e.g., skeletal muscle cell), epithelial cell (e.g., lung epithelial cell), diseased cell (e.g., tumor cell).

Methods for introducing nucleotide constructs into plants and other host cells are known in the art including, but not limited to, stable transformation methods, transient transformation methods, and virus-mediated methods.

The methods result in a transformed organism, such as a plant, including whole plants, as well as plant organs (*e.g.*, leaves, stems, roots, etc.), seeds, plant cells, propagules, embryos and progeny of the same. Plant cells can be differentiated or undifferentiated (*e.g.* callus, suspension culture cells, protoplasts, leaf cells, root cells, phloem cells, pollen).

"Transgenic organisms" or "transformed organisms" or "stably transformed" organisms or cells or tissues refers to organisms that have incorporated or integrated a polynucleotide encoding an RGN, crRNA, and/or tracrRNA of the invention. It is recognized that other exogenous or endogenous nucleic acid sequences or DNA fragments may also be incorporated into the host cell.

Agrobacterium-and biolistic-mediated transformation remain the two predominantly employed approaches for transformation of plant cells. However, transformation of a host cell may be performed by infection, transfection, microinjection, electroporation, microprojection, biolistics or particle bombardment, electroporation, silica/carbon fibers, ultrasound mediated, PEG mediated, calcium phosphate co-precipitation, polycation DMSO technique, DEAE dextran procedure, and viral mediated, liposome mediated and the like. Viral-mediated introduction of a polynucleotide encoding an RGN, crRNA, and/or tracrRNA includes retroviral, lentiviral, adenoviral, and adeno-associated viral mediated introduction and expression, as well as the use of Caulimoviruses, Geminiviruses, and RNA plant viruses.

Transformation protocols as well as protocols for introducing polypeptides or polynucleotide sequences into plants may vary depending on the type of host cell (*e.g.*, monocot or dicot plant cell) targeted for transformation. Methods for transformation are known in the art and include those set forth in US Patent Nos: 8,575,425; 7,692,068; 8,802,934; 7,541,517; each of which is herein incorporated by reference. See, also, Rakoczy-Trojanowska, M. (2002) *Cell Mol Biol Lett.* 7:849-858; Jones *et al.* (2005) *Plant Methods* 1:5; Rivera *et al.* (2012) *Physics of Life Reviews* 9:308-345; Bartlett *et al.* (2008) *Plant Methods* 4:1-12; Bates, G.W. (1999) *Methods in Molecular Biology* 111:359-366; Binns and Thomashow (1988) *Annual Reviews in Microbiology* 42:575-606; Christou, P. (1992) *The Plant Journal* 2:275-281; Christou, P. (1995) *Euphytica* 85:13-27; Tzfira *et al.* (2004) *TRENDS in Genetics* 20:375-383; Yao *et al.* (2006) *Journal of Experimental Botany* 57:3737-3746; Zupan and Zambryski (1995) *Plant Physiology* 107:1041-1047; Jones *et al.* (2005) *Plant Methods* 1:5;

Transformation may result in stable or transient incorporation of the nucleic acid into the cell. "Stable transformation" is intended to mean that the nucleotide construct introduced into a host cell integrates into the genome of the host cell and is capable of being inherited by the progeny thereof. "Transient transformation" is intended to mean that a polynucleotide is introduced into the host cell and does not integrate into the genome of the host cell.

Methods for transformation of chloroplasts are known in the art. See, for example, Svab et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:8526-8530; Svab and Maliga (1993) *Proc. Natl. Acad. Sci. USA* 90:913-917; Svab and Maliga (1993) *EMBO J.* 12:601-606. The method relies on particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination. Additionally, plastid transformation can be accomplished by transactivation of a silent plastid-borne transgene by tissue-preferred expression of a nuclear-encoded and plastid-directed RNA polymerase. Such a system has been reported in McBride et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:7301-7305.

The cells that have been transformed may be grown into a transgenic organism, such as a plant, in accordance with conventional ways. See, for example, McCormick et al. (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same transformed strain or different strains, and the resulting hybrid having constitutive expression of the desired phenotypic characteristic identified. Two or more generations may be grown to ensure that expression of the desired phenotypic characteristic is stably maintained and inherited and then seeds harvested to ensure expression of the desired phenotypic characteristic has been achieved. In this manner, the present invention provides transformed seed (also referred to as "transgenic seed") having a nucleotide construct of the invention, for example, an expression cassette of the invention, stably incorporated into their genome.

Alternatively, cells that have been transformed may be introduced into an organism. These cells could have originated from the organism, wherein the cells are transformed in an *ex vivo* approach.

The sequences provided herein may be used for transformation of any plant species, including, but not limited to, monocots and dicots. Examples of plants of interest include, but are not limited to, corn (maize), sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape, Brassica sp., alfalfa, rye, millet, safflower, peanuts, sweet potato, cassava, coffee, coconut, pineapple, citrus trees, cocoa, tea, banana, avocado, fig, guava, mango, olive, papaya, cashew, macadamia, almond, oats, vegetables, ornamentals, and conifers.

Vegetables include, but are not limited to, tomatoes, lettuce, green beans, lima beans, peas, and members of the genus *Curcumis* such as cucumber, cantaloupe, and musk melon. Ornamentals include, but are not limited to, azalea, hydrangea, hibiscus, roses, tulips, daffodils, petunias, carnation, poinsettia, and chrysanthemum. Preferably, plants of the present invention are crop plants (for example, maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, oilseed rape, etc.).

As used herein, the term plant includes plant cells, plant protoplasts, plant cell tissue cultures from which plants can be regenerated, plant calli, plant clumps, and plant cells that are intact in plants or parts of plants such as embryos, pollen, ovules, seeds, leaves, flowers, branches, fruit, kernels, ears,

cobs, husks, stalks, roots, root tips, anthers, and the like. Grain is intended to mean the mature seed produced by commercial growers for purposes other than growing or reproducing the species. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the introduced polynucleotides. Further provided is a processed plant product or byproduct that retains the sequences disclosed herein, including for example, soymeal.

The polynucleotides encoding the RGNs, crRNAs, and/or tracrRNAs or comprising the crRNAs and/or tracrRNAs can also be used to transform any prokaryotic species, including but not limited to, archaea and bacteria (e.g., *Bacillus* sp., *Klebsiella* sp., *Streptomyces* sp., *Rhizobium* sp., *Escherichia* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Vibrio* sp., *Yersinia* sp., *Mycoplasma* sp., *Agrobacterium*, *Lactobacillus* sp.).

The polynucleotides encoding the RGNs, crRNAs, and/or tracrRNAs or comprising the crRNAs and/or tracrRNAs can be used to transform any eukaryotic species, including but not limited to animals (e.g., mammals, insects, fish, birds, and reptiles), fungi, amoeba, algae, and yeast.

Conventional viral and non-viral based gene transfer methods can be used to introduce nucleic acids in mammalian, insect, or avian cells or target tissues. Such methods can be used to administer nucleic acids encoding components of an RGN system to cells in culture, or in a host organism. Non-viral vector delivery systems include DNA plasmids, RNA (e.g. a transcript of a vector described herein), naked nucleic acid, and nucleic acid complexed with a delivery vehicle, such as a liposome. Viral vector delivery systems include DNA and RNA viruses, which have either episomal or integrated genomes after delivery to the cell. For a review of gene therapy procedures, see Anderson, Science 256: 808- 813 (1992); Nabel & Feigner, TIBTECH 11:211-217 (1993); Mitani & Caskey, TIBTECH 11:162-166 (1993); Dillon, TIBTECH 11:167-175 (1993); Miller, Nature 357:455-460 (1992); Van Brunt, Biotechnology 6(10): 1149-1154 (1988); Vigne, Restorative Neurology and Neuroscience 8:35-36 (1995); Kremer & Perricaudet, British Medical Bulletin 51(1):31-44 (1995); Haddada et al., in Current Topics in Microbiology and Immunology, Doerfler and Bohm (eds) (1995); and Yu et al., Gene Therapy 1:13-26 (1994).

Methods of non-viral delivery of nucleic acids include lipofection, nucleofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipid: nucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., TransfectamTM and LipofectinTM). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Feigner, WO 91/17424; WO 91/16024. Delivery can be to cells (e.g. in vitro or ex vivo administration) or target tissues (e.g. in vivo administration). The preparation of lipid:nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science 270:404-410 (1995); Blaese et al., Cancer Gene Ther. 2:291- 297 (1995); Behr et al.,

Bioconjugate Chem. 5:382-389 (1994); Remy et al., Bioconjugate Chem. 5:647-654 (1994); Gao et al., Gene Therapy 2:710-722 (1995); Ahmad et al., Cancer Res. 52:4817-4820 (1992); U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

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

 The tropism of a retrovirus can be altered by incorporating foreign envelope proteins,
15 expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system would therefore depend on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors,
20 which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Widely used retroviral vectors include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., J. Viral. 66:2731-2739 (1992); Johann et al., J. Viral. 66:1635-1640 (1992); Sommnerfelt et al., Viral. 176:58-59 (1990);
25 Wilson et al., J. Viral. 63:2374-2378 (1989); Miller et al., J. Viral. 65:2220-2224 (1991); PCT/US94/05700).

 In applications where transient expression is preferred, adenoviral based systems may be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division. With such vectors, high titer and levels of expression have been
30 obtained. This vector can be produced in large quantities in a relatively simple system. Adeno-associated virus ("AAV") vectors may also be used to transduce cells with target nucleic acids, e.g., in the in vitro production of nucleic acids and peptides, and for in vivo and ex vivo gene therapy procedures (see, e.g., West et al., Virology 160:38-47 (1987); U.S. Pat. No. 4,797,368; WO 93/24641; Katin, Human Gene Therapy 5:793-801 (1994); Muzyczka, J. Clin. Invest. 94:1351
35 (1994). Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173,414; Tratschin et al., Mol. Cell. Biol. 5:3251-3260 (1985); Tratschin, et al., Mol. Cell. Biol. 4:2072-2081 (1984); Hermonat & Muzyczka, PNAS 81:6466-6470

(1984); and Samulski et al., *J. Viral.* 63:03822-3828 (1989). Packaging cells are typically used to form virus particles that are capable of infecting a host cell. Such cells include 293 cells, which package adenovirus, and ψ J2 cells or PA317 cells, which package retrovirus.

Viral vectors used in gene therapy are usually generated by producing a cell line that packages a nucleic acid vector into a viral particle. The vectors typically contain the minimal viral sequences required for packaging and subsequent integration into a host, other viral sequences being replaced by an expression cassette for the polynucleotide(s) to be expressed. The missing viral functions are typically supplied in trans by the packaging cell line. For example, AAV vectors used in gene therapy typically only possess ITR sequences from the AAV genome which are required for packaging and integration into the host genome. Viral DNA is packaged in a cell line, which contains a helper plasmid encoding the other AAV genes, namely rep and cap, but lacking ITR sequences.

The cell line may also be infected with adenovirus as a helper. The helper virus promotes replication of the AAV vector and expression of AAV genes from the helper plasmid. The helper plasmid is not packaged in significant amounts due to a lack of ITR sequences. Contamination with adenovirus can be reduced by, e.g., heat treatment to which adenovirus is more sensitive than AAV. Additional methods for the delivery of nucleic acids to cells are known to those skilled in the art. See, for example, US20030087817, incorporated herein by reference.

In some embodiments, a host cell is transiently or non-transiently transfected with one or more vectors described herein. In some embodiments, a cell is transfected as it naturally occurs in a subject. In some embodiments, a cell that is transfected is taken from a subject. In some embodiments, the cell is derived from cells taken from a subject, such as a cell line. In some embodiments, the cell line may be mammalian, insect, or avian cells. A wide variety of cell lines for tissue culture are known in the art. Examples of cell lines include, but are not limited to, C8161, CCRF-CEM, MOLT, mIMCD-3, NHDF, HeLaS3, Huhl, Huh4, Huh7, HUVEC, HASMC, HEKn, HEKa, MiaPaCell, Panel, PC-3, TFI, CTLL-2, CIR, Rat6, CVI, RPTE, AIO, T24, 182, A375, ARH-77, Calul, SW480, SW620, SKOV3, SK-UT, CaCo2, P388D1, SEM-K2, WEHI- 231, HB56, TIB55, lurkat, 145.01, LRMB, Bcl-1, BC-3, IC21, DLD2, Raw264.7, NRK, NRK-52E, MRC5, MEF, Hep G2, HeLa B, HeLa T4. COS, COS-1, COS-6, COS-M6A, BS-C-1 monkey kidney epithelial, BALB/3T3 mouse embryo fibroblast, 3T3 Swiss, 3T3-L1, 132-d5 human fetal fibroblasts; 10.1 mouse fibroblasts, 293-T, 3T3, 721, 9L, A2780, A2780ADR, A2780cis, A172, A20, A253, A431, A-549, ALC, B16, B35, BCP-I cells, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C3H-10T1/2, C6/36, Cal-27, CHO, CHO-7, CHO-IR, CHO-K1, CHO-K2, CHO-T, CHO Dhfr^{-/-}, COR-L23, COR-L23/CPR, COR-L235010, CORL23/ R23, COS-7, COV-434, CML T1, CMT, CT26, D17, DH82, DU145, DuCaP, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, HEK-293, HeLa, Hepalclc7, HL-60, HMEC, HT-29, lurkat, *IY* cells, K562 cells, Ku812, KCL22, KGI, KYOI, LNCap, Ma-Mel 1-48, MC-38, MCF-7, MCF-10A, MDA-MB-231, MDA-MB-468, MDA-MB-435, MDCKII, MDCKII, MOR/ 0.2R, MONO-MAC 6, MTD-1A, MyEnd, NCI-H69/CPR,

NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NALM-1, NW-145, OPCN/OPCT cell lines, Peer, PNT-1A/ PNT 2, RenCa, RIN-5F, RMA/RMAS, Saos-2 cells, Sf-9, SkBr3, T2, T-47D, T84, THP1 cell line, U373, U87, U937, VCaP, Vero cells, WM39, WT-49, X63, YAC-1, YAR, and transgenic varieties thereof. Cell lines are available from a variety of sources known to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassas, Va.)).

In some embodiments, a cell transfected with one or more vectors described herein is used to establish a new cell line comprising one or more vector-derived sequences. In some embodiments, a cell transiently transfected with the components of an RGN system as described herein (such as by transient transfection of one or more vectors, or transfection with RNA), and modified through the activity of an RGN system, is used to establish a new cell line comprising cells containing the modification but lacking any other exogenous sequence. In some embodiments, cells transiently or non-transiently transfected with one or more vectors described herein, or cell lines derived from such cells are used in assessing one or more test compounds.

In some embodiments, one or more vectors described herein are used to produce a non-human transgenic animal or transgenic plant. In some embodiments, the transgenic animal is a mammal, such as a mouse, rat, hamster, rabbit, cow, or pig. In some embodiments, the transgenic animal is a bird, such as a chicken or a duck. In some embodiments, the transgenic animal is an insect, such as a mosquito or a tick.

V. Variants and Fragments of Polypeptides and Polynucleotides

The present disclosure provides active variants and fragments of a naturally-occurring (*i.e.*, wild-type) RNA-guided nuclease, the amino acid sequence of which is set forth as any one of SEQ ID NOs: 1-12, as well as active variants and fragments of naturally-occurring CRISPR repeats, such as any one of the sequences set forth as SEQ ID NOs: 13-24, and active variant and fragments of naturally-occurring tracrRNAs, such as any one of the sequences set forth as SEQ ID NOs: 25-36, and polynucleotides encoding the same.

While the activity of a variant or fragment may be altered compared to the polynucleotide or polypeptide of interest, the variant and fragment should retain the functionality of the polynucleotide or polypeptide of interest. For example, a variant or fragment may have increased activity, decreased activity, different spectrum of activity or any other alteration in activity when compared to the polynucleotide or polypeptide of interest.

Fragments and variants of naturally-occurring RGN polypeptides, such as those disclosed herein, will retain sequence-specific, RNA-guided DNA-binding activity. In particular embodiments, fragments and variants of naturally-occurring RGN polypeptides, such as those disclosed herein, will retain nuclease activity (single-stranded or double-stranded).

Fragments and variants of naturally-occurring CRISPR repeats, such as those disclosed herein, will retain the ability, when part of a guide RNA (comprising a tracrRNA), to bind to and

guide an RNA-guided nuclease (complexed with the guide RNA) to a target nucleotide sequence in a sequence-specific manner.

Fragments and variants of naturally-occurring tracrRNAs, such as those disclosed herein, will retain the ability, when part of a guide RNA (comprising a CRISPR RNA), to guide an RNA-guided
5 nuclease (complexed with the guide RNA) to a target nucleotide sequence in a sequence-specific manner.

The term "fragment" refers to a portion of a polynucleotide or polypeptide sequence of the invention. "Fragments" or "biologically active portions" include polynucleotides comprising a sufficient number of contiguous nucleotides to retain the biological activity (*i.e.*, binding to and
10 directing an RGN in a sequence-specific manner to a target nucleotide sequence when comprised within a guide RNA). "Fragments" or "biologically active portions" include polypeptides comprising a sufficient number of contiguous amino acid residues to retain the biological activity (*i.e.*, binding to a target nucleotide sequence in a sequence-specific manner when complexed with a guide RNA).

Fragments of the RGN proteins include those that are shorter than the full-length sequences due to the
15 use of an alternate downstream start site. A biologically active portion of an RGN protein can be a polypeptide that comprises, for example, 10, 25, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700 or more contiguous amino acid residues of any one of SEQ ID NOs: 1-12. Such biologically active portions can be prepared by recombinant techniques and evaluated for
20 sequence-specific, RNA-guided DNA-binding activity. A biologically active fragment of a CRISPR repeat sequence can comprise at least 8 contiguous amino acids of any one of SEQ ID NOs:13-24. A biologically active portion of a CRISPR repeat sequence can be a polynucleotide that comprises, for example, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 contiguous nucleotides of any one of SEQ ID NOs: 13-24. A biologically active portion of a tracrRNA can be a polynucleotide
25 that comprises, for example, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more contiguous nucleotides of any one of SEQ ID NOs:25-36.

In general, "variants" is intended to mean substantially similar sequences. For polynucleotides, a variant comprises a deletion and/or addition of one or more nucleotides at one or
30 more internal sites within the native polynucleotide and/or a substitution of one or more nucleotides at one or more sites in the native polynucleotide. As used herein, a "native" or "wild type" polynucleotide or polypeptide comprises a naturally occurring nucleotide sequence or amino acid sequence, respectively. For polynucleotides, conservative variants include those sequences that, because of the degeneracy of the genetic code, encode the native amino acid sequence of the gene of
35 interest. Naturally occurring allelic variants such as these can be identified with the use of well-known molecular biology techniques, as, for example, with polymerase chain reaction (PCR) and hybridization techniques as outlined below. Variant polynucleotides also include synthetically

derived polynucleotides, such as those generated, for example, by using site-directed mutagenesis but which still encode the polypeptide or the polynucleotide of interest. Generally, variants of a particular polynucleotide disclosed herein will have at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity to that particular polynucleotide as determined by sequence alignment programs and parameters described elsewhere herein.

Variants of a particular polynucleotide disclosed herein (*i.e.*, the reference polynucleotide) can also be evaluated by comparison of the percent sequence identity between the polypeptide encoded by a variant polynucleotide and the polypeptide encoded by the reference polynucleotide.

Percent sequence identity between any two polypeptides can be calculated using sequence alignment programs and parameters described elsewhere herein. Where any given pair of polynucleotides disclosed herein is evaluated by comparison of the percent sequence identity shared by the two polypeptides they encode, the percent sequence identity between the two encoded polypeptides is at least about 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more sequence identity.

In particular embodiments, the presently disclosed polynucleotides encode an RNA-guided nuclease polypeptide comprising an amino acid sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater identity to any one of the amino acid sequences set forth as SEQ ID NOs: 1-12.

A biologically active variant of an RGN polypeptide of the invention may differ by as few as about 1-15 amino acid residues, as few as about 1-10, such as about 6-10, as few as 5, as few as 4, as few as 3, as few as 2, or as few as 1 amino acid residue. In specific embodiments, the polypeptides can comprise an N-terminal or a C-terminal truncation, which can comprise at least a deletion of 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700 amino acids or more from either the N or C terminus of the polypeptide.

In certain embodiments, the presently disclosed polynucleotides comprise or encode a CRISPR repeat comprising a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater identity to any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24.

The presently disclosed polynucleotides can comprise or encode a tracrRNA comprising a nucleotide sequence having at least 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or greater identity to any one of the nucleotide sequences set forth as SEQ ID NOs: 25-36.

Biologically active variants of a CRISPR repeat or tracrRNA of the invention may differ by as few as about 1-15 nucleotides, as few as about 1-10, such as about 6-10, as few as 5, as few as 4, as few as 3, as few as 2, or as few as 1 nucleotide. In specific embodiments, the polynucleotides can comprise a 5' or 3' truncation, which can comprise at least a deletion of 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 90, 95, 100, 105, 110 nucleotides or more from either the 5' or 3' end of the polynucleotide.

It is recognized that modifications may be made to the RGN polypeptides, CRISPR repeats, and tracrRNAs provided herein creating variant proteins and polynucleotides. Changes designed by man may be introduced through the application of site-directed mutagenesis techniques. Alternatively, native, as yet-unknown or as yet unidentified polynucleotides and/or polypeptides structurally and/or functionally-related to the sequences disclosed herein may also be identified that fall within the scope of the present invention. Conservative amino acid substitutions may be made in nonconserved regions that do not alter the function of the RGN proteins. Alternatively, modifications may be made that improve the activity of the RGN.

Variant polynucleotides and proteins also encompass sequences and proteins derived from a mutagenic and recombinogenic procedure such as DNA shuffling. With such a procedure, one or more different RGN proteins disclosed herein (e.g., SEQ ID NOs: 1-12) is manipulated to create a new RGN protein possessing the desired properties. In this manner, libraries of recombinant polynucleotides are generated from a population of related sequence polynucleotides comprising sequence regions that have substantial sequence identity and can be homologously recombined *in vitro* or *in vivo*. For example, using this approach, sequence motifs encoding a domain of interest may be shuffled between the RGN sequences provided herein and other known RGN genes to obtain a new gene coding for a protein with an improved property of interest, such as an increased K_m in the case of an enzyme. Strategies for such DNA shuffling are known in the art. See, for example, Stemmer (1994) *Proc. Natl. Acad. Sci. USA* 91:10747-10751; Stemmer (1994) *Nature* 370:389-391; Cramer *et al.* (1997) *Nature Biotech.* 15:436-438; Moore *et al.* (1997) *J. Mol. Biol.* 272:336-347; Zhang *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Cramer *et al.* (1998) *Nature* 391:288-291; and U.S. Patent Nos. 5,605,793 and 5,837,458. A "shuffled" nucleic acid is a nucleic acid produced by a shuffling procedure such as any shuffling procedure set forth herein. Shuffled nucleic acids are produced by recombining (physically or virtually) two or more nucleic acids (or character strings), for example in an artificial, and optionally recursive, fashion. Generally, one or more screening steps are used in shuffling processes to identify nucleic acids of interest; this screening step can be performed before or after any recombination step. In some (but not all) shuffling embodiments, it is desirable to perform multiple rounds of recombination prior to selection to increase the diversity of the pool to be screened. The overall process of recombination and selection are optionally repeated recursively. Depending on context, shuffling can refer to an overall process of recombination and selection, or, alternately, can simply refer to the recombinational portions of the overall process.

As used herein, "sequence identity" or "identity" in the context of two polynucleotides or polypeptide sequences makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence over a specified comparison window. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (*e.g.*, charge or hydrophobicity) and therefore do not change the functional properties of the molecule. When sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences that differ by such conservative substitutions are said to have "sequence similarity" or "similarity". Means for making this adjustment are well known to those of skill in the art. Typically, this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, *e.g.*, as implemented in the program PC/GENE (Intelligenetics, Mountain View, California).

As used herein, "percentage of sequence identity" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity.

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using GAP Version 10 using the following parameters: % identity and % similarity for a nucleotide sequence using GAP Weight of 50 and Length Weight of 3, and the nwsgapdna.cmp scoring matrix; % identity and % similarity for an amino acid sequence using GAP Weight of 8 and Length Weight of 2, and the BLOSUM62 scoring matrix; or any equivalent program thereof. By "equivalent program" is intended any sequence comparison program that, for any two sequences in question, generates an alignment having identical nucleotide or amino acid residue matches and an identical percent sequence identity when compared to the corresponding alignment generated by GAP Version 10.

Two sequences are "optimally aligned" when they are aligned for similarity scoring using a defined amino acid substitution matrix (*e.g.*, BLOSUM62), gap existence penalty and gap extension penalty so as to arrive at the highest score possible for that pair of sequences. Amino acid substitution

matrices and their use in quantifying the similarity between two sequences are well-known in the art and described, *e.g.*, in Dayhoff et al. (1978) "A model of evolutionary change in proteins." In "Atlas of Protein Sequence and Structure," Vol. 5, Suppl. 3 (ed. M. O. Dayhoff), pp. 345-352. Natl. Biomed. Res. Found., Washington, D.C. and Henikoff et al. (1992) Proc. Natl. Acad. Sci. USA 89:10915-10919. The BLOSUM62 matrix is often used as a default scoring substitution matrix in sequence alignment protocols. The gap existence penalty is imposed for the introduction of a single amino acid gap in one of the aligned sequences, and the gap extension penalty is imposed for each additional empty amino acid position inserted into an already opened gap. The alignment is defined by the amino acid positions of each sequence at which the alignment begins and ends, and optionally by the insertion of a gap or multiple gaps in one or both sequences, so as to arrive at the highest possible score. While optimal alignment and scoring can be accomplished manually, the process is facilitated by the use of a computer-implemented alignment algorithm, *e.g.*, gapped BLAST 2.0, described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, and made available to the public at the National Center for Biotechnology Information Website (www.ncbi.nlm.nih.gov). Optimal alignments, including multiple alignments, can be prepared using, *e.g.*, PSI-BLAST, available through www.ncbi.nlm.nih.gov and described by Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402.

With respect to an amino acid sequence that is optimally aligned with a reference sequence, an amino acid residue "corresponds to" the position in the reference sequence with which the residue is paired in the alignment. The "position" is denoted by a number that sequentially identifies each amino acid in the reference sequence based on its position relative to the N-terminus. Owing to deletions, insertion, truncations, fusions, etc., that must be taken into account when determining an optimal alignment, in general the amino acid residue number in a test sequence as determined by simply counting from the N-terminal will not necessarily be the same as the number of its corresponding position in the reference sequence. For example, in a case where there is a deletion in an aligned test sequence, there will be no amino acid that corresponds to a position in the reference sequence at the site of deletion. Where there is an insertion in an aligned reference sequence, that insertion will not correspond to any amino acid position in the reference sequence. In the case of truncations or fusions there can be stretches of amino acids in either the reference or aligned sequence that do not correspond to any amino acid in the corresponding sequence.

VI. Antibodies

Antibodies to the RGN polypeptides or ribonucleoproteins comprising the RGN polypeptides of the present invention, including those having any one of the amino acid sequences set forth as SEQ ID NOs: 1-12 or active variants or fragments thereof, are also encompassed. Methods for producing antibodies are well known in the art (see, for example, Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.; and U.S. Pat. No. 4,196,265). These antibodies can be used in kits for the detection and isolation of RGN polypeptides

or ribonucleoproteins. Thus, this disclosure provides kits comprising antibodies that specifically bind to the polypeptides or ribonucleoproteins described herein, including, for example, polypeptides having any one of the amino acid sequences set forth as SEQ ID NOs: 1-12.

5 *VII. Systems and Ribonucleoprotein Complexes for Binding a Target Sequence of Interest and Methods of Making the Same*

The present disclosure provides a system for binding a target sequence of interest, wherein the system comprises at least one guide RNA or a nucleotide sequence encoding the same, and at least one RNA-guided nuclease or a nucleotide sequence encoding the same. The guide RNA hybridizes to
10 the target sequence of interest and also forms a complex with the RGN polypeptide, thereby directing the RGN polypeptide to bind to the target sequence. In some of these embodiments, the RGN comprises any one of the amino acid sequences set forth as SEQ ID NOs: 1-12, or an active variant or fragment thereof. In various embodiments, the guide RNA comprises a CRISPR repeat sequence comprising any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24, or an active variant
15 or fragment thereof. In particular embodiments, the guide RNA comprises a tracrRNA comprising any one of the nucleotide sequences set forth as SEQ ID NOs: 25-36, or an active variant or fragment thereof. The guide RNA of the system can be a single guide RNA or a dual-guide RNA. In particular embodiments, the system comprises an RNA-guided nuclease that is heterologous to the guide RNA, wherein the RGN and guide RNA are not found complexed to one another (i.e., bound to one another)
20 in nature.

The system for binding a target sequence of interest provided herein can be a ribonucleoprotein complex, which is at least one molecule of an RNA bound to at least one protein. The ribonucleoprotein complexes provided herein comprise at least one guide RNA as the RNA component and an RNA-guided nuclease as the protein component. Such ribonucleoprotein
25 complexes can be purified from a cell or organism that naturally expresses an RGN polypeptide and has been engineered to express a particular guide RNA that is specific for a target sequence of interest. Alternatively, the ribonucleoprotein complex can be purified from a cell or organism that has been transformed with polynucleotides that encode an RGN polypeptide and a guide RNA and cultured under conditions to allow for the expression of the RGN polypeptide and guide RNA. Thus,
30 methods are provided for making an RGN polypeptide or an RGN ribonucleoprotein complex. Such methods comprise culturing a cell comprising a nucleotide sequence encoding an RGN polypeptide, and in some embodiments a nucleotide sequence encoding a guide RNA, under conditions in which the RGN polypeptide (and in some embodiments, the guide RNA) is expressed. The RGN polypeptide or RGN ribonucleoprotein can then be purified from a lysate of the cultured cells. In
35 embodiments, the nucleotide sequence encoding an RGN polypeptide includes a mRNA (messenger RNA). In some embodiments, methods for assembling an RNP complex comprise combining one or

more of the presently disclosed guide RNAs and one or more of the presently disclosed RGN polypeptides under conditions suitable for formation of the RNP complex.

Methods for purifying an RGN polypeptide or RGN ribonucleoprotein complex from a lysate of a biological sample are known in the art (*e.g.*, size exclusion and/or affinity chromatography, 2D-PAGE, HPLC, reversed-phase chromatography, immunoprecipitation). In particular methods, the RGN polypeptide is recombinantly produced and comprises a purification tag to aid in its purification, including but not limited to, glutathione-S-transferase (GST), chitin binding protein (CBP), maltose binding protein, thioredoxin (TRX), poly(NANP), tandem affinity purification (TAP) tag, myc, AcV5, AU1, AU5, E, ECS, E2, FLAG (*e.g.*, 3X FLAG tag), HA, nus, Softag 1, Softag 3, Strep, SBP, Glu-Glu, HSV, KT3, S, S1, T7, V5, VSV-G, 6xHis, 10xHis, biotin carboxyl carrier protein (BCCP), and calmodulin. Generally, the tagged RGN polypeptide or RGN ribonucleoprotein complex is purified using immobilized metal affinity chromatography. It will be appreciated that other similar methods known in the art may be used, including other forms of chromatography or for example immunoprecipitation, either alone or in combination.

An "isolated" or "purified" polypeptide, or biologically active portion thereof, is substantially or essentially free from components that normally accompany or interact with the polypeptide as found in its naturally occurring environment. Thus, an isolated or purified polypeptide is substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized. A protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of contaminating protein. When the protein of the invention or biologically active portion thereof is recombinantly produced, optimally culture medium represents less than about 30%, 20%, 10%, 5%, or 1% (by dry weight) of chemical precursors or non-protein-of-interest chemicals. Similarly, an "isolated" polynucleotide or nucleic acid molecule is removed from its naturally occurring environment. An isolated polynucleotide is substantially free of chemical precursors or other chemicals when chemically synthesized or has been removed from a genomic locus via the breaking of phosphodiester bonds. An isolated polynucleotide can be part of a vector, a composition of matter or can be contained within a cell so long as the cell is not the original environment of the polynucleotide.

Particular methods provided herein for binding and/or cleaving a target sequence of interest involve the use of an *in vitro* assembled RGN ribonucleoprotein complex. *In vitro* assembly of an RGN ribonucleoprotein complex can be performed using any method known in the art in which an RGN polypeptide is contacted with a guide RNA under conditions to allow for binding of the RGN polypeptide to the guide RNA. As used herein, "contact", "contacting", "contacted," refer to placing the components of a desired reaction together under conditions suitable for carrying out the desired reaction. The RGN polypeptide can be purified from a biological sample, cell lysate, or culture medium, produced via *in vitro* translation, or chemically synthesized. The guide RNA can be purified

from a biological sample, cell lysate, or culture medium, transcribed *in vitro*, or chemically synthesized. The RGN polypeptide and guide RNA can be brought into contact in solution (*e.g.*, buffered saline solution) to allow for *in vitro* assembly of the RGN ribonucleoprotein complex.

5 VIII. Methods of Binding, Cleaving, or Modifying a Target Sequence

The present disclosure provides methods for binding, cleaving, and/or modifying a target nucleotide sequence of interest. The methods include delivering a system comprising at least one guide RNA or a polynucleotide encoding the same, and at least one RGN polypeptide or a polynucleotide encoding the same to the target sequence or a cell, organelle, or embryo comprising
10 the target sequence. In some of these embodiments, the RGN comprises any one of the amino acid sequences set forth as SEQ ID NOs: 1-12, or an active variant or fragment thereof. In various embodiments, the guide RNA comprises a CRISPR repeat sequence comprising any one of the nucleotide sequences set forth as SEQ ID NOs: 13-24, or an active variant or fragment thereof. In particular embodiments, the guide RNA comprises a tracrRNA comprising any one of the nucleotide
15 sequences set forth as SEQ ID NOs: 25-36, or an active variant or fragment thereof. The guide RNA of the system can be a single guide RNA or a dual-guide RNA.

The RGN of the system may be a nuclease dead RGN, have nickase activity, or may be a fusion polypeptide. In some embodiments, the fusion polypeptide comprises a base-editing polypeptide, for example a cytosine deaminase or an adenine deaminase. In other embodiments, the
20 RGN fusion protein comprises a reverse transcriptase. In other embodiments, the RGN fusion protein comprises a polypeptide that recruits members of a functional nucleic acid repair complex, such as a member of the nucleotide excision repair (NER) or transcription coupled-nucleotide excision repair (TC-NER) pathway (Wei *et al.*, 2015, *PNAS USA* 112(27):E3495-504 ; Troelstra *et al.*, 1992, *Cell* 71:939-953; Marnef *et al.*, 2017, *J Mol Biol* 429(9):1277-1288), as described in U.S. Provisional
25 Application No. 62/966,203, which was filed on January 27, 2020, and is incorporated by reference in its entirety. In some embodiments, the RGN fusion protein comprises CSB (van den Boom *et al.*, 2004, *J Cell Biol* 166(1):27-36; van Gool *et al.*, 1997, *EMBO J* 16(19):5955-65; an example of which is set forth as SEQ ID NO: 324), which is a member of the TC-NER (nucleotide excision repair) pathway and functions in the recruitment of other members. In further embodiments, the RGN fusion
30 protein comprises an active domain of CSB, such as the acidic domain of CSB which comprises amino acid residues 356-394 of SEQ ID NO: 324 (Teng *et al.*, 2018, *Nat Commun* 9(1):4115).

In particular embodiments, the RGN and/or guide RNA is heterologous to the cell, organelle, or embryo to which the RGN and/or guide RNA (or polynucleotide(s) encoding at least one of the RGN and guide RNA) are introduced.

35 In those embodiments wherein the method comprises delivering a polynucleotide encoding a guide RNA and/or an RGN polypeptide, the cell or embryo can then be cultured under conditions in which the guide RNA and/or RGN polypeptide are expressed. In various embodiments, the method

comprises contacting a target sequence with an RGN ribonucleoprotein complex. The RGN ribonucleoprotein complex may comprise an RGN that is nuclease dead or has nickase activity. In some embodiments, the RGN of the ribonucleoprotein complex is a fusion polypeptide comprising a base-editing polypeptide. In certain embodiments, the method comprises introducing into a cell, organelle, or embryo comprising a target sequence an RGN ribonucleoprotein complex. The RGN ribonucleoprotein complex can be one that has been purified from a biological sample, recombinantly produced and subsequently purified, or *in vitro*-assembled as described herein. In those embodiments wherein the RGN ribonucleoprotein complex that is contacted with the target sequence or a cell organelle, or embryo has been assembled *in vitro*, the method can further comprise the *in vitro* assembly of the complex prior to contact with the target sequence, cell, organelle, or embryo.

A purified or *in vitro* assembled RGN ribonucleoprotein complex can be introduced into a cell, organelle, or embryo using any method known in the art, including, but not limited to electroporation. Alternatively, an RGN polypeptide and/or polynucleotide encoding or comprising the guide RNA can be introduced into a cell, organelle, or embryo using any method known in the art (*e.g.*, electroporation).

Upon delivery to or contact with the target sequence or cell, organelle, or embryo comprising the target sequence, the guide RNA directs the RGN to bind to the target sequence in a sequence-specific manner. In those embodiments wherein the RGN has nuclease activity, the RGN polypeptide cleaves the target sequence of interest upon binding. The target sequence can subsequently be modified via endogenous repair mechanisms, such as non-homologous end joining, or homology-directed repair with a provided donor polynucleotide.

Methods to measure binding of an RGN polypeptide to a target sequence are known in the art and include chromatin immunoprecipitation assays, gel mobility shift assays, DNA pull-down assays, reporter assays, microplate capture and detection assays. Likewise, methods to measure cleavage or modification of a target sequence are known in the art and include *in vitro* or *in vivo* cleavage assays wherein cleavage is confirmed using PCR, sequencing, or gel electrophoresis, with or without the attachment of an appropriate label (*e.g.*, radioisotope, fluorescent substance) to the target sequence to facilitate detection of degradation products. Alternatively, the nicking triggered exponential amplification reaction (NTEXPAR) assay can be used (see, *e.g.*, Zhang et al. (2016) *Chem. Sci.* 7:4951-4957). *In vivo* cleavage can be evaluated using the Surveyor assay (Guschin et al. (2010) *Methods Mol Biol* 649:247-256).

In some embodiments, the methods involve the use of a single type of RGN complexed with more than one guide RNA. The more than one guide RNA can target different regions of a single gene or can target multiple genes.

In those embodiments wherein a donor polynucleotide is not provided, a double-stranded break introduced by an RGN polypeptide can be repaired by a non-homologous end-joining (NHEJ) repair process. Due to the error-prone nature of NHEJ, repair of the double-stranded break can result

in a modification to the target sequence. As used herein, a “modification” in reference to a nucleic acid molecule refers to a change in the nucleotide sequence of the nucleic acid molecule, which can be a deletion, insertion, or substitution of one or more nucleotides, or a combination thereof.

Modification of the target sequence can result in the expression of an altered protein product or inactivation of a coding sequence.

In those embodiments wherein a donor polynucleotide is present, the donor sequence in the donor polynucleotide can be integrated into or exchanged with the target nucleotide sequence during the course of repair of the introduced double-stranded break, resulting in the introduction of the exogenous donor sequence. A donor polynucleotide thus comprises a donor sequence that is desired to be introduced into a target sequence of interest. In some embodiments, the donor sequence alters the original target nucleotide sequence such that the newly integrated donor sequence will not be recognized and cleaved by the RGN. Integration of the donor sequence can be enhanced by the inclusion within the donor polynucleotide of flanking sequences, referred to herein as “homology arms” that have substantial sequence identity with the sequences flanking the target nucleotide sequence, allowing for a homology-directed repair process. In some embodiments, homology arms have a length of at least 50 base pairs, at least 100 base pairs, and up to 2000 base pairs or more, and have at least 90%, at least 95%, or more, sequence homology to their corresponding sequence within the target nucleotide sequence.

In those embodiments wherein the RGN polypeptide introduces double-stranded staggered breaks, the donor polynucleotide can comprise a donor sequence flanked by compatible overhangs, allowing for direct ligation of the donor sequence to the cleaved target nucleotide sequence comprising overhangs by a non-homologous repair process during repair of the double-stranded break.

In those embodiments wherein the method involves the use of an RGN that is a nickase (*i.e.*, is only able to cleave a single strand of a double-stranded polynucleotide), the method can comprise introducing two RGN nickases that target identical or overlapping target sequences and cleave different strands of the polynucleotide. For example, an RGN nickase that only cleaves the positive (+) strand of a double-stranded polynucleotide can be introduced along with a second RGN nickase that only cleaves the negative (-) strand of a double-stranded polynucleotide.

In various embodiments, a method is provided for binding a target nucleotide sequence and detecting the target sequence, wherein the method comprises introducing into a cell, organelle, or embryo at least one guide RNA or a polynucleotide encoding the same, and at least one RGN polypeptide or a polynucleotide encoding the same, expressing the guide RNA and/or RGN polypeptide (if coding sequences are introduced), wherein the RGN polypeptide is a nuclease-dead RGN and further comprises a detectable label, and the method further comprises detecting the detectable label. The detectable label may be fused to the RGN as a fusion protein (*e.g.*, fluorescent

protein) or may be a small molecule conjugated to or incorporated within the RGN polypeptide that can be detected visually or by other means.

Also provided herein are methods for modulating the expression of a target sequence or a gene of interest under the regulation of a target sequence. The methods comprise introducing into a cell, organelle, or embryo at least one guide RNA or a polynucleotide encoding the same, and at least one RGN polypeptide or a polynucleotide encoding the same, expressing the guide RNA and/or RGN polypeptide (if coding sequences are introduced), wherein the RGN polypeptide is a nuclease-dead RGN. In some of these embodiments, the nuclease-dead RGN is a fusion protein comprising an expression modulator domain (*i.e.*, epigenetic modification domain, transcriptional activation domain or a transcriptional repressor domain) as described herein.

The present disclosure also provides methods for binding and/or modifying a target nucleotide sequence of interest. The methods include delivering a system comprising at least one guide RNA or a polynucleotide encoding the same, and at least one fusion polypeptide comprises an RGN of the invention and a base-editing polypeptide, for example a cytosine deaminase or an adenine deaminase, or a polynucleotide encoding the fusion polypeptide, to the target sequence or a cell, organelle, or embryo comprising the target sequence.

One of ordinary skill in the art will appreciate that any of the presently disclosed methods can be used to target a single target sequence or multiple target sequences. Thus, methods comprise the use of a single RGN polypeptide in combination with multiple, distinct guide RNAs, which can target multiple, distinct sequences within a single gene and/or multiple genes. Also encompassed herein are methods wherein multiple, distinct guide RNAs are introduced in combination with multiple, distinct RGN polypeptides. These guide RNAs and guide RNA/RGN polypeptide systems can target multiple, distinct sequences within a single gene and/or multiple genes.

In one aspect, the invention provides kits containing any one or more of the elements disclosed in the above methods and compositions. In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system comprises (a) a first regulatory element operably linked to a DNA sequence encoding the crRNA sequence and one or more insertion sites for inserting a guide sequence upstream of the encoded crRNA sequence, wherein when expressed, the guide sequence directs sequence-specific binding of an RGN complex to a target sequence in a eukaryotic cell, wherein the RGN complex comprises an RGN enzyme complexed with the guide RNA polynucleotide; and/or (b) a second regulatory element operably linked to an enzyme coding sequence encoding said RGN enzyme comprising a nuclear localization sequence. Elements may be provided individually or in combinations, and may be provided in any suitable container, such as a vial, a bottle, or a tube.

In some embodiments, the kit includes instructions in one or more languages. In some embodiments, a kit comprises one or more reagents for use in a process utilizing one or more of the elements described herein. Reagents may be provided in any suitable container. For example, a kit

may provide one or more reaction or storage buffers. Reagents may be provided in a form that is usable in a particular assay, or in a form that requires addition of one or more other components before use (e.g. in concentrate or lyophilized form). A buffer can be any buffer, including but not limited to a sodium carbonate buffer, a sodium bicarbonate buffer, a borate buffer, a Tris buffer, a MOPS buffer, a HEPES buffer, and combinations thereof. In some embodiments, the buffer is alkaline. In some embodiments, the buffer has a pH from about 7 to about 10.

In some embodiments, the kit comprises one or more oligonucleotides corresponding to a guide sequence for insertion into a vector so as to operably link the guide sequence and a regulatory element. In some embodiments, the kit comprises a homologous recombination template polynucleotide. In one aspect, the invention provides methods for using one or more elements of an RGN system. The RGN system of the invention provides an effective means for modifying a target polynucleotide. The RGN system of the invention has a wide variety of utility including modifying (e.g., deleting, inserting, translocating, inactivating, activating, base editing) a target polynucleotide in a multiplicity of cell types. As such the RGN system of the invention has a broad spectrum of applications in, e.g., gene therapy, drug screening, disease diagnosis, and prognosis. An exemplary RGN system, or RGN complex, comprises an RGN enzyme complexed with a guide sequence hybridized to a target sequence within the target polynucleotide.

IX. Target Polynucleotides

In one aspect, the invention provides for methods of modifying a target polynucleotide in a eukaryotic cell, which may be in vivo, ex vivo or in vitro. In some embodiments, the method comprises sampling a cell or population of cells from a human or non-human animal or plant (including microalgae) and modifying the cell or cells. Culturing may occur at any stage ex vivo. The cell or cells may even be re-introduced into the non-human animal or plant (including microalgae).

Using natural variability, plant breeders combine most useful genes for desirable qualities, such as yield, quality, uniformity, hardiness, and resistance against pests. These desirable qualities also include growth, day length preferences, temperature requirements, initiation date of floral or reproductive development, fatty acid content, insect resistance, disease resistance, nematode resistance, fungal resistance, herbicide resistance, tolerance to various environmental factors including drought, heat, wet, cold, wind, and adverse soil conditions including high salinity. The sources of these useful genes include native or foreign varieties, heirloom varieties, wild plant relatives, and induced mutations, e.g., treating plant material with mutagenic agents. Using the present invention, plant breeders are provided with a new tool to induce mutations. Accordingly, one skilled in the art can analyze the genome for sources of useful genes, and in varieties having desired characteristics or traits employ the present invention to induce the rise of useful genes, with more precision than previous mutagenic agents and hence accelerate and improve plant breeding programs.

The target polynucleotide of an RGN system can be any polynucleotide endogenous or exogenous to the eukaryotic cell. For example, the target polynucleotide can be a polynucleotide residing in the nucleus of the eukaryotic cell. The target polynucleotide can be a sequence coding a gene product (e.g., a protein) or a non-coding sequence (e.g., a regulatory polynucleotide or a junk DNA). Without wishing to be bound by theory, the target sequence should be associated with a PAM (protospacer adjacent motif); that is, a short sequence recognized by the RGN system. The precise sequence and length requirements for the PAM differ depending on the RGN used, but PAMs are typically 2-7 base pair sequences adjacent to the protospacer (that is, the target sequence).

The target polynucleotide of an RGN system may include a number of disease-associated genes and polynucleotides as well as signaling biochemical pathway-associated genes and polynucleotides. Examples of target polynucleotides include a sequence associated with a signaling biochemical pathway, e.g., a signaling biochemical pathway-associated gene or polynucleotide. Examples of target polynucleotides include a disease associated gene or polynucleotide. A "disease-associated" gene or polynucleotide refers to any gene or polynucleotide which is yielding transcription or translation products at an abnormal level or in an abnormal form in cells derived from a disease-affected tissues compared with tissues or cells of a non-disease control. It may be a gene that becomes expressed at an abnormally high level; it may be a gene that becomes expressed at an abnormally low level, where the altered expression correlates with the occurrence and/or progression of the disease. A disease-associated gene also refers to a gene possessing mutation(s) or genetic variation that is directly responsible or is in linkage disequilibrium with a gene(s) that is responsible for the etiology of a disease (e.g., a causal mutation). The causal mutation may be an expanded repeat (present at higher numbers than those in normal individuals) that leads to instability of transcribed mRNA, altered splicing, or instability of a translated product or a translated product with reduced activity. The transcribed or translated products may be known or unknown, and further may be at a normal or abnormal level. In some embodiments, the disease may be an animal disease. In some embodiments, the disease may be an avian disease. In other embodiments, the disease may be a mammalian disease. In further embodiments, the disease may be a human disease. Examples of disease-associated genes and polynucleotides in humans are provided in Table 6 and are also available from McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, Md.) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, Md.), available on the World Wide Web.

Although RGN systems are particularly useful for their relative ease in targeting to genomic sequences of interest, there still remains an issue of what the RGN can do to address a causal mutation. One approach is to produce a fusion protein between an RGN (preferably an inactive or nickase variant of the RGN) and a base-editing enzyme or the active domain of a base editing enzyme, such as a cytosine deaminase or an adenine deaminase base editor (U.S. Patent No. 9,840,699, herein incorporated by reference). In some embodiments, the methods comprise contacting a DNA molecule

with (a) a fusion protein comprising an RGN of the invention or a nickase variant thereof and a base-editing polypeptide such as a deaminase; and (b) a gRNA targeting the fusion protein of (a) to a target nucleotide sequence of the DNA strand; wherein the DNA molecule is contacted with the fusion protein and the gRNA in an amount effective and under conditions suitable for the deamination of a nucleobase. In some embodiments, the target DNA sequence comprises a sequence associated with a disease or disorder, and wherein the deamination of the nucleobase results in a sequence that is not associated with a disease or disorder. In some embodiments, the target DNA sequence resides in an allele of a crop plant, wherein the particular allele of the trait of interest results in a plant of lesser agronomic value. The deamination of the nucleobase results in an allele that improves the trait and increases the agronomic value of the plant.

In some embodiments, the DNA sequence comprises a T→C or A→G point mutation associated with a disease or disorder, and wherein the deamination of the mutant C or G base results in a sequence that is not associated with a disease or disorder. In some embodiments, the deamination corrects a point mutation in the sequence associated with the disease or disorder.

In some embodiments, the sequence associated with the disease or disorder encodes a protein, and wherein the deamination introduces a stop codon into the sequence associated with the disease or disorder, resulting in a truncation of the encoded protein. In some embodiments, the contacting is performed *in vivo* in a subject susceptible to having, having, or diagnosed with the disease or disorder. In some embodiments, the disease or disorder is a disease associated with a point mutation, or a single-base mutation, in the genome. In some embodiments, the disease is a genetic disease, a cancer, a metabolic disease, or a lysosomal storage disease.

X. Pharmaceutical Compositions and Methods of Treatment

Pharmaceutical compositions comprising the presently disclosed RGN polypeptides and active variants and fragments thereof, as well as polynucleotides encoding the same, the presently disclosed gRNAs or polynucleotides encoding the same, the presently disclosed systems, or cells comprising any of the RGN polypeptides or RGN-encoding polynucleotides, gRNA or gRNA-encoding polynucleotides, or the RGN systems, and a pharmaceutically acceptable carrier are provided.

A pharmaceutical composition is a composition that is employed to prevent, reduce in intensity, cure or otherwise treat a target condition or disease that comprises an active ingredient (i.e., RGN polypeptides, RGN-encoding polynucleotides, gRNA, gRNA-encoding polynucleotides, RGN systems, or cells comprising any one of these) and a pharmaceutically acceptable carrier.

As used herein, a “pharmaceutically acceptable carrier” refers to a material that does not cause significant irritation to an organism and does not abrogate the activity and properties of the active ingredient (i.e., RGN polypeptides, RGN-encoding polynucleotides, gRNA, gRNA-encoding polynucleotides, RGN systems, or cells comprising any one of these). Carriers must be of sufficiently

high purity and of sufficiently low toxicity to render them suitable for administration to a subject being treated. The carrier can be inert, or it can possess pharmaceutical benefits. In some embodiments, a pharmaceutically acceptable carrier comprises one or more compatible solid or liquid filler, diluents or encapsulating substances which are suitable for administration to a human or other vertebrate animal. In some embodiments, the pharmaceutically acceptable carrier is not naturally-occurring. In some embodiments, the pharmaceutically acceptable carrier and the active ingredient are not found together in nature.

Pharmaceutical compositions used in the presently disclosed methods can be formulated with suitable carriers, excipients, and other agents that provide suitable transfer, delivery, tolerance, and the like. A multitude of appropriate formulations are known to those skilled in the art. See, *e.g.*, Remington, *The Science and Practice of Pharmacy* (21st ed. 2005). Suitable formulations include, for example, powders, pastes, ointments, jellies, waxes, oils, lipids, lipid (cationic or anionic) containing vesicles (such as LIPOFECTIN vesicles), lipid nanoparticles, DNA conjugates, anhydrous absorption pastes, oil-in-water and water-in-oil emulsions, emulsions carbowax (polyethylene glycols of various molecular weights), semi-solid gels, and semi-solid mixtures containing carbowax. Pharmaceutical compositions for oral or parenteral use may be prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc.

In some embodiments wherein cells comprising or modified with the presently disclosed RGN, gRNAs, RGN systems or polynucleotides encoding the same are administered to a subject, the cells are administered as a suspension with a pharmaceutically acceptable carrier. One of skill in the art will recognize that a pharmaceutically acceptable carrier to be used in a cell composition will not include buffers, compounds, cryopreservation agents, preservatives, or other agents in amounts that substantially interfere with the viability of the cells to be delivered to the subject. A formulation comprising cells can include *e.g.*, osmotic buffers that permit cell membrane integrity to be maintained, and optionally, nutrients to maintain cell viability or enhance engraftment upon administration. Such formulations and suspensions are known to those of skill in the art and/or can be adapted for use with the cells described herein using routine experimentation.

A cell composition can also be emulsified or presented as a liposome composition, provided that the emulsification procedure does not adversely affect cell viability. The cells and any other active ingredient can be mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient, and in amounts suitable for use in the therapeutic methods described herein.

Additional agents included in a cell composition can include pharmaceutically acceptable salts of the components therein. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide) that are formed with inorganic acids, such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, tartaric, mandelic and

the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases, such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

Physiologically tolerable and pharmaceutically acceptable carriers are well known in the art.

5 Exemplary liquid carriers are sterile aqueous solutions that contain no materials in addition to the active ingredients and water, or contain a buffer such as sodium phosphate at physiological pH value, physiological saline or both, such as phosphate-buffered saline. Still further, aqueous carriers can contain more than one buffer salt, as well as salts such as sodium and potassium chlorides, dextrose, polyethylene glycol and other solutes. Liquid compositions can also contain liquid phases in addition
10 to and to the exclusion of water. Exemplary of such additional liquid phases are glycerin, vegetable oils such as cottonseed oil, and water-oil emulsions. The amount of an active compound used in the cell compositions that is effective in the treatment of a particular disorder or condition can depend on the nature of the disorder or condition, and can be determined by standard clinical techniques.

The presently disclosed RGN polypeptides, guide RNAs, RGN systems or polynucleotides
15 encoding the same can be formulated with pharmaceutically acceptable excipients such as carriers, solvents, stabilizers, adjuvants, diluents, etc., depending upon the particular mode of administration and dosage form. In some embodiments, these pharmaceutical compositions are formulated to achieve a physiologically compatible pH, and range from a pH of about 3 to a pH of about 11, about pH 3 to about pH 7, depending on the formulation and route of administration. In some embodiments, the pH
20 can be adjusted to a range from about pH 5.0 to about pH 8. In some embodiments, the compositions can comprise a therapeutically effective amount of at least one compound as described herein, together with one or more pharmaceutically acceptable excipients. In some embodiments, the compositions comprise a combination of the compounds described herein, or include a second active ingredient useful in the treatment or prevention of bacterial growth (for example and without
25 limitation, anti-bacterial or anti-microbial agents), or include a combination of reagents of the present disclosure.

Suitable excipients include, for example, carrier molecules that include large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Other exemplary
30 excipients can include antioxidants (for example and without limitation, ascorbic acid), chelating agents (for example and without limitation, EDTA), carbohydrates (for example and without limitation, dextrin, hydroxyalkylcellulose, and hydroxyalkylmethylcellulose), stearic acid, liquids (for example and without limitation, oils, water, saline, glycerol and ethanol), wetting or emulsifying agents, pH buffering substances, and the like.

35 In some embodiments, the formulations are provided in unit-dose or multi-dose containers, for example sealed ampules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring the addition of the sterile liquid carrier, for example, saline, water-for-injection, a semi-

liquid foam, or gel, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described. In some embodiments, the active ingredient is dissolved in a buffered liquid solution that is frozen in a unit-dose or multi-dose container and later thawed for injection or kept/stabilized under refrigeration until use.

The therapeutic agent(s) may be contained in controlled release systems. In order to prolong the effect of a drug, it often is desirable to slow the absorption of the drug from subcutaneous, intrathecal, or intramuscular injection. This may be accomplished by the use of a liquid suspension of crystalline or amorphous material with poor water solubility. The rate of absorption of the drug then depends upon its rate of dissolution which, in turn, may depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally administered drug form is accomplished by dissolving or suspending the drug in an oil vehicle. In some embodiments, the use of a long-term sustained release implant may be particularly suitable for treatment of chronic conditions. Long-term sustained release implants are well-known to those of ordinary skill in the art.

Methods of treating a disease in a subject in need thereof are provided herein. The methods comprise administering to a subject in need thereof an effective amount of a presently disclosed RGN polypeptide or active variant or fragment thereof or a polynucleotide encoding the same, a presently disclosed gRNA or a polynucleotide encoding the same, a presently disclosed RGN system, or a cell modified by or comprising any one of these compositions.

In some embodiments, the treatment comprises *in vivo* gene editing by administering a presently disclosed RGN polypeptide, gRNA, or RGN system or polynucleotide(s) encoding the same. In some embodiments, the treatment comprises *ex vivo* gene editing wherein cells are genetically modified *ex vivo* with a presently disclosed RGN polypeptide, gRNA, or RGN system or polynucleotide(s) encoding the same and then the modified cells are administered to a subject. In some embodiments, the genetically modified cells originate from the subject that is then administered the modified cells, and the transplanted cells are referred to herein as autologous. In some embodiments, the genetically modified cells originate from a different subject (i.e., donor) within the same species as the subject that is administered the modified cells (i.e., recipient), and the transplanted cells are referred to herein as allogeneic. In some examples described herein, the cells can be expanded in culture prior to administration to a subject in need thereof.

In some embodiments, the disease to be treated with the presently disclosed compositions is one that can be treated with immunotherapy, such as with a chimeric antigen receptor (CAR) T cell. Such diseases include but are not limited to cancer. In some embodiments, the disease to be treated with the presently disclosed compositions is associated with a causal mutation. As used herein, a “causal mutation” refers to a particular nucleotide, nucleotides, or nucleotide sequence in the genome that contributes to the severity or presence of a disease or disorder in a subject. The correction of the causal mutation leads to the improvement of at least one symptom resulting from a disease or

disorder. In some embodiments, the causal mutation is adjacent to a PAM site recognized by an RGN disclosed herein. The causal mutation can be corrected with a presently disclosed RGN or a fusion polypeptide comprising a presently disclosed RGN and a base-editing polypeptide (i.e., a base editor). Non-limiting examples of diseases associated with a causal mutation include cystic fibrosis, Hurler syndrome, Friedreich's Ataxia, Huntington's Disease, and sickle cell disease. In some embodiments, the disease to be treated with the presently disclosed RGNs is a disease listed in Table 6. Additional non-limiting examples of disease-associated genes and mutations are available from McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, Md.) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, Md.), available on the World Wide Web.

As used herein, "treatment" or "treating," or "palliating" or "ameliorating" are used interchangeably. These terms refer to an approach for obtaining beneficial or desired results including but not limited to a therapeutic benefit and/or a prophylactic benefit. By therapeutic benefit is meant any therapeutically relevant improvement in or effect on one or more diseases, conditions, or symptoms under treatment. For prophylactic benefit, the compositions may be administered to a subject at risk of developing a particular disease, condition, or symptom, or to a subject reporting one or more of the physiological symptoms of a disease, even though the disease, condition, or symptom may not have yet been manifested. In some embodiments, treatment may be administered after one or more symptoms have developed and/or after a disease has been diagnosed. In particular embodiments, treatment may be administered in the absence of symptoms, e.g., to prevent or delay onset of a symptom or inhibit onset or progression of a disease. For example, treatment may be administered to a susceptible individual prior to the onset of symptoms (e.g., in light of a history of symptoms and/or in light of genetic or other susceptibility factors). Treatment may also be continued after symptoms have resolved, for example, to prevent or delay their prevention or recurrence.

The term "effective amount" or "therapeutically effective amount" refers to the amount of an agent that is sufficient to effect beneficial or desired results. The therapeutically effective amount may vary depending upon one or more of: the subject and disease condition being treated, the weight and age of the subject, the severity of the disease condition, the manner of administration and the like, which can readily be determined by one of ordinary skill in the art. The specific dose may vary depending on one or more of: the particular agent chosen, the dosing regimen to be followed, whether it is administered in combination with other compounds, timing of administration, and the delivery system in which it is carried.

The term "administering" refers to the placement of an active ingredient into a subject, by a method or route that results in at least partial localization of the introduced active ingredient at a desired site, such as a site of injury or repair, such that a desired effect(s) is produced. In some embodiments, the disclosure provides methods comprising delivering any of the RGN polypeptides, nucleic acid molecules, ribonucleoprotein complexes, vectors, pharmaceutical compositions and/or

gRNAs described herein. In some embodiments, the disclosure further provides cells produced by such methods, and organisms (such as animals or plants) comprising or produced from such cells. In some embodiments, a RGN polypeptide and/or nucleic acid molecules as described herein in combination with (and optionally complexed with) a guide sequence is delivered to a cell.

5 In those embodiments wherein cells are administered, the cells can be administered by any appropriate route that results in delivery to a desired location in the subject where at least a portion of the implanted cells or components of the cells remain viable. The period of viability of the cells after administration to a subject can be as short as a few hours, e.g., twenty-four hours, to a few days, to as long as several years, or even the life time of the patient, i.e., long-term engraftment. For example, in
10 some aspects described herein, an effective amount of photoreceptor cells or retinal progenitor cells is administered via a systemic route of administration, such as an intraperitoneal or intravenous route.

In some embodiments, the administering comprises administering by viral delivery. Viral vectors comprising a nucleic acid encoding the RGN polypeptides, ribonucleoprotein complexes, or vectors disclosed herein may be administered directly to patients (i.e., *in vivo*) or they may be used to
15 treat cells *in vitro*, and the modified cells may optionally be administered to patients (i.e., *ex vivo*). Conventional viral based systems may include, without limitation, retroviral, lentivirus, adenoviral, adeno-associated and herpes simplex virus vectors for gene transfer. Integration in the host genome is possible with the retrovirus, lentivirus, and adeno-associated virus gene transfer methods, often resulting in long term expression of the inserted transgene. Lentiviral vectors are retroviral vectors
20 that are able to transduce or infect non-dividing cells and typically produce high viral titers. In applications where transient expression is preferred, adenoviral based systems may be used. Adenoviral based vectors are capable of very high transduction efficiency in many cell types and do not require cell division.

In some embodiments, the administering comprises administering by other non-viral delivery
25 of nucleic acids. Exemplary non-viral delivery methods, without limitation, include RNP complexes, lipofection, nucleofection, microinjection, biolistics, virosomes, liposomes, immunoliposomes, polycation or lipidnucleic acid conjugates, naked DNA, artificial virions, and agent-enhanced uptake of DNA. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355) and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and
30 neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Feigner, WO1991/17424; WO 1991/16024. Delivery can be to cells (e.g., *in vitro* or *ex vivo* administration) or target tissues (e.g., *in vivo* administration).

In some embodiments, the administering comprises administering by a method selected from the group consisting of: intravenously, subcutaneously, intramuscularly, orally, rectally, by aerosol,
35 parenterally, ophthalmically, pulmonarily, transdermally, vaginally, otically, nasally, and by topical administration, or any combination thereof. In some embodiments, for the delivery of cells, administration by injection or infusion is used.

As used herein, the term "subject" refers to any individual for whom diagnosis, treatment or therapy is desired. In some embodiments, the subject is an animal. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human being.

The efficacy of a treatment can be determined by the skilled clinician. However, a treatment is considered an "effective treatment," if any one or all of the signs or symptoms of a disease or disorder are altered in a beneficial manner (e.g., decreased by at least 10%), or other clinically accepted symptoms or markers of disease are improved or ameliorated. Efficacy can also be measured by failure of an individual to worsen as assessed by hospitalization or need for medical interventions (e.g., progression of the disease is halted or at least slowed). Methods of measuring these indicators are known to those of skill in the art. Treatment includes: (1) inhibiting the disease, e.g., arresting, or slowing the progression of symptoms; or (2) relieving the disease, e.g., causing regression of symptoms; and (3) preventing or reducing the likelihood of the development of symptoms.

Pharmaceutical compositions comprising the presently disclosed RGN polypeptides or polynucleotides encoding the same, the presently disclosed gRNAs or polynucleotides encoding the same, the presently disclosed systems, the presently disclosed ribonucleoprotein complexes or cells comprising any of the RGN polypeptides or RGN-encoding polynucleotides, gRNA or gRNA-encoding polynucleotides, or the systems, and a pharmaceutically acceptable carrier are provided.

As used herein, a "pharmaceutically acceptable carrier" refers to a material that does not cause significant irritation to an organism and does not abrogate the activity and properties of the active ingredient (e.g., an RGN polypeptide or nucleic acid molecule encoding the same). Carriers must be of sufficiently high purity and of sufficiently low toxicity to render them suitable for administration to a subject being treated. The carrier can be inert, or it can possess pharmaceutical benefits. In some embodiments, a pharmaceutically acceptable carrier comprises one or more compatible solid or liquid filler, diluents or encapsulating substances which are suitable for administration to a human or other vertebrate animal. In some embodiments, the pharmaceutical composition comprises a pharmaceutically acceptable carrier that is non-naturally occurring. In some embodiments, the pharmaceutically acceptable carrier and the active ingredient are not found together in nature and are thus, heterologous.

Pharmaceutical compositions used in the presently disclosed methods can be formulated with suitable carriers, excipients, and other agents that provide suitable transfer, delivery, tolerance, and the like. A multitude of appropriate formulations are known to those skilled in the art. See, e.g., Remington, The Science and Practice of Pharmacy (21st ed. 2005). Non-limiting examples include a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. Administered intravenously, particular

carriers are physiological saline or phosphate buffered saline (PBS). Pharmaceutical compositions for oral or parenteral use may be prepared into dosage forms in a unit dose suited to fit a dose of the active ingredients. Such dosage forms in a unit dose include, for example, tablets, pills, capsules, injections (ampoules), suppositories, etc. These compositions also may contain adjuvants including preservative agents, wetting agents, emulsifying agents, and dispersing agents. Prevention of the action of microorganisms may be ensured by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, and the like. It also may be desirable to include isotonic agents, for example, sugars, sodium chloride and the like. Prolonged absorption of the injectable pharmaceutical form may be brought about by the use of agents delaying absorption, for example, aluminum monostearate and gelatin.

In some embodiments wherein cells comprising or modified with the presently disclosed RGNs, gRNAs, systems, or polynucleotides encoding the same are administered to a subject, the cells are administered as a suspension with a pharmaceutically acceptable carrier. One of skill in the art will recognize that a pharmaceutically acceptable carrier to be used in a cell composition will not include buffers, compounds, cryopreservation agents, preservatives, or other agents in amounts that substantially interfere with the viability of the cells to be delivered to the subject. A formulation comprising cells can include e.g., osmotic buffers that permit cell membrane integrity to be maintained, and optionally, nutrients to maintain cell viability or enhance engraftment upon administration. Such formulations and suspensions are known to those of skill in the art and/or can be adapted for use with the cells described herein using routine experimentation.

A cell composition can also be emulsified or presented as a liposome composition, provided that the emulsification procedure does not adversely affect cell viability. The cells and any other active ingredient can be mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient, and in amounts suitable for use in the therapeutic methods described herein.

Additional agents included in a cell composition can include pharmaceutically acceptable salts of the components therein. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide) that are formed with inorganic acids, such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, tartaric, mandelic and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases, such as, for example, sodium, potassium, ammonium, calcium or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

Suitable routes of administering the pharmaceutical compositions described herein include, without limitation: topical, subcutaneous, transdermal, intradermal, intralesional, intraarticular, intraperitoneal, intravesical, transmucosal, gingival, intradental, intracochlear, transtympanic, intraorgan, epidural, intrathecal, intramuscular, intravenous, intravascular, intraosseous, periocular, intratumoral, intracerebral, and intracerebroventricular administration.

In some embodiments, a pharmaceutical composition described herein is administered locally to a diseased site (e.g., the lung). In some embodiments, the pharmaceutical composition described herein is administered to a subject by injection, inhalation (e.g., of an aerosol), by means of a catheter, by means of a suppository, or by means of an implant, the implant being of a porous, non-porous, or gelatinous material, including a membrane, such as a sialastic membrane, or a fiber. In some
5 embodiments, the pharmaceutical composition is formulated for delivery to a subject, e.g., for gene editing.

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

20 In some embodiments, the pharmaceutical composition can be contained within a lipid particle or vesicle, such as a liposome or microcrystal, which is also suitable for parenteral administration.

Although the descriptions of pharmaceutical compositions provided herein are principally directed to pharmaceutical compositions which are suitable for administration to humans, it will be
25 understood by the skilled artisan that such compositions are generally suitable for administration to animals or organisms of all sorts.

A. Modifying causal mutations using base-editing

An example of a genetically inherited disease which could be corrected using an approach
30 that relies on an RGN-base editor fusion protein of the invention is Hurler Syndrome. Hurler Syndrome, also known as MPS-1, is the result of a deficiency of α -L-iduronidase (IDUA) resulting in a lysosomal storage disease characterized at the molecular level by the accumulation of dermatan sulfate and heparan sulfate in lysosomes. This disease is generally an inherited genetic disorder caused by mutations in the IDUA gene encoding α -L-iduronidase. Common IDUA mutations are
35 W402X and Q70X, both nonsense mutations resulting in premature termination of translation. Such mutations are well addressed by precise genome editing (PGE) approaches, since reversion of a single nucleotide, for example by a base-editing approach, would restore the wild-type coding sequence and

result in protein expression controlled by the endogenous regulatory mechanisms of the genetic locus. Additionally, since heterozygotes are known to be asymptomatic, a PGE therapy that targets one of these mutations would be useful to a large proportion of patients with this disease, as only one of the mutated alleles needs to be corrected (Bunge et al. (1994) Hum. Mol. Genet. 3(6): 861-866, herein
5 incorporated by reference).

Current treatments for Hurler Syndrome include enzyme replacement therapy and bone marrow transplants (Vellodi et al. (1997) Arch. Dis. Child. 76(2): 92-99; Peters et al. (1998) Blood 91(7): 2601-2608, herein incorporated by reference). While enzyme replacement therapy has had a dramatic effect on the survival and quality of life of Hurler Syndrome patients, this approach requires
10 costly and time-consuming weekly infusions. Additional approaches include the delivery of the IDUA gene on an expression vector or the insertion of the gene into a highly expressed locus such as that of serum albumin (U.S. Patent No. 9,956,247, herein incorporated by reference). However, these approaches do not restore the original IDUA locus to the correct coding sequence. A genome-editing strategy would have a number of advantages, most notably that regulation of gene expression would
15 be controlled by the natural mechanisms present in healthy individuals. Additionally, using base editing does not necessitate causing a double stranded DNA breaks, which could lead to large chromosomal rearrangements, cell death, or oncogenicity by the disruption of tumor suppression mechanisms. A general strategy may be directed toward using RGN-base editor fusion proteins of the invention, for example those comprising LPG10136, LPG10139, LPG10134, or LPG10145, to target
20 and correct certain disease-causing mutations in the human genome. It will be appreciated that similar approaches to target diseases that can be corrected by base-editing may also be pursued. It will be further appreciated that similar approaches to target disease-causing mutations in other species, particularly common household pets or livestock, can also be deployed using the RGNs of the invention. Common household pets and livestock include dogs, cats, horses, pigs, cows, sheep,
25 chickens, donkeys, snakes, ferrets, and fish including salmon and shrimp.

B. Modifying causal mutations by targeted deletion

RGNs of the invention could also be useful in human therapeutic approaches where the causal mutation is more complicated. For example, some diseases such as Friedreich's Ataxia and
30 Huntington's Disease are the result of a significant increase in repeats of a three nucleotide motif at a particular region of a gene, which affects the ability of the expressed protein to function or to be expressed. Friedreich's Ataxia (FRDA) is an autosomal recessive disease resulting in progressive degeneration of nervous tissue in the spinal cord. Reduced levels of the frataxin (FXN) protein in the mitochondria cause oxidative damages and iron deficiencies at the cellular level. The reduced FXN
35 expression has been linked to a GAA triplet expansion within the intron 1 of the somatic and germline FXN gene. In FRDA patients, the GAA repeat frequently consists of more than 70, sometimes even more than 1000 (most commonly 600-900) triplets, whereas unaffected individuals have about 40

repeats or less (Pandolfo et al. (2012) Handbook of Clinical Neurology 103: 275-294; Campuzano et al. (1996) Science 271: 1423-1427; Pandolfo (2002) Adv. Exp. Med. Biol. 516: 99-118; all herein incorporated by reference).

The expansion of the trinucleotide repeat sequence causing Friedreich's Ataxia (FRDA) occurs in a defined genetic locus within the FXN gene, referred to as the FRDA instability region. RNA guided nucleases (RGNs) may be used for excising the instability region in FRDA patient cells. This approach requires 1) an RGN and guide RNA sequence that can be programmed to target the allele in the human genome; and 2) a delivery approach for the RGN and guide sequence. Many nucleases used for genome editing, such as the commonly used Cas9 nuclease from *S. pyogenes* (SpCas9), are too large to be packaged into adeno-associated viral (AAV) vectors, especially when considering the length of the SpCas9 gene and the guide RNA in addition to other genetic elements required for functional expression cassettes. This makes an approach using SpCas9 more difficult.

Certain RNA guided nucleases of the invention, for example, LPG10134, LPG10145, LPG10136, and LPG10139, are well suited for packaging into an AAV vector along with a guide RNA. The present invention encompasses a strategy using RGNs of the invention in which a region of genomic instability is removed. Such a strategy is applicable to other diseases and disorders which have a similar genetic basis, such as Huntington's Disease. Similar strategies using RGNs of the invention may also be applicable to similar diseases and disorders in non-human animals of agronomic or economic importance, including dogs, cats, horses, pigs, cows, sheep, chickens, donkeys, snakes, ferrets, and fish including salmon and shrimp.

C. Modifying causal mutations by targeted mutagenesis

RGNs of the invention could also be to introduce disruptive mutations that may result in a beneficial effect. Genetic defects in the genes encoding hemoglobin, particularly the beta globin chain (the HBB gene), can be responsible for a number of diseases known as hemoglobinopathies, including sickle cell anemia and thalassemias.

In adult humans, hemoglobin is a heterotetramer comprising two alpha (α)-like globin chains and two beta (β)-like globin chains and 4 heme groups. In adults the $\alpha_2\beta_2$ tetramer is referred to as Hemoglobin A (HbA) or adult hemoglobin. Typically, the alpha and beta globin chains are synthesized in an approximate 1:1 ratio and this ratio seems to be critical in terms of hemoglobin and red blood cell (RBC) stabilization. In a developing fetus, a different form of hemoglobin, fetal hemoglobin (HbF), is produced which has a higher binding affinity for oxygen than Hemoglobin A such that oxygen can be delivered to the baby's system via the mother's blood stream. Fetal hemoglobin also contains two α globin chains, but in place of the adult β -globin chains, it has two fetal gamma (γ)-globin chains (i.e., fetal hemoglobin is $\alpha_2\gamma_2$). The regulation of the switch from production of gamma- to beta-globin is quite complex, and primarily involves a down-regulation of gamma globin transcription with a simultaneous up-regulation of beta globin transcription. At

approximately 30 weeks of gestation, the synthesis of gamma globin in the fetus starts to drop while the production of beta globin increases. By approximately 10 months of age, the newborn's hemoglobin is nearly all $\alpha_2\beta_2$ although some HbF persists into adulthood (approximately 1-3% of total hemoglobin). In the majority of patients with hemoglobinopathies, the genes encoding gamma globin remain present, but expression is relatively low due to normal gene repression occurring around parturition as described above.

Sickle cell disease is caused by a V6E mutation in the β globin gene (HBB) (a GAG to GTG at the DNA level), where the resultant hemoglobin is referred to as "hemoglobinS" or "HbS." Under lower oxygen conditions, HbS molecules aggregate and form fibrous precipitates. These aggregates cause the abnormality or 'sickling' of the RBCs, resulting in a loss of flexibility of the cells. The sickling RBCs are no longer able to squeeze into the capillary beds and can result in vaso-occlusive crisis in sickle cell patients. In addition, sickled RBCs are more fragile than normal RBCs, and tend towards hemolysis, eventually leading to anemia in the patient.

Treatment and management of sickle cell patients is a life-long proposition involving antibiotic treatment, pain management and transfusions during acute episodes. One approach is the use of hydroxyurea, which exerts its effects in part by increasing the production of gamma globin. Long term side effects of chronic hydroxyurea therapy are still unknown, however, and treatment gives unwanted side effects and can have variable efficacy from patient to patient. Despite an increase in the efficacy of sickle cell treatments, the life expectancy of patients is still only in the mid to late 50's and the associated morbidities of the disease have a profound impact on a patient's quality of life.

Thalassemias (alpha thalassemias and beta thalassemia) are also diseases relating to hemoglobin and typically involve a reduced expression of globin chains. This can occur through mutations in the regulatory regions of the genes or from a mutation in a globin coding sequence that results in reduced expression or reduced levels or functional globin protein. Treatment of thalassemias usually involves blood transfusions and iron chelation therapy. Bone marrow transplants are also being used for treatment of people with severe thalassemias if an appropriate donor can be identified, but this procedure can have significant risks.

One approach that has been proposed for the treatment of both sickle cell disease (SCD) and beta thalassemias is to increase the expression of gamma globin so that HbF functionally replaces the aberrant adult hemoglobin. As mentioned above, treatment of SCD patients with hydroxyurea is thought to be successful in part due to its effect on increasing gamma globin expression (DeSimone (1982) Proc Nat'l Acad Sci USA 79(14):4428-31; Ley, et al., (1982) N. Engl. J. Medicine, 307: 1469-1475; Ley, et al., (1983) Blood 62: 370-380; Constantoulakis et al., (1988) Blood 72(6):1961-1967, all herein incorporated by reference). Increasing the expression of HbF involves identification of genes whose products play a role in the regulation of gamma globin expression. One such gene is BCL11A. BCL11A encodes a zinc finger protein that expressed in adult erythroid precursor cells,

and down-regulation of its expression leads to an increase in gamma globin expression (Sankaran et al (2008) Science 322: 1839, herein incorporated by reference). Use of an inhibitory RNA targeted to the BCL11A gene has been proposed (e.g., U.S. Patent Publication 2011/0182867, herein incorporated by reference) but this technology has several potential drawbacks, including that complete knock down may not be achieved, delivery of such RNAs may be problematic, and the RNAs must be present continuously, requiring multiple treatments for life.

RGNs of the invention, for example LPG10134, LPG10145, LPG10136, or LPG10139, may be used to target the BCL11A enhancer region to disrupt expression of BCL11A, thereby increasing gamma globin expression. This targeted disruption can be achieved by non-homologous end joining (NHEJ), whereby an RGN of the invention targets to a particular sequence within the BCL11A enhancer region, makes a double-stranded break, and the cell's machinery repairs the break, typically simultaneously introducing deleterious mutations. Similar to what is described for other disease targets, RGNs of the invention may have advantages over other known RGNs due to their relatively small size, which enables packaging expression cassettes for the RGN and its guide RNA into a single AAV vector for *in vivo* delivery. Similar strategies using RGNs of the invention may also be applicable to similar diseases and disorders in both humans and in non-human animals of agronomic or economic importance.

XI. Cells Comprising a Genetic Modification

Provided herein are cells and organisms comprising a target sequence of interest that has been modified using a process mediated by an RGN, crRNA, and/or tracrRNA as described herein. In some of these embodiments, the RGN comprises any one of the amino acid sequences set forth as SEQ ID NOs: 1-12, or an active variant or fragment thereof. In various embodiments, the guide RNA comprises a CRISPR repeat sequence comprising any one of the nucleotide sequences set forth as SEQ ID NOs:13-24, or an active variant or fragment thereof. In particular embodiments, the guide RNA comprises a tracrRNA comprising any one of the nucleotide sequences set forth as SEQ ID NOs:25-36, or an active variant or fragment thereof. The guide RNA of the system can be a single guide RNA or a dual-guide RNA.

The modified cells can be eukaryotic (e.g., mammalian, plant, insect, avian cell) or prokaryotic. Also provided are organelles and embryos comprising at least one nucleotide sequence that has been modified by a process utilizing an RGN, crRNA, and/or tracrRNA as described herein. The genetically modified cells, organisms, organelles, and embryos can be heterozygous or homozygous for the modified nucleotide sequence.

The chromosomal modification of the cell, organism, organelle, or embryo can result in altered expression (up-regulation or down-regulation), inactivation, or the expression of an altered protein product or an integrated sequence. In those embodiments wherein the chromosomal modification results in either the inactivation of a gene or the expression of a non-functional protein

product, the genetically modified cell, organism, organelle, or embryo is referred to as a “knock out”. The knock out phenotype can be the result of a deletion mutation (*i.e.*, deletion of at least one nucleotide), an insertion mutation (*i.e.*, insertion of at least one nucleotide), or a nonsense mutation (*i.e.*, substitution of at least one nucleotide such that a stop codon is introduced).

Alternatively, the chromosomal modification of a cell, organism, organelle, or embryo can produce a “knock in”, which results from the chromosomal integration of a nucleotide sequence that encodes a protein. In some of these embodiments, the coding sequence is integrated into the chromosome such that the chromosomal sequence encoding the wild-type protein is inactivated, but the exogenously introduced protein is expressed.

In other embodiments, the chromosomal modification results in the production of a variant protein product. The expressed variant protein product can have at least one amino acid substitution and/or the addition or deletion of at least one amino acid. The variant protein product encoded by the altered chromosomal sequence can exhibit modified characteristics or activities when compared to the wild-type protein, including but not limited to altered enzymatic activity or substrate specificity.

In yet other embodiments, the chromosomal modification can result in an altered expression pattern of a protein. As a non-limiting example, chromosomal alterations in the regulatory regions controlling the expression of a protein product can result in the overexpression or downregulation of the protein product or an altered tissue or temporal expression pattern.

The cells that have been modified can be grown into an organism, such as a plant, in accordance with conventional ways. See, for example, McCormick et al. (1986) *Plant Cell Reports* 5:81-84. These plants may then be grown, and either pollinated with the same modified strain or different strains, and the resulting hybrid having the genetic modification. The present invention provides genetically modified seed. Progeny, variants, and mutants of the regenerated plants are also included within the scope of the invention, provided that these parts comprise the genetic modification. Further provided is a processed plant product or byproduct that retains the genetic modification, including for example, soymeal.

The methods provided herein may be used for modification of any plant species, including, but not limited to, monocots and dicots. Examples of plants of interest include, but are not limited to, corn (maize), sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, and oilseed rape, Brassica sp., alfalfa, rye, millet, safflower, peanuts, sweet potato, cassava, coffee, coconut, pineapple, citrus trees, cocoa, tea, banana, avocado, fig, guava, mango, olive, papaya, cashew, macadamia, almond, oats, vegetables, ornamentals, and conifers.

Vegetables include, but are not limited to, tomatoes, lettuce, green beans, lima beans, peas, and members of the genus *Curcumis* such as cucumber, cantaloupe, and musk melon. Ornamentals include, but are not limited to, azalea, hydrangea, hibiscus, roses, tulips, daffodils, petunias, carnation, poinsettia, and chrysanthemum. Preferably, plants of the present invention are crop plants (for

example, maize, sorghum, wheat, sunflower, tomato, crucifers, peppers, potato, cotton, rice, soybean, sugarbeet, sugarcane, tobacco, barley, oilseed rape, etc.).

The methods provided herein can also be used to genetically modify any prokaryotic species, including but not limited to, archaea and bacteria (*e.g.*, *Bacillus* sp., *Klebsiella* sp., *Streptomyces* sp.,
5 *Rhizobium* sp., *Escherichia* sp., *Pseudomonas* sp., *Salmonella* sp., *Shigella* sp., *Vibrio* sp., *Yersinia* sp., *Mycoplasma* sp., *Agrobacterium*, *Lactobacillus* sp.).

The methods provided herein can be used to genetically modify any eukaryotic species or cells therefrom, including but not limited to animals (*e.g.*, mammals, insects, fish, birds, and reptiles), fungi, amoeba, algae, and yeast. In some embodiments, the cell that is modified by the presently
10 disclosed methods include cells of hematopoietic origin, such as cells of the immune system including but not limited to B cells, T cells, natural killer (NK) cells, pluripotent stem cells, induced pluripotent stem cells, chimeric antigen receptor T (CAR-T) cells, monocytes, macrophages, and dendritic cells.

Cells that have been modified may be introduced into an organism. These cells could have originated from the same organism (*e.g.*, person) in the case of autologous cellular transplants,
15 wherein the cells are modified in an *ex vivo* approach. Alternatively, the cells originated from another organism within the same species (*e.g.*, another person) in the case of allogeneic cellular transplants.

XIII. Kits

Some aspects of this disclosure provide kits comprising an RGN polypeptide of the invention.
20 In addition, in some embodiments, the kit comprises suitable reagents, buffers, and/or instructions for using the RGN polypeptide, *e.g.*, for *in vitro* or *in vivo* DNA or RNA editing. In some embodiments, the kit comprises instructions regarding the design and use of suitable gRNAs for targeted editing of a nucleic acid sequence.

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

The article “a” and “an” are used herein to refer to one or more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, “a polypeptide” means one or more
35 polypeptides.

All publications and patent applications mentioned in the specification are indicative of the level of those skilled in the art to which this disclosure pertains. All publications and patent

applications are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and
5 modifications may be practiced within the scope of the appended embodiments.

Non-limiting embodiments include:

1. A nucleic acid molecule comprising a polynucleotide encoding an RNA-guided
nuclease (RGN) polypeptide, wherein said polynucleotide comprises a nucleotide sequence encoding
10 an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any
one of SEQ ID NOs: 1-12;

wherein said RGN polypeptide is capable of binding a target DNA sequence in an RNA-
guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said
target DNA sequence.

2. The nucleic acid molecule of embodiment 1, wherein said polynucleotide encoding an
RGN polypeptide is operably linked to a promoter heterologous to said polynucleotide.

3. The nucleic acid molecule of embodiment 1 or 2, wherein said RGN polypeptide
comprises an amino acid sequence having at least 95% sequence identity to any one of SEQ ID
NOs: 1-12.

4. The nucleic acid molecule of embodiment 1 or 2, wherein said RGN polypeptide
comprises an amino acid sequence having 100% sequence identity to any one of SEQ ID NOs: 1-12.

5. The nucleic acid molecule of any one of embodiments 1-4, wherein said RGN
polypeptide is capable of cleaving said target DNA sequence upon binding.

6. The nucleic acid molecule of embodiment 5, wherein said RGN polypeptide is
25 capable of generating a double-stranded break.

7. The nucleic acid molecule of embodiment 5, wherein said RGN polypeptide is
capable of generating a single-stranded break.

8. The nucleic acid molecule of any one of embodiments 1-4, wherein said RGN
polypeptide is nuclease inactive or is a nickase.

9. The nucleic acid molecule of any of embodiment 1-5, 7 and 8, wherein the RGN
polypeptide is operably linked to a prime editing polypeptide.

10. The nucleic acid molecule of embodiment 9, wherein said prime editing polypeptide
comprises a DNA polymerase.

11. The nucleic acid molecule of embodiment 9, wherein said prime editing polypeptide
35 comprises a reverse transcriptase.

12. The nucleic acid molecule of any one of embodiments 1-8, wherein the RGN
polypeptide is operably linked to a base-editing polypeptide.

13. The nucleic acid molecule of embodiment 12, wherein the base-editing polypeptide is a deaminase.

14. The nucleic acid molecule of embodiment 13, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

15. The nucleic acid molecule of embodiment 13, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

16. The nucleic acid molecule of embodiment 13, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

17. The nucleic acid molecule of any one of embodiments 1-16, wherein the RGN polypeptide comprises one or more nuclear localization signals.

18. The nucleic acid molecule of any one of embodiments 1-17, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

19. The nucleic acid molecule of any one of embodiments 1-18, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

20. A vector comprising the nucleic acid molecule of any one of embodiments 1-19.

21. The vector of embodiment 20, further comprising at least one nucleotide sequence encoding said gRNA capable of hybridizing to said target DNA sequence.

22. The vector of embodiment 21, wherein the guide RNA is selected from the group consisting of:

a) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25; wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;

b) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26; wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;

c) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27; wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;

- d) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16; and
 - ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28;
- 5 wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;
- e) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17; and
 - 10 ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;
- f) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18; and
 - 15 ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;
- g) a guide RNA comprising:
- 20 i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19; and
 - ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;
- 25 h) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20; and
 - ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32;
- 30 wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;
- i) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21; and
 - ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33;
- 35 wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;
- j) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 10;

k) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

l) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

23. The vector of embodiment 21, wherein the guide RNA is selected from the group consisting of:

a) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1;

b) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2;

c) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 3;

- d) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16; and
 - ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28;
- 5 wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 4;
- e) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 17; and
 - 10 ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 5;
- f) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18; and
 - 15 ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6;
- g) a guide RNA comprising:
- 20 i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19; and
 - ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31;
- wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 7;
- 25 h) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20; and
 - ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32;
- 30 wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 8;
- i) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21; and
 - ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33;
- 35 wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 9;
- j) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 10;

k) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 11; and

l) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24; and

ii) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 12.

24. The vector of embodiment 21, wherein the guide RNA is selected from the group consisting of:

a) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 25;

wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 1;

b) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 26;

wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 2;

c) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 27;

wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 3;

- d) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16; and
 - ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 28;
- 5 wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 4;
- e) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17; and
 - 10 ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 29;
- wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 5;
- f) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18; and
 - 15 ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 30;
- wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6;
- g) a guide RNA comprising:
- 20 i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19; and
 - ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 31;
- wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 7;
- 25 h) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20; and
 - ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 32;
- 30 wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 8;
- i) a guide RNA comprising:
- i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21; and
 - ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 33;
- 35 wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 9;
- j) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 34; wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 10;

k) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 35; wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 11; and

l) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24; and

ii) a tracrRNA having 100% sequence identity to SEQ ID NO: 36; wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 12.

25. The vector of any one of embodiments 21-24, where said gRNA is a single guide RNA (sgRNA).

26. The vector of embodiment 25, wherein said sgRNA further comprises an extension comprising an edit template for prime editing.

27. The vector of any one of embodiments 21-24, wherein said gRNA is a dual-guide RNA.

28. A cell comprising the nucleic acid molecule of any one of embodiments 1-19 or the vector of any one of embodiments 20-27.

29. The cell of embodiment 28, wherein the cell is a prokaryotic cell.

30. The cell of embodiment 28, wherein the cell is a eukaryotic cell.

31. The cell of embodiment 30, wherein the eukaryotic cell is a mammalian cell.

32. The cell of embodiment 31, wherein the mammalian cell is a human cell.

33. The cell of embodiment 32, wherein the human cell is an immune cell.

34. The cell of embodiment 33, wherein the immune cell is a stem cell.

35. The cell of embodiment 34, wherein the stem cell is an induced pluripotent stem cell.

36. The cell of embodiment 30, wherein the eukaryotic cell is an insect or avian cell.

37. The cell of embodiment 30, wherein the eukaryotic cell is a fungal cell.

38. The cell of embodiment 30, wherein the eukaryotic cell is a plant cell.

39. A plant comprising the cell of embodiment 38.

40. A seed comprising the cell of embodiment 38.

41. A method for making an RGN polypeptide comprising culturing the cell of any one of embodiments 28-38 under conditions in which the RGN polypeptide is expressed.

42. A method for making an RGN polypeptide comprising introducing into a cell a heterologous nucleic acid molecule comprising a nucleotide sequence encoding an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12;

wherein said RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence;

and culturing said cell under conditions in which the RGN polypeptide is expressed.

43. The method of embodiment 42, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

44. The method of embodiment 42, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to any one of SEQ ID NOs: 1-12.

45. The method of any one of embodiments 41-44, further comprising purifying said RGN polypeptide.

46. The method of any one of embodiments 41-44, wherein said cell further expresses one or more guide RNAs capable of binding to said RGN polypeptide to form an RGN ribonucleoprotein complex.

47. The method of embodiment 46, further comprising purifying said RGN ribonucleoprotein complex.

48. An RNA-guided nuclease (RGN) polypeptide, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; and

wherein said RGN polypeptide is capable of binding a target DNA sequence of a DNA molecule in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence.

49. The RGN polypeptide of embodiment 48, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

50. The RGN polypeptide of embodiment 48, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to any one of SEQ ID NOs: 1-12.

51. The RGN polypeptide of any one of embodiments 48-50, wherein said RGN polypeptide is an isolated RGN polypeptide.

52. The RGN polypeptide of any one of embodiments 48-51, wherein said RGN polypeptide is capable of cleaving said target DNA sequence upon binding.

53. The RGN polypeptide of embodiment 52, wherein cleavage by said RGN polypeptide generates a double-stranded break.

54. The RGN polypeptide of embodiment 52, wherein cleavage by said RGN polypeptide generates a single-stranded break.

55. The RGN polypeptide of any one of embodiments 48-51, wherein said RGN polypeptide is nuclease inactive or a nickase.

56. The RGN polypeptide of any of embodiment 48-52, 54, and 55, wherein the RGN polypeptide is operably linked to a prime editing polypeptide.

57. The RGN polypeptide of embodiment 56, wherein said prime editing polypeptide comprises a DNA polymerase.

58. The RGN polypeptide of embodiment 56, wherein said prime editing polypeptide comprises a reverse transcriptase.

59. The RGN polypeptide of any one of embodiments 48-55, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

60. The RGN polypeptide of embodiment 59, wherein the base-editing polypeptide is a deaminase.

61. The RGN polypeptide of embodiment 60, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

62. The RGN polypeptide of embodiment 60, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

63. The RGN polypeptide of embodiment 60, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

64. The RGN polypeptide of any one of embodiments 48-63, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

65. The RGN polypeptide of any one of embodiments 48-64, wherein the RGN polypeptide comprises one or more nuclear localization signals.

66. A ribonucleoprotein (RNP) complex comprising the RGN polypeptide of any one of embodiments 48-65 and a guide RNA (gRNA) bound to the RGN polypeptide.

67. The RNP complex of embodiment 66, wherein said gRNA is a single guide RNA (sgRNA).

68. The RNP complex of embodiment 67, wherein said gRNA comprises an extension comprising an edit template for prime editing.

69. A nucleic acid molecule comprising a CRISPR RNA (crRNA) or a polynucleotide encoding a crRNA, wherein said crRNA comprises a spacer sequence and a CRISPR repeat sequence, wherein said CRISPR repeat sequence comprises a nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 13-24;

wherein a guide RNA comprising:

a) said crRNA; and

b) a trans-activating CRISPR RNA (tracrRNA) hybridized to said CRISPR repeat sequence of said crRNA;

is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of said crRNA when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide.

70. The nucleic acid molecule of embodiment 69, wherein said polynucleotide encoding a crRNA is operably linked to a promoter heterologous to said polynucleotide.

71. The nucleic acid molecule of embodiment 69 or 70, wherein said CRISPR repeat sequence comprises a nucleotide sequence having at least 95% sequence identity to any one of SEQ ID NOs: 13-24.

72. The nucleic acid molecule of embodiment 69 or 70, wherein said CRISPR repeat sequence comprises a nucleotide sequence having 100% sequence identity to any one of SEQ ID NOs: 13-24.

73. A vector comprising the nucleic acid molecule comprising said polynucleotide encoding said crRNA of any one of embodiments 69-72.

74. The vector of embodiment 73, wherein said vector further comprises a polynucleotide encoding said tracrRNA.

75. The vector of embodiment 74, wherein said tracrRNA is selected from the group consisting of:

a) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13;

b) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 14;

c) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15;

d) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16;

e) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17;

f) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18;

g) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19;

h) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20;

i) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21;

j) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22;

k) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23; and

5 l) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24.

76. The vector of embodiment 74, wherein said tracrRNA is selected from the group consisting of:

a) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25, wherein said
10 CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 13;

b) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 14;

c) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 15;

15 d) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 16;

e) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 17;

20 f) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 18;

g) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 19;

h) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 20;

25 i) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 21;

j) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 22;

30 k) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 23; and

l) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 24.

77. The vector of embodiment 74, wherein said tracrRNA is selected from the group consisting of:

35 a) a tracrRNA having 100% sequence identity to SEQ ID NO: 25, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 13;

b) a tracrRNA having 100% sequence identity to SEQ ID NO: 26, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 14;

c) a tracrRNA having 100% sequence identity to SEQ ID NO: 27, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 15;

5 d) a tracrRNA having 100% sequence identity to SEQ ID NO: 28, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 16;

e) a tracrRNA having 100% sequence identity to SEQ ID NO: 29, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 17;

10 f) a tracrRNA having 100% sequence identity to SEQ ID NO: 30, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 18;

g) a tracrRNA having 100% sequence identity to SEQ ID NO: 31, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 19;

h) a tracrRNA having 100% sequence identity to SEQ ID NO: 32, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 20;

15 i) a tracrRNA having 100% sequence identity to SEQ ID NO: 33, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 21;

j) a tracrRNA having 100% sequence identity to SEQ ID NO: 34, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 22;

20 k) a tracrRNA having 100% sequence identity to SEQ ID NO: 35, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 23; and

l) a tracrRNA having 100% sequence identity to SEQ ID NO: 36, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 24.

25 78. The vector of any one of embodiments 74-77, wherein said polynucleotide encoding said crRNA and said polynucleotide encoding said tracrRNA are operably linked to the same promoter and are encoded as a single guide RNA (sgRNA).

79. The vector of embodiment 78, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

30 80. The vector of any one of embodiments 74-77, wherein said polynucleotide encoding said crRNA and said polynucleotide encoding said tracrRNA are operably linked to separate promoters.

81. The vector of any one of embodiments 74-80, wherein said vector further comprises a polynucleotide encoding said RGN polypeptide.

82. The vector of embodiment 81, wherein said RGN polypeptide is selected from the group consisting of:

35 a) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 1, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 2, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 3, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 4, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 5, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 6, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 7, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 8, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 9, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 10, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 11, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 12, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 36.

83. The vector of embodiment 81, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 1, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 2, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 3, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 4, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 16 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 5, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 17 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 6, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 18 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 7, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 19 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 8, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 20 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 9, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 21 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 10, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 22 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 11, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 23 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 12, wherein said CRISPR repeat sequence has at least 95% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 36.

84. The vector of embodiment 81, wherein said RGN polypeptide is selected from the group consisting of:

- a) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 1, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 13 and said tracrRNA has 100% sequence identity to SEQ ID NO: 25;
- b) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 2, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 14 and said tracrRNA has 100% sequence identity to SEQ ID NO: 26;
- c) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 3, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 15 and said tracrRNA has 100% sequence identity to SEQ ID NO: 27;
- d) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 4, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 16 and said tracrRNA has 100% sequence identity to SEQ ID NO: 28;
- e) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 5, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 17 and said tracrRNA has 100% sequence identity to SEQ ID NO: 29;
- f) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 6, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 18 and said tracrRNA has 100% sequence identity to SEQ ID NO: 30;
- g) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 7, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 19 and said tracrRNA has 100% sequence identity to SEQ ID NO: 31;
- h) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 8, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 20 and said tracrRNA has 100% sequence identity to SEQ ID NO: 32;
- i) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 9, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 21 and said tracrRNA has 100% sequence identity to SEQ ID NO: 33;
- j) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 10, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 22 and said tracrRNA has 100% sequence identity to SEQ ID NO: 34;
- k) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 11, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 23 and said tracrRNA has 100% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 12, wherein said CRISPR repeat sequence has 100% sequence identity to SEQ ID NO: 24 and said tracrRNA has 100% sequence identity to SEQ ID NO: 36.

85. A nucleic acid molecule comprising a trans-activating CRISPR RNA (tracrRNA) or a polynucleotide encoding a tracrRNA comprising a nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 25-36;

wherein a guide RNA comprising:

a) said tracrRNA; and

b) a crRNA comprising a spacer sequence and a CRISPR repeat sequence,

wherein said tracrRNA hybridizes with said CRISPR repeat sequence of said crRNA; is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of said crRNA when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide.

86. The nucleic acid molecule of embodiment 85, wherein said polynucleotide encoding a tracrRNA is operably linked to a promoter heterologous to said polynucleotide.

87. The nucleic acid molecule of embodiment 85 or 86, wherein said tracrRNA comprises a nucleotide sequence having at least 95% sequence identity to any one of SEQ ID NOs: 25-36.

88. The nucleic acid molecule of embodiment 85 or 86, wherein said tracrRNA comprises a nucleotide sequence having 100% sequence identity to any one of SEQ ID NOs: 25-36.

89. A vector comprising the nucleic acid molecule comprising said polynucleotide encoding said tracrRNA of any one of embodiments 85-88.

90. The vector of embodiment 89, wherein said vector further comprises a polynucleotide encoding said crRNA.

91. The vector of embodiment 90, wherein said crRNA comprises a CRISPR repeat sequence selected from the group consisting of:

a) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 25;

b) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 26;

c) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 27;

d) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 28;

e) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 29;

f) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 30;

g) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 31;

5 h) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 32;

i) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 33;

10 j) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 34;

k) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 35; and

l) a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24, wherein said tracrRNA has at least 90% sequence identity to SEQ ID NO: 36.

15 92. The vector of embodiment 90, wherein said crRNA comprises a CRISPR repeat sequence selected from the group consisting of:

a) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 25;

20 b) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 26;

c) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 27;

d) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 28;

25 e) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 17, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 29;

f) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 30;

30 g) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 31;

h) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 32;

i) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 33;

35 j) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 34;

k) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 35; and

l) a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24, wherein said tracrRNA has at least 95% sequence identity to SEQ ID NO: 36.

93. The vector of embodiment 90, wherein said crRNA comprises a CRISPR repeat sequence selected from the group consisting of:

a) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 25;

b) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 26;

c) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 27;

d) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 28;

e) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 29;

f) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 30;

g) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 31;

h) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 32;

i) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 33;

j) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 34;

k) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 35; and

l) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24, wherein said tracrRNA has 100% sequence identity to SEQ ID NO: 36.

94. The vector of any one of embodiments 90-93, wherein said polynucleotide encoding said crRNA and said polynucleotide encoding said tracrRNA are operably linked to the same promoter and are encoded as a single guide RNA (sgRNA).

95. The vector of embodiment 94, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

96. The vector of any one of embodiments 90-93, wherein said polynucleotide encoding said crRNA and said polynucleotide encoding said tracrRNA are operably linked to separate promoters.

97. The vector of any one of embodiments 90-96, wherein said vector further comprises a polynucleotide encoding said RGN polypeptide.

98. The vector of embodiment 97, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 1, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 2, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 3, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 4, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 5, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 6, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 7, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 8, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 9, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 10, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 11, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 12, wherein said crRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 36.

99. The vector of embodiment 97, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 1, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 2, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 3, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 4, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 5, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 17 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 6, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 7, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 8, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 9, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 10, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 11, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having at least 95% sequence identity to SEQ ID NO: 12, wherein said crRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 95% sequence identity to SEQ ID NO: 36.

100. The vector of embodiment 97, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 1, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13 and said tracrRNA has 100% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 2, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14 and said tracrRNA has 100% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 3, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15 and said tracrRNA has 100% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 4, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16 and said tracrRNA has 100% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 5, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17 and said tracrRNA has 100% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 6, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and said tracrRNA has 100% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 7, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19 and said tracrRNA has 100% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 8, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20 and said tracrRNA has 100% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 9, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21 and said tracrRNA has 100% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 10, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22 and said tracrRNA has 100% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 11, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23 and said tracrRNA has 100% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having 100% sequence identity to SEQ ID NO: 12, wherein said crRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24 and said tracrRNA has 100% sequence identity to SEQ ID NO: 36.

101. A cell comprising the nucleic acid molecule of any one of embodiments 69-72 and 85-88, the vector of any one of embodiments 73-84 and 89-100, the single guide RNA of embodiment 274 or 275, or the double guide RNA of embodiment 276.

102. The cell of embodiment 101, wherein the cell is a prokaryotic cell.

103. The cell of embodiment 101, wherein the cell is a eukaryotic cell.

104. The cell of embodiment 103, wherein the eukaryotic cell is a mammalian cell.

105. The cell of embodiment 104, wherein the mammalian cell is a human cell.

106. The cell of embodiment 105, wherein the human cell is an immune cell.

107. The cell of embodiment 106, wherein the immune cell is a stem cell.

108. The cell of embodiment 107, wherein the stem cell is an induced pluripotent stem cell.

109. The cell of embodiment 103, wherein the eukaryotic cell is an insect or avian cell.

110. The cell of embodiment 103, wherein the eukaryotic cell is a fungal cell.

111. The cell of embodiment 103, wherein the eukaryotic cell is a plant cell.

112. A plant comprising the cell of embodiment 111.

113. A seed comprising the cell of embodiment 111.

114. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12 or a polynucleotide comprising a nucleotide sequence encoding the RGN polypeptide;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

115. The system of embodiment 114, wherein at least one of said nucleotide sequences encoding the one or more guide RNAs and said nucleotide sequence encoding the RGN polypeptide is operably linked to a promoter heterologous to said nucleotide sequence.

116. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

117. The system of any one of embodiments 114-116, wherein at least one of said nucleotides sequences encoding the one or more guide RNAs is operably linked to a promoter heterologous to said nucleotide sequence.

118. The system of any one of embodiments 114-117, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

119. The system of any one of embodiments 114-117, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to any one of SEQ ID NOs: 1-12.

120. The system of any one of embodiments 114-119, wherein said RGN polypeptide and said one or more guide RNAs are not found complexed to one another in nature.

121. The system of any one of embodiments 114-120, wherein said target DNA sequence is a eukaryotic target DNA sequence.

122. The system of any one of embodiments 114-121, wherein said gRNA is a single guide RNA (sgRNA).

123. The system of embodiment 122, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

124. The system of any one of embodiments 114-121, wherein said gRNA is a dual-guide RNA.

125. The system of any one of embodiments 114-124, wherein said gRNA is selected from the group consisting of:

- 5 a) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;
- 10 b) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;
- 15 c) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;
- 20 d) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;
- 25 e) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;
- 30 f) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;
- g) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;
- 35 h) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

5 j) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NOs:10;

10 k) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

15 l) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

126. The system of any one of embodiments 114-124, wherein said gRNA is selected from the group consisting of:

20 a) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1;

25 b) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2;

30 c) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 4;

35 e) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29, wherein

said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30, wherein
5 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31, wherein
10 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32, wherein
said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33, wherein
15 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34, wherein
20 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NOs: 10;

k) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35, wherein
25 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36, wherein
30 said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 12.

127. The system of any one of embodiments 114-124, wherein said gRNA is selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having 100% sequence identity to SEQ ID NO: 25, wherein said
35 RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having 100% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 2;

5 c) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having 100% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 3;

10 d) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having 100% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 4;

15 e) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having 100% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 5;

20 f) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having 100% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 7;

25 h) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having 100% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 8;

30 i) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having 100% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 9;

35 j) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having 100% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NOs: 10;

k) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having 100% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having 100% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 12.

128. The system of any one of embodiments 114-127, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

129. The system of any one of embodiments 114-127, wherein the target DNA sequence is within a cell.

130. The system of any one of embodiments 114-129, wherein the one or more guide RNAs is capable of hybridizing to the target DNA sequence and the guide RNA is capable of forming a complex with the RGN polypeptide to direct cleavage of the target DNA sequence.

131. The system of embodiment 130, wherein the cleavage generates a double-stranded break.

132. The system of embodiment 130, wherein the cleavage generates a single-stranded break.

133. The system of any one of embodiments 114-129, wherein said RGN polypeptide is nuclease inactive or is a nickase.

134. The system of any one of embodiments 114-130, 132, and 133, wherein said RGN polypeptide is operably linked to a prime editing polypeptide.

135. The system of embodiment 134, wherein said prime editing polypeptide comprises a DNA polymerase.

136. The system of embodiment 134, wherein said prime editing polypeptide comprises a reverse transcriptase.

137. The system of any one of embodiments 114-133, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

138. The system of embodiment 137, wherein the base-editing polypeptide is a deaminase.

139. The system of embodiment 138, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

140. The system of embodiment 138, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

141. The system of embodiment 138, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

142. The system of any one of embodiments 114-141, wherein the RGN polypeptide comprises one or more nuclear localization signals.

143. The system of any one of embodiments 114-142, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

144. The system of any one of embodiments 114-143, wherein the nucleotide sequences encoding the one or more guide RNAs and the nucleotide sequence encoding the RGN polypeptide are located on one vector.

145. The system of any one of embodiments 114-144, wherein said system further comprises one or more donor polynucleotides.

146. A cell comprising the system of any one of embodiments 114-145.

147. The cell of embodiment 146, wherein the cell is a prokaryotic cell.

148. The cell of embodiment 146, wherein the cell is a eukaryotic cell.

149. The cell of embodiment 148, wherein the eukaryotic cell is a mammalian cell.

150. The cell of embodiment 149, wherein the mammalian cell is a human cell.

151. The cell of embodiment 150, wherein the human cell is an immune cell.

152. The cell of embodiment 151, wherein the immune cell is a stem cell.

153. The cell of embodiment 152, wherein the stem cell is an induced pluripotent stem cell.

154. The cell of embodiment 148, wherein the eukaryotic cell is an insect or avian cell.

155. The cell of embodiment 148, wherein the eukaryotic cell is a fungal cell.

156. The cell of embodiment 148, wherein the eukaryotic cell is a plant cell.

157. A plant comprising the cell of embodiment 156.

158. A seed comprising the cell of embodiment 156.

159. A pharmaceutical composition comprising the nucleic acid molecule of any one of embodiments 1-19, 69-72, and 85-88, the vector of any one of embodiments 20-27, 73-84, and 89-100, the cell of any one of embodiments 30-35, 103-108, and 148-153, the RGN polypeptide of any one of embodiments 48-65, the RNP complex of any one of embodiments 66-68, or the system of any one of embodiments 114-145, and a pharmaceutically acceptable carrier.

160. The pharmaceutical composition of embodiment 159, wherein the pharmaceutically acceptable carrier is heterologous to said nucleic acid molecule, said vector, said cell, said RGN polypeptide, or said system.

161. The pharmaceutical composition of embodiment 159 or 160, wherein the pharmaceutically acceptable carrier is not naturally-occurring.

162. A method for binding a target DNA sequence of a DNA molecule comprising delivering a system according to any one of embodiments 114-145, to said target DNA sequence or a cell comprising the target DNA sequence.

163. The method of embodiment 162, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

164. The method of embodiment 162, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby modulating expression of said target DNA sequence or a gene under transcriptional control by said target DNA sequence.

165. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule comprising delivering a system according to any one of embodiments 114-145 to said target DNA sequence or a cell comprising the DNA molecule, wherein cleavage or modification of said target DNA sequence occurs.

166. The method of embodiment 165, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

167. The method of embodiment 165, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

168. The method of embodiment 165, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

169. A method for binding a target DNA sequence of a DNA molecule comprising:

a) assembling an RNA-guided nuclease (RGN) ribonucleotide complex by combining:

i) one or more guide RNAs capable of hybridizing to the target DNA sequence;

and

ii) an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs:1-12;

under conditions suitable for formation of the RGN ribonucleotide complex; and

b) contacting said target DNA sequence or a cell comprising said target DNA sequence with the assembled RGN ribonucleotide complex;

wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence.

170. The method of embodiment 169, wherein said method is performed *in vitro*, *in vivo*, or *ex vivo*.

171. The method of embodiment 169 or 170, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

172. The method of embodiment 169 or 170, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby allowing for the modulation of expression of said target DNA sequence.

173. The method of embodiment 169 or 170, wherein said RGN polypeptide is operably linked to a prime editing polypeptide, thereby allowing for the modification of said target DNA sequence.

174. The method of embodiment 173, wherein said prime editing polypeptide comprises a DNA polymerase.

175. The method of embodiment 173, wherein said prime editing polypeptide comprises a reverse transcriptase.

5 176. The method of embodiment 169 or 170, wherein said RGN polypeptide is operably linked to a base-editing polypeptide, thereby allowing for the modification of said target DNA sequence.

177. The method of embodiment 176, wherein said base-editing polypeptide comprises a deaminase.

10 178. The method of embodiment 177, wherein said deaminase is a cytosine deaminase or an adenine deaminase.

179. The method of embodiment 177, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

180. The method of embodiment 178, wherein the deaminase has 100% sequence identity
15 to an amino acid sequence of any one of SEQ ID NOs: 377-448.

181. The method of embodiment 169 or 170, wherein said RGN polypeptide is capable of cleaving said target DNA sequence, thereby allowing for the cleaving and/or modifying of said target DNA sequence.

182. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule,
20 comprising contacting the DNA molecule with:

a) an RNA-guided nuclease (RGN) polypeptide, wherein said RGN comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; and

b) one or more guide RNAs capable of targeting the RGN of (a) to the target DNA sequence;

25 wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence and cleavage and/or modification of said target DNA sequence occurs.

183. The method of embodiment 182, wherein cleavage by said RGN polypeptide generates a double-stranded break.

30 184. The method of embodiment 182, wherein cleavage by said RGN polypeptide generates a single-stranded break.

185. The method of embodiment 182, wherein said RGN polypeptide is nuclease inactive or a nickase.

35 186. The method of any one of embodiments 182, 184, and 185, wherein said RGN is operably linked to a prime editing polypeptide, thereby allowing for the modification of said target DNA sequence.

187. The method of embodiment 186, wherein said prime editing polypeptide comprises a DNA polymerase.

188. The method of embodiment 186, wherein said prime editing polypeptide comprises a reverse transcriptase.

5 189. The method of any one of embodiments 182-185, wherein said RGN polypeptide is operably linked to a base-editing polypeptide.

190. The method of embodiment 189, wherein the base-editing polypeptide is a deaminase.

10 191. The method of embodiment 189, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

192. The method of embodiment 190, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

193. The method of embodiment 190, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

15 194. The method of embodiment 182, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

195. The method of embodiment 182, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

20 196. The method of embodiment 182, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

197. The method of any one of embodiments 169-196, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

198. The method of any one of embodiments 169-197, wherein said target DNA sequence is a eukaryotic target DNA sequence.

25 199. The method of any one of embodiments 169-198, wherein said gRNA is a single guide RNA (sgRNA).

200. The method of embodiment 199, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

30 201. The method of any one of embodiments 169-198, wherein said gRNA is a dual-guide RNA.

202. The method of any one of embodiments 169-201, wherein said RGN comprises an amino acid sequence having at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

203. The method of any one of embodiments 169-201, wherein said RGN comprises an amino acid sequence having 100% sequence identity to any one of SEQ ID NOs: 1-12.

35 204. The method of any one of embodiments 169-201, wherein:

a) said RGN has at least 90% sequence identity to SEQ ID NO: 1, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25;

b) said RGN has at least 90% sequence identity to SEQ ID NO: 2, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26;

c) said RGN has at least 90% sequence identity to SEQ ID NO: 3, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27;

d) said RGN has at least 90% sequence identity to SEQ ID NO: 4, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28;

e) said RGN has at least 90% sequence identity to SEQ ID NO: 5, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29;

f) said RGN has at least 90% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30;

g) said RGN has at least 90% sequence identity to SEQ ID NO: 7, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31;

h) said RGN has at least 90% sequence identity to SEQ ID NO: 8, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32;

i) said RGN has at least 90% sequence identity to SEQ ID NO: 9, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33;

j) said RGN has at least 90% sequence identity to SEQ ID NO: 10, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34;

k) said RGN has at least 90% sequence identity to SEQ ID NO: 11, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35; or

l) said RGN has at least 90% sequence identity to SEQ ID NO: 12, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36.

205. The method of any one of embodiments 169-201, wherein:

a) said RGN has at least 95% sequence identity to SEQ ID NO: 1, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25;

b) said RGN has at least 95% sequence identity to SEQ ID NO: 2, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26;

c) said RGN has at least 95% sequence identity to SEQ ID NO: 3, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27;

d) said RGN has at least 95% sequence identity to SEQ ID NO: 4, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28;

e) said RGN has at least 95% sequence identity to SEQ ID NO: 5, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29;

f) said RGN has at least 95% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30;

g) said RGN has at least 95% sequence identity to SEQ ID NO: 7, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31;

h) said RGN has at least 95% sequence identity to SEQ ID NO: 8, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32;

i) said RGN has at least 95% sequence identity to SEQ ID NO: 9, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33;

j) said RGN has at least 95% sequence identity to SEQ ID NO: 10, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34;

k) said RGN has at least 95% sequence identity to SEQ ID NO: 11, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35; or

l) said RGN has at least 95% sequence identity to SEQ ID NO: 12, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36.

206. The method of any one of embodiments 169-201, wherein:

a) said RGN has 100% sequence identity to SEQ ID NO: 1, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having 100% sequence identity to SEQ ID NO: 25;

b) said RGN has 100% sequence identity to SEQ ID NO: 2, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having 100% sequence identity to SEQ ID NO: 26;

c) said RGN has 100% sequence identity to SEQ ID NO: 3, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having 100% sequence identity to SEQ ID NO: 27;

d) said RGN has 100% sequence identity to SEQ ID NO: 4, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having 100% sequence identity to SEQ ID NO: 28;

e) said RGN has 100% sequence identity to SEQ ID NO: 5, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having 100% sequence identity to SEQ ID NO: 29;

f) said RGN has 100% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30;

g) said RGN has 100% sequence identity to SEQ ID NO: 7, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having 100% sequence identity to SEQ ID NO: 31;

h) said RGN has 100% sequence identity to SEQ ID NO: 8, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having 100% sequence identity to SEQ ID NO: 32;

i) said RGN has 100% sequence identity to SEQ ID NO: 9, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having 100% sequence identity to SEQ ID NO: 33;

j) said RGN has 100% sequence identity to SEQ ID NO: 10, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having 100% sequence identity to SEQ ID NO: 34;

k) said RGN has 100% sequence identity to SEQ ID NO: 11, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having 100% sequence identity to SEQ ID NO: 35; or

l) said RGN has 100% sequence identity to SEQ ID NO: 12, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having 100% sequence identity to SEQ ID NO: 36.

207. The method of any one of embodiments 162-206, wherein the target DNA sequence is within a cell.

208. The method of embodiment 207, wherein the cell is a eukaryotic cell.

209. The method of embodiment 208, wherein the eukaryotic cell is a mammalian cell.

5 210. The method of embodiment 209, wherein said mammalian cell is a human cell.

211. The method of embodiment 210, wherein said human cell is an immune cell.

212. The method of embodiment 211, wherein said immune cell is a stem cell.

213. The method of embodiment 212, wherein said stem cell is an induced pluripotent stem cell.

10 214. The method of embodiment 208, wherein the eukaryotic cell is an insect or avian cell.

215. The method of embodiment 207, wherein the cell is a prokaryotic cell.

216. The method of embodiment 208, wherein the eukaryotic cell is a fungal cell.

217. The method of embodiment 208, wherein the eukaryotic cell is a plant cell.

15 218. The method of any one of embodiments 207-217, further comprising culturing the cell under conditions in which the RGN polypeptide is expressed and cleaves and modifies the target DNA sequence to produce a DNA molecule comprising a modified target DNA sequence; and selecting a cell comprising said modified target DNA sequence.

219. A cell comprising a modified target DNA sequence according to the method of embodiment 218.

20 220. The cell of embodiment 219, wherein the cell is a eukaryotic cell.

221. The cell of embodiment 220, wherein the eukaryotic cell is a mammalian cell.

222. The cell of embodiment 221, wherein said mammalian cell is a human cell.

223. The cell of embodiment 222, wherein said human cell is an immune cell.

224. The cell of embodiment 223, wherein said immune cell is a stem cell.

25 225. The cell of embodiment 224, wherein said stem cell is an induced pluripotent stem cell.

226. The cell of embodiment 220, wherein the eukaryotic cell is an insect or avian cell.

227. The cell of embodiment 219, wherein the cell is a prokaryotic cell.

228. The cell of embodiment 220, wherein the eukaryotic cell is a fungal cell.

30 229. The cell of embodiment 220, wherein the eukaryotic cell is a plant cell.

230. A plant comprising the cell of embodiment 229.

231. A seed comprising the cell of embodiment 229.

232. A pharmaceutical composition comprising the cell of any one of embodiments 220-225 and a pharmaceutically acceptable carrier.

35 233. A method for producing a genetically modified cell with a correction in a causal mutation for a genetically inherited disease, the method comprising introducing into the cell:

a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12, or a polynucleotide encoding said RGN polypeptide, wherein said polynucleotide encoding the RGN polypeptide is operably linked to a promoter to enable expression of the RGN polypeptide in the cell;
 5 and

b) a guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell

whereby the RGN and gRNA target to the genomic location of the causal mutation and
 10 modify the genomic sequence to remove the causal mutation.

234. The method of embodiment 233, wherein the RGN is nuclease inactive or a nickase.

235. The method of embodiment 233 or 234, wherein the RGN is operably linked to a prime editing polypeptide.

236. The method of embodiment 235, wherein the prime editing polypeptide comprises a
 15 DNA polymerase.

237. The method of embodiment 235, wherein the prime editing polypeptide comprises a reverse transcriptase.

238. The method of any one of embodiments 235-237, wherein said gRNA is a single guide RNA and comprises an extension comprising an edit template for prime editing.

20 239. The method of embodiment 233 or 234, wherein the RGN is operably linked to a polypeptide which has base-editing activity.

240. The method of embodiment 239, wherein the base-editing polypeptide is a deaminase.

241. The method of embodiment 240, wherein the polypeptide with base-editing activity is
 25 a cytosine deaminase or an adenine deaminase.

242. The method of embodiment 240, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

243. The method of embodiment 240, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

30 244. The method of any one of embodiments 240-243, wherein the genetically inherited disease is caused by a single nucleotide polymorphism.

245. The method of any one of embodiments 240-243, wherein the genetically inherited disease is Hurler Syndrome.

246. The method of embodiment 244, wherein the gRNA further comprises a spacer
 35 sequence that targets a region proximal to the causal single nucleotide polymorphism.

247. A method for producing a genetically modified cell with a deletion in a causal mutation, the method comprising introducing into the cell:

a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12, or a polynucleotide encoding said RGN polypeptide, wherein said polynucleotide encoding the RGN polypeptide is operably linked to a promoter to enable expression of the RGN polypeptide in the cell;
 5 and

b) a first guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell, and further wherein the gRNA comprises a spacer sequence that targets the 5' flank of the causal mutation; and

10 c) a second guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell, and further wherein said second gRNA comprises a spacer sequence that targets the 3' flank of the causal mutation;

whereby the RGN and the two gRNAs target to the causal mutation and at least a portion of
 15 the causal mutation is removed.

248. The method of embodiment 247, wherein the genetically inherited disease is Friedrich's Ataxia or Huntington's Disease.

249. The method of embodiment 247, wherein the first gRNA further comprises a spacer sequence that targets a region within or proximal to the causal mutation.

20 250. The method of embodiment 249, wherein the second gRNA further comprises a spacer sequence that targets a region within or proximal to the causal mutation.

251. The method of any one of embodiments 233-250, wherein said RGN polypeptide has at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

252. The method of any one of embodiments 233-250, wherein said RGN polypeptide has
 25 100% sequence identity to any one of SEQ ID NOs: 1-12.

253. The method of any one of embodiments 233-250, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA is selected from a gRNA selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to
 30 SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to
 SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein
 35 said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;

5 d) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;

10 e) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;

15 f) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;

20 g) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;

25 i) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

30 j) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 10;

35 k) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

5 254. The method of any one of embodiments 233-250, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA is selected from a gRNA selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25, wherein
10 said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26, wherein
15 said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27, wherein
said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 3;

20 d) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28, wherein
said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to
25 SEQ ID NO: 17 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29, wherein
said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30, wherein
30 said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31, wherein
35 said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32, wherein

said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 10;

k) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 12.

255. The method of any one of embodiments 233-250, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA is selected from a gRNA selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having 100% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having 100% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having 100% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having 100% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having 100% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having 100% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having 100% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having 100% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having 100% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 10;

k) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having 100% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having 100% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 12.

256. The method of any one of embodiments 233-255, wherein the cell is an animal cell.

257. The method of embodiment 256, wherein the animal cell is a mammalian cell.

258. The method of embodiment 256, wherein the cell is derived from a dog, cat, mouse, rat, rabbit, horse, cow, pig, or human.

259. A method for producing a genetically modified mammalian hematopoietic progenitor cell having decreased BCL11A mRNA and protein expression, the method comprising introducing into an isolated human hematopoietic progenitor cell:

a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12, or a polynucleotide encoding said RGN polypeptide, wherein said polynucleotide encoding the RGN polypeptide is operably linked to a promoter to enable expression of the RGN polypeptide in the cell; and

b) a guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell,

whereby the RGN and gRNA are expressed in the cell and cleave at the BCL11A enhancer region, resulting in genetic modification of the human hematopoietic progenitor cell and reducing the mRNA and/or protein expression of BCL11A.

260. The method of embodiment 259, wherein said RGN polypeptide has at least 95% sequence identity to any one of SEQ ID NOs: 1-12.

261. The method of embodiment 259, wherein said RGN polypeptide has 100% sequence identity to any one of SEQ ID NOs: 1-12.

262. The method of embodiment 259, wherein said gRNA is selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;

5 i) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

10 j) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 10;

15 k) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

20 l) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

263. The method of embodiment 259, wherein said gRNA is selected from the group consisting of:

25 a) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 1;

30 b) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 3;

35 d) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 28, wherein

said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 10;

k) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 12.

264. The method of embodiment 259, wherein said gRNA is selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having 100% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having 100% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having 100% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having 100% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having 100% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having 100% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having 100% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 8;

i) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having 100% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having 100% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 10;

k) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having 100% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having 100% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide has an amino acid sequence having 100% sequence identity to SEQ ID NO: 12.

265. The method of any one of embodiments 259-264, wherein the gRNA further comprises a spacer sequence that targets a region within or proximal to the BCL11A enhancer region.

266. A method of treating a disease, disorder, or condition, said method comprising administering to a subject in need thereof an effective amount of a pharmaceutical composition of any one of embodiments 159-161 and 232.

267. The method of embodiment 266, wherein said disease, disorder, or condition is associated with a causal mutation and said effective amount of said pharmaceutical composition corrects said causal mutation.

268. The method of embodiment 266 or 267, wherein said subject is at risk of developing said disease, disorder, or condition.

269. Use of the nucleic acid molecule of any one of embodiments 1-19, 69-72, and 85-88, the vector of any one of embodiments 20-27, 73-84, and 89-100, the cell of any one of embodiments 30-35, 103-108, 148-153, and 220-225, the RGN polypeptide of any one of embodiments 48-65, the RNP complex of any one of embodiments 66-68, or the system of any one of embodiments 114-145 for the treatment of a disease, disorder, or condition in a subject in need thereof.

270. The use of embodiment 269, wherein said disease, disorder, or condition is associated with a causal mutation and said treating comprises correcting said causal mutation.

271. The use of embodiment 269 or 270, wherein said subject is at risk of developing said disease, disorder, or condition.

272. Use of the nucleic acid molecule of any one of embodiments 1-19, 69-72, and 85-88, the vector of any one of embodiments 20-27, 73-84, and 89-100, the cell of any one of embodiments 30-35, 103-108, 148-153, and 220-225, the RGN polypeptide of any one of embodiments 48-65, the RNP complex of any one of embodiments 66-68, or the system of any one of embodiments 114-145 for the manufacture of a medicament useful for treating a disease, disorder, or condition.

273. The use of embodiment 272, wherein said disease is associated with a causal mutation and an effective amount of said medicament corrects said causal mutation.

274. A single guide RNA comprising the nucleic acid molecule comprising said crRNA of any one of embodiments 69-72 and the nucleic acid molecule comprising said tracrRNA of any one of embodiments 85-88.

275. The single guide RNA of embodiment 274, wherein said single guide RNA further comprises an extension comprising an edit template for prime editing.

276. A dual guide RNA comprising the nucleic acid molecule comprising said crRNA of any one of embodiments 69-72 and the nucleic acid molecule comprising said tracrRNA of any one of embodiments 85-88.

277. A nucleic acid molecule comprising a polynucleotide encoding an RNA-guided nuclease (RGN) polypeptide, wherein said polynucleotide comprises a nucleotide sequence encoding

an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:6;

wherein said RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence.

278. The nucleic acid molecule of embodiment 277, wherein said polynucleotide encoding an RGN polypeptide is operably linked to a promoter heterologous to said polynucleotide.

279. The nucleic acid molecule of embodiment 277 or 278, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO:6.

280. The nucleic acid molecule of embodiment 277 or 278, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6.

281. The nucleic acid molecule of any one of embodiments 277-280, wherein said RGN polypeptide is capable of cleaving said target DNA sequence upon binding.

282. The nucleic acid molecule of embodiment 281, wherein said RGN polypeptide is capable of generating a double-stranded break.

283. The nucleic acid molecule of embodiment 281, wherein said RGN polypeptide is capable of generating a single-stranded break.

284. The nucleic acid molecule of any one of embodiments 277-280, wherein said RGN polypeptide is nuclease inactive or is a nickase.

285. The nucleic acid molecule of any of embodiment 277-280, 283 and 284, wherein the RGN polypeptide is operably linked to a prime editing polypeptide.

286. The nucleic acid molecule of embodiment 285, wherein said prime editing polypeptide comprises a DNA polymerase.

287. The nucleic acid molecule of embodiment 285, wherein said prime editing polypeptide comprises a reverse transcriptase.

288. The nucleic acid molecule of any one of embodiments 277-284, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

289. The nucleic acid molecule of embodiment 288, wherein the base-editing polypeptide is a deaminase.

290. The nucleic acid molecule of embodiment 289, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

291. The nucleic acid molecule of embodiment 289, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

292. The nucleic acid molecule of embodiment 289, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

293. The nucleic acid molecule of any one of embodiments 277-292, wherein the RGN polypeptide comprises one or more nuclear localization signals.

294. The nucleic acid molecule of any one of embodiments 277-293, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

295. The nucleic acid molecule of any one of embodiments 277-294, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

296. The nucleic acid molecule of embodiment 295, wherein said PAM has the sequence set forth as SEQ ID NO: 78 or 465.

297. A vector comprising the nucleic acid molecule of any one of embodiments 277-296.

298. The vector of embodiment 297, further comprising at least one nucleotide sequence encoding said gRNA capable of hybridizing to said target DNA sequence.

299. The vector of embodiment 298, wherein the guide RNA comprises:

a) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18; and

b) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30.

300. The vector of embodiment 298, wherein the guide RNA comprises:

a) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18; and

b) a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30.

301. The vector of embodiment 298, wherein the guide RNA comprises:

a) a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18; and

b) a tracrRNA having 100% sequence identity to SEQ ID NO: 30.

302. The vector of any one of embodiments 298-301, where said gRNA is a single guide RNA (sgRNA).

303. The vector of embodiment 302, wherein said sgRNA further comprises an extension comprising an edit template for prime editing.

304. The vector of any one of embodiments 298-301, wherein said gRNA is a dual-guide RNA.

305. A cell comprising the nucleic acid molecule of any one of embodiments 277-296 or the vector of any one of embodiments 297-304.

306. An RNA-guided nuclease (RGN) polypeptide, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6; and

wherein said RGN polypeptide is capable of binding a target DNA sequence of a DNA molecule in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence.

307. The RGN polypeptide of embodiment 306, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6.

308. The RGN polypeptide of embodiment 306, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6.

309. The RGN polypeptide of any one of embodiments 306-308, wherein said RGN polypeptide is an isolated RGN polypeptide.

5 310. The RGN polypeptide of any one of embodiments 306-309, wherein said RGN polypeptide is capable of cleaving said target DNA sequence upon binding.

311. The RGN polypeptide of embodiment 310, wherein cleavage by said RGN polypeptide generates a double-stranded break.

10 312. The RGN polypeptide of embodiment 310, wherein cleavage by said RGN polypeptide generates a single-stranded break.

313. The RGN polypeptide of any one of embodiments 306-309, wherein said RGN polypeptide is nuclease inactive or a nickase.

314. The RGN polypeptide of any of embodiment 306-310, 312, and 313, wherein the RGN polypeptide is operably linked to a prime editing polypeptide.

15 315. The RGN polypeptide of embodiment 314, wherein said prime editing polypeptide comprises a DNA polymerase.

316. The RGN polypeptide of embodiment 314, wherein said prime editing polypeptide comprises a reverse transcriptase.

20 317. The RGN polypeptide of any one of embodiments 306-316, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

318. The RGN polypeptide of embodiment 317, wherein the base-editing polypeptide is a deaminase.

319. The RGN polypeptide of embodiment 318, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

25 320. The RGN polypeptide of embodiment 318, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

321. The RGN polypeptide of embodiment 318, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

30 322. The RGN polypeptide of any one of embodiments 306-321, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

323. The RGN polypeptide of embodiment 322, wherein said PAM has the sequence set forth as SEQ ID NO: 78 or 465.

324. The RGN polypeptide of any one of embodiments 306-323, wherein the RGN polypeptide comprises one or more nuclear localization signals.

35 325. A ribonucleoprotein (RNP) complex comprising the RGN polypeptide of any one of embodiments 306-324 and a guide RNA (gRNA) bound to the RGN polypeptide.

326. The RNP complex of embodiment 325, wherein said gRNA is a single guide RNA (sgRNA).

327. The RNP complex of embodiment 326, wherein said gRNA comprises an extension comprising an edit template for prime editing.

5 328. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

10 b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6 or a polynucleotide comprising a nucleotide sequence encoding the RGN polypeptide;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

15 wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

329. The system of embodiment 328, wherein at least one of said nucleotide sequences encoding the one or more guide RNAs and said nucleotide sequence encoding the RGN polypeptide is operably linked to a promoter heterologous to said nucleotide sequence.

20 330. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

25 b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

30 wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

331. The system of any one of embodiments 328-330, wherein at least one of said nucleotides sequences encoding the one or more guide RNAs is operably linked to a promoter heterologous to said nucleotide sequence.

35 332. The system of any one of embodiments 328-331, wherein said RGN polypeptide comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6.

333. The system of any one of embodiments 328-331, wherein said RGN polypeptide comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6.

334. The system of any one of embodiments 328-333, wherein said RGN polypeptide and said one or more guide RNAs are not found complexed to one another in nature.

5 335. The system of any one of embodiments 328-334, wherein said target DNA sequence is a eukaryotic target DNA sequence.

336. The system of any one of embodiments 328-335, wherein said gRNA is a single guide RNA (sgRNA).

10 337. The system of embodiment 336, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

338. The system of any one of embodiments 328-336, wherein said gRNA is a dual-guide RNA.

15 339. The system of any one of embodiments 328-338, wherein said gRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30.

340. The system of any one of embodiments 328-338, wherein said gRNA comprises a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30.

20 341. The system of any one of embodiments 328-338, wherein said gRNA comprises a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30.

342. The system of any one of embodiments 328-341, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

25 343. The system of embodiment 342, wherein said PAM has the sequence set forth as SEQ ID NO: 78 or 465.

344. The system of any one of embodiments 328-341, wherein the target DNA sequence is within a cell.

30 345. The system of any one of embodiments 328-344, wherein the one or more guide RNAs is capable of hybridizing to the target DNA sequence and the guide RNA is capable of forming a complex with the RGN polypeptide to direct cleavage of the target DNA sequence.

346. The system of embodiment 345, wherein the cleavage generates a double-stranded break.

347. The system of embodiment 345, wherein the cleavage generates a single-stranded break.

35 348. The system of any one of embodiments 328-344, wherein said RGN polypeptide is nuclease inactive or is a nickase.

349. The system of any one of embodiments 328-344, 347, and 348, wherein said RGN polypeptide is operably linked to a prime editing polypeptide.

350. The system of embodiment 349, wherein said prime editing polypeptide comprises a DNA polymerase.

5 351. The system of embodiment 349, wherein said prime editing polypeptide comprises a reverse transcriptase.

352. The system of any one of embodiments 328-348, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

353. The system of embodiment 352, wherein the base-editing polypeptide is a deaminase.

10 354. The system of embodiment 353, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

355. The system of embodiment 353, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

15 356. The system of embodiment 353, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

357. The system of any one of embodiments 328-355, wherein the RGN polypeptide comprises one or more nuclear localization signals.

358. The system of any one of embodiments 328-357, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

20 359. The system of any one of embodiments 328-358, wherein the nucleotide sequences encoding the one or more guide RNAs and the nucleotide sequence encoding the RGN polypeptide are located on one vector.

360. The system of any one of embodiments 328-359, wherein said system further comprises one or more donor polynucleotides.

25 361. A cell comprising the system of any one of embodiments 328-360.

362. A pharmaceutical composition comprising the nucleic acid molecule of any one of embodiments 277-296, the vector of any one of embodiments 297-304, the cell of embodiment 305 or 361, the RGN polypeptide of any one of embodiments 306-324, the RNP complex of any one of embodiments 325-327, or the system of any one of embodiments 328-360, and a pharmaceutically acceptable carrier.

30 363. The pharmaceutical composition of embodiment 362, wherein the pharmaceutically acceptable carrier is heterologous to said nucleic acid molecule, said vector, said cell, said RGN polypeptide, or said system.

35 364. The pharmaceutical composition of embodiment 362 or 363, wherein the pharmaceutically acceptable carrier is not naturally-occurring.

365. A method for binding a target DNA sequence of a DNA molecule comprising delivering a system according to any one of embodiments 328-360, to said target DNA sequence or a cell comprising the target DNA sequence.

366. The method of embodiment 365, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

367. The method of embodiment 365, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby modulating expression of said target DNA sequence or a gene under transcriptional control by said target DNA sequence.

368. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule comprising delivering a system according to any one of embodiments 328-360 to said target DNA sequence or a cell comprising the DNA molecule, wherein cleavage or modification of said target DNA sequence occurs.

369. The method of embodiment 368, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

370. The method of embodiment 368, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

371. The method of embodiment 368, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

372. A method for binding a target DNA sequence of a DNA molecule comprising:

a) assembling an RNA-guided nuclease (RGN) ribonucleotide complex by combining:

i) one or more guide RNAs capable of hybridizing to the target DNA sequence;

and

ii) an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:6;

under conditions suitable for formation of the RGN ribonucleotide complex; and

b) contacting said target DNA sequence or a cell comprising said target DNA sequence with the assembled RGN ribonucleotide complex;

wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence.

373. The method of embodiment 372, wherein said method is performed *in vitro*, *in vivo*, or *ex vivo*.

374. The method of embodiment 372 or 373, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

375. The method of embodiment 372 or 373, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby allowing for the modulation of expression of said target DNA sequence.

376. The method of embodiment 372 or 373, wherein said RGN polypeptide is operably linked to a prime editing polypeptide, thereby allowing for the modification of said target DNA sequence.

377. The method of embodiment 376, wherein said prime editing polypeptide comprises a DNA polymerase.

378. The method of embodiment 376, wherein said prime editing polypeptide comprises a reverse transcriptase.

379. The method of embodiment 372 or 373, wherein said RGN polypeptide is operably linked to a base-editing polypeptide, thereby allowing for the modification of said target DNA sequence.

380. The method of embodiment 379, wherein said base-editing polypeptide comprises a deaminase.

381. The method of embodiment 380, wherein said deaminase is a cytosine deaminase or an adenine deaminase.

382. The method of embodiment 380, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

383. The method of embodiment 380, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

384. The method of embodiment 372 or 373, wherein said RGN polypeptide is capable of cleaving said target DNA sequence, thereby allowing for the cleaving and/or modifying of said target DNA sequence.

385. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule, comprising contacting the DNA molecule with:

a) an RNA-guided nuclease (RGN) polypeptide, wherein said RGN comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6; and

b) one or more guide RNAs capable of targeting the RGN of (a) to the target DNA sequence;

wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence and cleavage and/or modification of said target DNA sequence occurs.

386. The method of embodiment 385, wherein cleavage by said RGN polypeptide generates a double-stranded break.

387. The method of embodiment 385, wherein cleavage by said RGN polypeptide generates a single-stranded break.

388. The method of embodiment 385, wherein said RGN polypeptide is nuclease inactive or a nickase.

389. The method of any one of embodiments 385, 387, and 388, wherein said RGN polypeptide is operably linked to a prime editing polypeptide, thereby allowing for the modification of said target DNA sequence.

390. The method of embodiment 389, wherein said prime editing polypeptide comprises a DNA polymerase.

391. The method of embodiment 389, wherein said prime editing polypeptide comprises a reverse transcriptase.

392. The method of any one of embodiments 385-388, wherein said RGN polypeptide is operably linked to a base-editing polypeptide.

393. The method of embodiment 392, wherein the base-editing polypeptide is a deaminase.

394. The method of embodiment 392, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

395. The method of embodiment 393, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

396. The method of embodiment 393, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

397. The method of embodiment 385, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

398. The method of embodiment 385, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

399. The method of embodiment 385, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

400. The method of any one of embodiments 372-399, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

401. The method of embodiment 400, wherein said PAM has the sequence set forth as SEQ ID NO: 78 or 465.

402. The method of any one of embodiments 372-401, wherein said target DNA sequence is a eukaryotic target DNA sequence.

403. The method of any one of embodiments 372-402, wherein said gRNA is a single guide RNA (sgRNA).

404. The method of embodiment 403, wherein said sgRNA comprises an extension comprising an edit template for prime editing.

405. The method of any one of embodiments 372-403, wherein said gRNA is a dual-guide RNA.

406. The method of any one of embodiments 372-405, wherein said RGN comprises an amino acid sequence having at least 95% sequence identity to SEQ ID NO: 6.

407. The method of any one of embodiments 372-405, wherein said RGN comprises an amino acid sequence having 100% sequence identity to SEQ ID NO: 6.

408. The method of any one of embodiments 372-405, wherein said RGN has at least 90% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30.

409. The method of any one of embodiments 372-405, wherein said RGN has at least 95% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30.

410. The method of any one of embodiments 372-405, wherein said RGN has 100% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30.

411. The method of any one of embodiments 365-183, wherein the target DNA sequence is within a cell.

412. The method of embodiment 411, further comprising culturing the cell under conditions in which the RGN polypeptide is expressed and cleaves and modifies the target DNA sequence to produce a DNA molecule comprising a modified target DNA sequence; and selecting a cell comprising said modified target DNA sequence.

413. A cell comprising a modified target DNA sequence according to the method of embodiment 412.

414. A pharmaceutical composition comprising the cell of embodiment 413 and a pharmaceutically acceptable carrier.

415. A method for producing a genetically modified cell with a correction in a causal mutation for a genetically inherited disease, the method comprising introducing into the cell:

a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6, or a polynucleotide encoding said RGN polypeptide, wherein said polynucleotide encoding the RGN polypeptide is operably linked to a promoter to enable expression of the RGN polypeptide in the cell; and

b) a guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell

whereby the RGN and gRNA target to the genomic location of the causal mutation and modify the genomic sequence to remove the causal mutation.

416. The method of embodiment 415, wherein the RGN is nuclease inactive or a nickase.

417. The method of embodiment 415 or 416, wherein the RGN is operably linked to a prime editing polypeptide.

418. The method of embodiment 417, wherein the prime editing polypeptide comprises a DNA polymerase.

419. The method of embodiment 417, wherein the prime editing polypeptide comprises a reverse transcriptase.

420. The method of any one of embodiments 417-419, wherein said gRNA comprises an extension comprising an edit template for prime editing.

421. The method of embodiment 415 or 416, wherein the RGN is operably linked to a polypeptide which has base-editing activity.

422. The method of embodiment 421, wherein the base-editing polypeptide is a deaminase.

423. The method of embodiment 422, wherein the polypeptide with base-editing activity is a cytosine deaminase or an adenine deaminase.

424. The method of embodiment 422, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

425. The method of embodiment 422, wherein the deaminase has 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

426. The method of any one of embodiments 415-425, wherein the genetically inherited disease is caused by a single nucleotide polymorphism.

427. The method of embodiment 426, wherein the gRNA further comprises a spacer sequence that targets a region proximal to the causal single nucleotide polymorphism.

428. A method for producing a genetically modified cell with a deletion in a causal mutation, the method comprising introducing into the cell:

a) an RNA-guided nuclease (RGN) polypeptide, wherein the RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6, or a polynucleotide encoding said RGN polypeptide, wherein said polynucleotide encoding the RGN polypeptide is operably linked to a promoter to enable expression of the RGN polypeptide in the cell;

b) a first guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell, and further wherein the gRNA comprises a spacer sequence that targets the 5' flank of the causal mutation; and

c) a second guide RNA (gRNA) or a polynucleotide encoding said gRNA, wherein said polynucleotide encoding the gRNA is operably linked to a promoter to enable expression of the gRNA in the cell, and further wherein said second gRNA comprises a spacer sequence that targets the 3' flank of the causal mutation;

whereby the RGN and the two gRNAs target to the causal mutation and at least a portion of the causal mutation is removed.

429. The method of embodiment 428, wherein the first gRNA further comprises a spacer sequence that targets a region within or proximal to the causal mutation.

5 430. The method of embodiment 429, wherein the second gRNA further comprises a spacer sequence that targets a region within or proximal to the causal mutation.

431. The method of any one of embodiments 415-430, wherein said RGN polypeptide has at least 95% sequence identity to SEQ ID NO: 6.

10 432. The method of any one of embodiments 415-430, wherein said RGN polypeptide has 100% sequence identity to SEQ ID NO: 6.

433. The method of any one of embodiments 415-430, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA comprises a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence
15 having at least 90% sequence identity to SEQ ID NO: 6.

434. The method of any one of embodiments 415-430, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA comprise a CRISPR repeat sequence having at least 95% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence
20 having at least 95% sequence identity to SEQ ID NO: 6.

435. The method of any one of embodiments 415-430, wherein said gRNA, said first gRNA, said second gRNA, or said first gRNA and said second gRNA comprise a CRISPR repeat sequence having 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having 100% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide has an amino acid sequence having 100%
25 sequence identity to SEQ ID NO: 6.

436. A method of treating a disease, disorder, or condition, said method comprising administering to a subject in need thereof an effective amount of a pharmaceutical composition of any one of embodiments 362-364 and 414.

30 437. The method of embodiment 436, wherein said disease, disorder, or condition is associated with a causal mutation and said effective amount of said pharmaceutical composition corrects said causal mutation.

438. The method of embodiment 436 or 437, wherein said subject is at risk of developing said disease, disorder, or condition.

35 439. Use of the nucleic acid molecule of any one of embodiments 277-296, the vector of any one of embodiments 297-304, the cell of embodiment 305 or 361, the RGN polypeptide of any one of embodiments 306-324, the RNP complex of any one of embodiments 325-327, or the system

of any one of embodiments 328-360 for the treatment of a disease, disorder, or condition in a subject in need thereof.

440. The use of embodiment 439, wherein said disease, disorder, or condition is associated with a causal mutation and said treating comprises correcting said causal mutation.

441. The use of embodiment 439 or 440, wherein said subject is at risk of developing said disease, disorder, or condition.

442. Use of the nucleic acid molecule of any one of embodiments 277-296, the vector of any one of embodiments 297-304, the cell of embodiment 305 or 361, the RGN polypeptide of any one of embodiments 306-324, the RNP complex of any one of embodiments 325-327, or the system of any one of embodiments 328-360 for the manufacture of a medicament useful for treating a disease, disorder, or condition.

443. The use of embodiment 442, wherein said disease is associated with a causal mutation and an effective amount of said medicament corrects said causal mutation.

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1. Identification of RNA-guided nuclease

Twelve distinct CRISPR-associated RNA-guided nucleases (RGNs) were identified and are described in Table 1 below. Table 1 provides the name of each RGN, its amino acid sequence, the source from which it was derived, and processed crRNA and tracrRNA sequences (see Example 2 for methods of identification). Table 1 further provides a generic single guide RNA (sgRNA) sequence, where the poly-N indicates the location of the spacer sequence which determines the nucleic acid target sequence of the sgRNA. For RGN systems LPG10134 and LPG10141, the conserved sequence in the base of the hairpin stem of the tracrRNA is CNANNA (SEQ ID NO: 322). For LPG10136, LPG10138, and LPG10139, the sequence in the same location is UNANNG (SEQ ID NO: 321). For RGN system LPG10145, the conserved sequence in the base of the hairpin stem of the tracrRNA is UNANNC (SEQ ID NO: 318). For LPG10146, LPG10147, LPG10150, LPG10155, LPG10159 and LPG10160, the sequence in the same location is UNANNA (SEQ ID NO: 319).

Table 1: Summary of SEQ IDs and CRISPR associated systems

RGN ID	SEQ ID NO.	Source	crRNA repeat seq (SEQ ID NO.)	tracrRNA (SEQ ID NO.)	sgRNA backbone (SEQ ID NO)
LPG10134	1	<i>Brevundimonas vesicularis</i>	13	25	37
LPG10136	2	<i>Bacillus_I endophyticus</i>	14	26	38
LPG10138	3	<i>Bacillus_C megaterium</i>	15	27	39
LPG10139	4	<i>Bacillus_C megaterium</i>	16	28	40
LPG10141	5	<i>Bosea thiooxidans</i>	17	29	41
LPG10145	6	undetermined	18	30	42
LPG10146	7	<i>Bifidobacterium thermacidophilum</i>	19	31	43
LPG10147	8	undetermined	20	32	44
LPG10150	9	undetermined	21	33	45
LPG10155	10	<i>Chryseobacterium geocarposphaerae</i>	22	34	46
LPG10159	11	Contaminated/multiple	23	35	47
LPG10160	12	<i>Chryseobacterium ureilyticum</i>	24	36	48

Example 2: Guide RNA identification and sgRNA construction

Guide RNAs were determined through identification of tracrRNAs and crRNAs encoded in the genomic CRISPR loci. An internal database of validated and predicted tracrRNAs was used to determine a putative RNA. When no homology-based tracrRNA could be identified, the anti-repeat portion of the tracrRNA was identified using permissive BLASTn parameters using the consensus CRISPR repeat following the protocol determined in Briner, Cold Spring Harb Protoc 7: pbd. prot086785 (2016). Manual curation of RNAs was performed using secondary structure prediction by RNAfold, an RNA folding software. sgRNA cassettes were prepared by DNA synthesis and were generally designed as follows (5'→3'): 20-30 bp spacer sequence, operably linked at its 3' end to the processed repeat portion of the crRNA, operably linked to a 4 bp noncomplementary linker (AAAG; SEQ ID NO: 323), operably linked at its 3' end to the processed tracrRNA. Other 4 bp noncomplementary linkers may also be used.

For *in vitro* assays, sgRNAs were synthesized by *in vitro* transcription of the sgRNA cassettes with a GeneArt™ Precision gRNA Synthesis Kit (ThermoFisher). Processed crRNA and tracrRNA sequences for each of the RGN polypeptides are identified and are set forth in Table 1. See Example 3 for the sgRNAs constructed for PAM libraries 1 and 2.

Example 3: Determination of PAM requirements for each RGN

PAM requirements for each RGN were determined using an in vitro translation PAM determination assay essentially adapted from Karvelis et al. (2015) Genome Biol 253. Briefly, two plasmid libraries (L1 and L2) were generated in a pUC18 backbone (ampR), with each containing a distinct 30bp protospacer (target) sequence flanked by 8 random nucleotides (i.e., the PAM region). The target sequence and flanking PAM region of library 1 and library 2 for each RGN are set forth in Table 2.

Briefly, the proteins were translated in vitro using the PURExpress In Vitro Protein Synthesis kit (New England Biolabs) starting from a T7 promoter driven bacterial expression plasmid.

In the presence of the appropriate sgRNA, plasmids containing a PAM that is recognizable by the RGN will be cleaved. Adapters were ligated to cleaved DNA using the NEBNext Ultra II DNA Library Prep Kit (New England Biolabs), and after cleanup, the product was PCR amplified using primers complementary to the ligated adapter and plasmid backbone sequence such that the enriched PAM sequences were contained in the amplicon. Deep sequencing (75bp single end reads) was performed on a MiSeq (Illumina) by a service provider (MoGene, St. Louis, MO). Typically, 500,000 reads were obtained per amplicon. PAM regions were extracted, counted, and normalized to total reads for each sample. PAMs that led to plasmid cleavage were identified by being enriched when compared to controls (i.e., the starting frequencies for the PAM in the libraries). To represent PAM requirements for a novel RGN, the depletion ratios (frequency in sample/frequency in control) for all sequences in the region in question were converted to enrichment values with a $-\log$ base 2 transformation. Sufficient PAMs were defined as those with enrichment values >3.5 . PAMs above this threshold in both libraries were collected and used to generate web logos, which for example can be generated using a web-based service on the internet known as “weblogo”. PAM sequences were identified and reported when there was a consistent pattern in the top enriched PAMs. A consensus PAM (having an enrichment factor (EF) >3.5) for each RGN is provided in Table 2. The PAM orientation is also indicated in Table 2.

Table 2: PAM or PAM-like determination

RGN ID	sgRNA L1 (SEQ ID NO.)	sgRNA L2 (SEQ ID NO.)	PAM (SEQ ID NO.)	PAM orientation
LPG10134	49	61	73	5'-target-PAM-3'
LPG10136	50	62	74	5'-target-PAM-3'
LPG10138	51	63	75	5'-target-PAM-3'
LPG10139	52	64	76	5'-target-PAM-3'
LPG10141	53	65	77	5'-target-PAM-3'
LPG10145	54	66	78	5'-target-PAM-3'
LPG10146	55	67	79	5'-target-PAM-3'
LPG10147	56	68	80	5'-target-PAM-3'

RGN ID	sgRNA L1 (SEQ ID NO.)	sgRNA L2 (SEQ ID NO.)	PAM (SEQ ID NO.)	PAM orientation
LPG10150	57	69	81	5'-target-PAM-3'
LPG10155	58	70	82	5'-target-PAM-3'
LPG10159	59	71	83	5'-target-PAM-3'
LPG10160	60	72	84	5'-target-PAM-3'

Example 4: Demonstration of gene editing activity in mammalian cells

RGN expression cassettes were produced and introduced into vectors for mammalian expression. Each RGN was codon-optimized for human expression and operably fused at the 5' end to an SV40 nuclear localization sequence (NLS; SEQ ID NO: 316) and to 3xFLAG tags (SEQ ID NO: 326), and operably fused at the 3' end to nucleoplasmin NLS sequences (SEQ ID NO: 317). Each expression cassette was under control of a cytomegalovirus (CMV) promoter (SEQ ID NO: 327). It is known in the art that the CMV transcription enhancer (SEQ ID NO: 328) may also be included in constructs comprising the CMV promoter. Guide RNA expression constructs encoding a single gRNA, each under the control of a human RNA polymerase III U6 promoter (SEQ ID NO: 329), were produced and introduced into the pTwist High Copy Amp vector. Sequences for the target sequences for each guide are provided in Table 3.

Several of the constructs described above were introduced into mammalian cells. One day prior to transfection, 1×10^5 HEK293T cells (Sigma) were plated in 24-well dishes in Dulbecco's modified Eagle medium (DMEM) plus 10% (vol/vol) fetal bovine serum (Gibco) and 1% Penicillin-Streptomycin (Gibco). The next day when the cells were at 50-60% confluency, 500 ng of an RGN expression plasmid plus 500 ng of a single gRNA expression plasmid were co-transfected using 1.5 μ L of Lipofectamine 3000 (Thermo Scientific) per well, following the manufacturer's instructions. After 48 hours of growth, total genomic DNA was harvested using a genomic DNA isolation kit (Machery-Nagel) according to the manufacturer's instructions.

The total genomic DNA was then analyzed to determine the rate of editing for each RGN for each genomic target. First, oligonucleotides were produced to be used for PCR amplification and subsequent analysis of the amplified genomic target site.

All PCR reactions were performed using 10 μ L of 2X Master Mix Phusion High-Fidelity DNA polymerase (Thermo Scientific) in a 20 μ L reaction including 0.5 μ M of each primer. Large genomic regions encompassing each target gene were first amplified using PCR#1 primers, using a program of: 98°C., 1 min; 30 cycles of [98°C., 10 sec; 62°C., 15 sec; 72°C., 5 min]; 72°C., 5 min; 12°C., forever. One microliter of this PCR reaction was then further amplified using primers specific for each guide (PCR#2 primers), using a program of: 98°C., 1 min; 35 cycles of [98°C., 10 sec; 67°C., 15 sec; 72°C., 30 sec]; 72°C., 5 min; 12°C., forever. Primers for PCR#2 include Nextera Read 1 and Read 2 Transposase Adapter overhang sequences for Illumina sequencing.

A number of different genes in the human genome were targeted for RNA-guided cleavage. These loci are included in Table 3 below.

Table 3: Target and sgRNA sequences for guide RNAs used to test gene editing activity in mammalian cells

RGN ID	Gene	Guide ID	Target Sequence (SEQ ID NO)
LPG10134	B2M	SGN002644	554
LPG10134	B2M	SGN002645	555
LPG10134	B2M	SGN002646	556
LPG10134	B2M	SGN002647	557
LPG10134	B2M	SGN002648	558
LPG10134	TRAC	SGN002649	559
LPG10134	TRAC	SGN002650	560
LPG10134	TRAC	SGN002651	561
LPG10134	TRAC	SGN002652	562
LPG10134	TRAC	SGN002653	563
LPG10136	B2M	SGN002654	564
LPG10136	B2M	SGN002655	565
LPG10136	B2M	SGN002656	566
LPG10136	B2M	SGN002657	567
LPG10136	B2M	SGN002658	568
LPG10136	TRAC	SGN002659	569
LPG10136	TRAC	SGN002660	570
LPG10136	TRAC	SGN002661	571
LPG10136	TRAC	SGN002662	572
LPG10136	TRAC	SGN002663	573
LPG10138	B2M	SGN002664	574
LPG10138	B2M	SGN002665	575
LPG10138	B2M	SGN002666	576
LPG10138	B2M	SGN002667	577
LPG10138	B2M	SGN002668	578
LPG10138	TRAC	SGN002669	579
LPG10138	TRAC	SGN002670	580
LPG10138	TRAC	SGN002671	581
LPG10138	TRAC	SGN002672	582
LPG10138	TRAC	SGN002673	583
LPG10139	B2M	SGN002674	584
LPG10139	B2M	SGN002675	585
LPG10139	B2M	SGN002676	586

RGN ID	Gene	Guide ID	Target Sequence (SEQ ID NO)
LPG10139	B2M	SGN002677	587
LPG10139	B2M	SGN002678	588
LPG10139	TRAC	SGN002679	589
LPG10139	TRAC	SGN002680	590
LPG10139	TRAC	SGN002681	591
LPG10139	TRAC	SGN002682	592
LPG10139	TRAC	SGN002683	593
LPG10141	B2M	SGN002684	594
LPG10141	B2M	SGN002685	595
LPG10141	B2M	SGN002686	596
LPG10141	B2M	SGN002687	597
LPG10141	B2M	SGN002688	598
LPG10141	TRAC	SGN002689	599
LPG10141	TRAC	SGN002690	600
LPG10141	TRAC	SGN002691	601
LPG10141	TRAC	SGN002692	602
LPG10141	TRAC	SGN002693	603
LPG10145	B2M	SGN002698	604
LPG10145	B2M	SGN002699	605
LPG10145	B2M	SGN002700	606
LPG10145	B2M	SGN002701	607
LPG10145	B2M	SGN002702	608
LPG10145	TRAC	SGN002703	609
LPG10145	TRAC	SGN002704	610
LPG10145	TRAC	SGN002705	611
LPG10145	TRAC	SGN002706	612
LPG10145	TRAC	SGN002707	613
LPG10146	B2M	SGN002708	614
LPG10146	B2M	SGN002709	615
LPG10146	B2M	SGN002710	616
LPG10146	B2M	SGN002711	617
LPG10146	B2M	SGN002712	618
LPG10146	TRAC	SGN002713	619
LPG10146	TRAC	SGN002714	620
LPG10146	TRAC	SGN002715	621
LPG10146	TRAC	SGN002716	622
LPG10146	TRAC	SGN002717	623
LPG10147	B2M	SGN002718	624
LPG10147	B2M	SGN002719	625

RGN ID	Gene	Guide ID	Target Sequence (SEQ ID NO)
LPG10147	TRAC	SGN002720	626
LPG10147	TRAC	SGN002721	627
LPG10147	TRAC	SGN002722	628
LPG10147	TRAC	SGN002723	629
LPG10150	B2M	SGN002724	630
LPG10150	B2M	SGN002725	631
LPG10150	B2M	SGN002726	632
LPG10150	B2M	SGN002727	633
LPG10150	B2M	SGN002728	634
LPG10150	TRAC	SGN002729	635
LPG10150	TRAC	SGN002730	636
LPG10150	TRAC	SGN002731	637
LPG10150	TRAC	SGN002732	638
LPG10150	TRAC	SGN002733	639
LPG10155	B2M	SGN002734	640
LPG10155	B2M	SGN002735	641
LPG10155	TRAC	SGN002736	642
LPG10155	TRAC	SGN002737	643
LPG10155	TRAC	SGN002738	644
LPG10155	TRAC	SGN002739	645
LPG10159	B2M	SGN002740	646
LPG10159	B2M	SGN002741	647
LPG10159	B2M	SGN002742	648
LPG10159	B2M	SGN002743	649
LPG10159	B2M	SGN002744	650
LPG10159	TRAC	SGN002745	651
LPG10159	TRAC	SGN002746	652
LPG10159	TRAC	SGN002747	653
LPG10159	TRAC	SGN002748	654
LPG10159	TRAC	SGN002749	655
LPG10160	B2M	SGN002750	656
LPG10160	B2M	SGN002751	657
LPG10160	B2M	SGN002752	658
LPG10160	B2M	SGN002753	659
LPG10160	B2M	SGN002754	660
LPG10160	TRAC	SGN002755	661
LPG10160	TRAC	SGN002756	662
LPG10160	TRAC	SGN002757	663
LPG10160	TRAC	SGN002758	664

RGN ID	Gene	Guide ID	Target Sequence (SEQ ID NO)
LPG10160	TRAC	SGN002759	665

Purified genomic DNA was subjected to PCR#1 and PCR#2 as above. Following the second PCR amplification, DNA was cleaned using a PCR cleanup kit (Zymo) according to the manufacturer's instructions and eluted in water. 200-500ng of purified PCR#2 product was combined with 2 μ L of 10X NEB Buffer 2 and water in a 20 μ L reaction and annealed to form heteroduplex DNA using a program of: 95°C., 5 min; 95-85°C, cooled at a rate of 2°C / sec; 85-25°C, cooled at a rate of 0.1°C / sec.; 12°C., forever. Following annealing 5 μ L of DNA was removed as a no enzyme control, and 1 μ L of T7 Endonuclease I (NEB) was added and the reaction incubated at 37°C for 1 hr. After incubation 5x FlashGel loading dye (Lonza) was added and 5 μ L of each reaction and controls were analyzed by a 2.2% agarose FlashGel (Lonza) using gel electrophoresis. Following visualization of the gel, the percentage of non-homologous end joining (NHEJ) was determined using the following equation: %NHEJ events = $100 \times [1 - (1 - \text{fraction cleaved})^{1/2}]$, where (fraction cleaved) is defined as: (density of digested products)/(density of digested products + undigested parental band).

For some samples, SURVEYOR® was used to analyze the results following expression in mammalian cells. Cells were incubated at 37° C for 72 h post-transfection before genomic DNA extraction. Genomic DNA was extracted using the QuickExtract DNA Extraction Solution (Epicentre) following the manufacturer's protocol. The genomic region flanking the RGN target site was PCR amplified, and products were purified using QiaQuick Spin Column (Qiagen) following the manufacturer's protocol. 200-500 ng total of the purified PCR products were mixed with 1 μ L 10 $\times$ Taq DNA Polymerase PCR buffer (Enzymatics) and ultrapure water to a final volume of 10 μ L, and subjected to a re-annealing process to enable heteroduplex formation: 95° C for 10 min, 95° C to 85° C ramping at -2° C/s, 85° C to 25° C at -0.25° C/s, and 25° C hold for 1 min.

After reannealing, products were treated with SURVEYOR® nuclease and SURVEYOR® enhancer S (Integrated DNA Technologies) following the manufacturer's recommended protocol and analyzed on 4-20% Novex TBE polyacrylamide gels (Life Technologies). Gels were stained with SYBR Gold DNA stain (Life Technologies) for 10 min and imaged with a Gel Doc gel imaging system (Bio-rad). Quantification was based on relative band intensities. Indel percentage was determined by the formula, $100 \times (1 - (1 - (b+c)/(a+b+c))^{1/2})$, where a is the integrated intensity of the undigested PCR product, and b and c are the integrated intensities of each cleavage product.

Additionally, products from PCR#2 containing Illumina overhang sequences underwent library preparation following the Illumina 16S Metagenomic Sequencing Library protocol. Deep sequencing was performed on an Illumina Mi-Seq platform by a service provider (MOGene). Typically, 200,000 of 250 bp paired-end reads (2 x 100,000 reads) are generated per amplicon. The

reads were analyzed using CRISPResso (Pinello, et al. 2016 Nature Biotech, 34:695-697) to calculate the rates of editing. Output alignments were hand-curated to confirm insertion and deletion sites as well as identify microhomology sites at the recombination sites. The rates of editing are shown in Table 4. All experiments were performed in human cells. The “target sequence” is the targeted sequence within the gene target. For each target sequence, the guide RNA comprised the complementary RNA target sequence and the appropriate sgRNA depending on the RGN used. A selected breakdown of experiments by guide RNA is shown in Tables 5.1 and 5.2 and depicted in Figure 1.

Table 4: Editing rate by plasmid delivery

RGN	SGN	Rep1	Rep2	Rep3
LPG10134	SGN002644	0	0.06	1.76
LPG10134	SGN002645	0	0	1.43
LPG10134	SGN002646	0	0	0.04
LPG10134	SGN002647	0	0	0
LPG10134	SGN002648	0	0	2.15
LPG10134	SGN002649	0	0	0
LPG10134	SGN002650	0	0	0
LPG10134	SGN002651	0	0	0
LPG10134	SGN002652	0	0	0
LPG10134	SGN002653	0	0	0
LPG10136	SGN002654	5.74	3.57	8
LPG10136	SGN002655	5.18	5.36	6.86
LPG10136	SGN002656	3.4	2.06	5.7
LPG10136	SGN002657	4.14	3.01	6.77
LPG10136	SGN002658	0.05	0	0
LPG10136	SGN002659	0.33	0.15	0.87
LPG10136	SGN002660	1.89	0.82	4.38
LPG10136	SGN002661	3.56	3.81	4.82
LPG10136	SGN002662	2.53	1.9	3.99
LPG10136	SGN002663	0.51	0.33	0.67
LPG10138	SGN002664	0.47	0.46	2.75
LPG10138	SGN002665	0.92	3.79	4.84
LPG10138	SGN002666	0.12	0.22	0.88
LPG10138	SGN002667	0.91	3.13	3.18
LPG10138	SGN002668	0	0	0
LPG10138	SGN002669	0.14	0.42	1.92
LPG10138	SGN002670	0	0	0.14
LPG10138	SGN002671	2.54	2.56	3.21
LPG10138	SGN002672	0.1	1.11	0.79
LPG10138	SGN002673	0	0	0.87
LPG10139	SGN002674	0.27	0.56	2.97
LPG10139	SGN002675	3.95	3.92	5.99

RGN	SGN	Rep1	Rep2	Rep3
LPG10139	SGN002676	0	0.12	1.36
LPG10139	SGN002677	0.88	0.24	3.27
LPG10139	SGN002678	0	0	0
LPG10139	SGN002679	1.68	0.47	3.26
LPG10139	SGN002680	0	0	0.16
LPG10139	SGN002681	3.53	4.09	7.03
LPG10139	SGN002682	0.94	0.51	3.32
LPG10139	SGN002683	0.35	0.44	0.93
LPG10141	SGN002684	0	0	0.3
LPG10141	SGN002685	0	0	0.43
LPG10141	SGN002686	0	0	0.14
LPG10141	SGN002687	0	0	2.1
LPG10141	SGN002688	0	0	0
LPG10141	SGN002689	0	0	0
LPG10141	SGN002690	0	0	0
LPG10141	SGN002691	0	0	0
LPG10141	SGN002692	0	0	0
LPG10141	SGN002693	0	0	0
LPG10145	SGN002698	9.25	9.03	13.74
LPG10145	SGN002699	3.19	4.3	6.29
LPG10145	SGN002700	1.43	0.31	4.26
LPG10145	SGN002701	3.9	5.07	6.85
LPG10145	SGN002702	9.87	4.92	11.76
LPG10145	SGN002703	0.08	0.07	0.61
LPG10145	SGN002704	3.04	1.09	4.83
LPG10145	SGN002705	0	0	0
LPG10145	SGN002706	4.36	1.96	4.7
LPG10145	SGN002707	8.54	8.09	7.36
LPG10146	SGN002708	0.85	0	1.09
LPG10146	SGN002709	0	0	0.19
LPG10146	SGN002710	0.29	1.08	1.09
LPG10146	SGN002711	0	0	0.71
LPG10146	SGN002712	2.42	1.57	3.01
LPG10146	SGN002713	0	0	0
LPG10146	SGN002714	0	0	0
LPG10146	SGN002715	0	0	0
LPG10146	SGN002716	0	0	0
LPG10146	SGN002717	0	0	0
LPG10147	SGN002718	0	0	0
LPG10147	SGN002719	0	0	0
LPG10147	SGN002720	0	0	0
LPG10147	SGN002721	0	0	0
LPG10147	SGN002722	0	0	0

RGN	SGN	Rep1	Rep2	Rep3
LPG10147	SGN002723	0	0	0
LPG10150	SGN002724	2.15	3.12	1.25
LPG10150	SGN002725	1.29	1.1	0.28
LPG10150	SGN002726	0.05	0	0
LPG10150	SGN002727	0.03	0	0
LPG10150	SGN002728	0.06	0.1	0
LPG10150	SGN002729	0	0	0
LPG10150	SGN002730	0	0	0
LPG10150	SGN002731	0.08	0.2	0
LPG10150	SGN002732	0	0	0
LPG10150	SGN002733	0.72	0.17	0.09
LPG10155	SGN002734	0	0	0
LPG10155	SGN002735	0	0.15	0
LPG10155	SGN002735	0.42	0	0
LPG10155	SGN002736	0	0	0
LPG10155	SGN002737	0	0	0
LPG10155	SGN002738	0	0	0
LPG10159	SGN002738	0	0	0
LPG10159	SGN002739	0	0	0
LPG10159	SGN002740	0	0	0
LPG10159	SGN002741	0	0	0
LPG10159	SGN002742	0	0	0
LPG10159	SGN002744	0	0	0
LPG10159	SGN002745	0	0	0
LPG10159	SGN002747		0	0
LPG10159	SGN002748	0	0	0
LPG10159	SGN002749	0	0	0
LPG10160	SGN002750	0	0	0
LPG10160	SGN002751	0	0	0
LPG10160	SGN002752	0	0	0
LPG10160	SGN002753	0	0	0
LPG10160	SGN002754	0	0	0
LPG10160	SGN002755	0	0	0
LPG10160	SGN002756	0	0	0
LPG10160	SGN002757	0	0	0
LPG10160	SGN002758	0	0	0
LPG10160	SGN002759	0	0	0

LPG10136 showed an average editing rate around 3.01% across 10 guides in three independent experiments. LPG10145 showed an average editing rate around 4.63% across 10 guides in three independent editing experiments, with three guides editing around 10%. LPG10138, LPG10139, LPG10141, LPG10146, and LPG10150 also showed indel formation by amplicon sequencing with at least one guide RNA demonstrating these nucleases are active in mammalian cells.

Table 5.1: Example INDEL formation for LPG10136

#Reads	Edited Sequence	Category	Size	INDEL Location	% Reads	% of INDELs
261890	CTCAGGTACTCCAAAGATTCAGG TTTACTCACGTCATCCAGCAGAGA	WT	0	0	92.82	0
1935	CTCAGGTACTCCAAAGATTCAGGT TT----ACGTCATCCAGCAGAGA	Deletion	4	3	0.69	9.55
1806	CTCAGGTACTCCAAAGATTCAGGT TTAC-----TCATCCAGCAGAGA	Deletion	5	0	0.64	8.92
929	CTCAGGTACTCCAAAGAT-----T CACGTCATCCAGCAGAGA	Deletion	10	5	0.33	4.59
828	CTCAGGTACTCCAAAGATTCAGGT TTACT-ACGTCATCCAGCAGAGA	Deletion	1	3	0.29	4.09
803	CTCAGGTACTCCAAAGATTCAGGT TTACTCAACGTCATCCAGCAGAG	Insertion	1	3	0.28	3.96
802	CTCAGGTACTCCAAAGATTCAGGT TTAC-----TCCAGCAGAGA	Deletion	8	-3	0.28	3.96
622	CTCAGGTACTCCAAAGATTCAGGT TTACT—CGTCATCCAGCAGAGA	Deletion	2	2	0.22	3.07
409	CTCAGGTACTCCAAAG-----A CGTCATCCAGCAGAGA	Deletion	14	3	0.14	2.02
380	CTCAGGTACTCCAAAGATTCAGGT TTACTCCACGTCATCCAGCAGAG	Insertion	1	4	0.13	1.88
373	CTCAGGTACTCCAAAGATTCAGGT TTACT-----CAGCAGAGA	Deletion	9	-5	0.13	1.84
342	CTCAGGTACTCCAAAGATTCA---- ----ACGTCATCCAGCAGAGA	Deletion	9	3	0.12	1.69
340	CTCAGGTACTCCAAAG----- -----A	Deletion	133	-116	0.12	1.68
335	CTCAGGTACTCCAAAGAT----- ---TCATCCAGCAGAGA	Deletion	15	0	0.12	1.65
302	CTCAGGTACTCCAAAGATTCAGGT TTA—CACGTCATCCAGCAGAGA	Deletion	2	4	0.11	1.49
302	CTCAGGTACTCCAAAGAT----- ACGTCATCCAGCAGAGA	Deletion	12	3	0.11	1.49
293	CTCAGGTACTCCAAAGATTCAG---- -----GTCATCCAGCAGAGA	Deletion	10	1	0.1	1.45
289	CTCAGGTACTCCAAAGATTCAGGT TTACTC-CGTCATCCAGCAGAGA	Deletion	1	2	0.1	1.43
287	CTCAGGTACTCCAAAGATTCAGGT T----ACGTCATCCAGCAGAGA	Deletion	5	3	0.1	1.42
277	CTCAGGTACTCCAAAGATTCAGGT T----- -----T	Deletion	168	-160	0.1	1.37
271	CTCAGGTACTCCAAAGATTCAGGT TTA---ACGTCATCCAGCAGAGA	Deletion	3	3	0.1	1.34

Edited alleles that account for >0.1% of overall editing results are shown above. Deletions are shown by dashes. The most frequent editing outcome for this guide was small deletions and insertions.

5

Table 5.2: Example INDEL formation for LPG10145

#Reads	Edited Sequence	Category	Size	INDEL Location	% Reads	% of INDELs
270438	ATGTCTCGCTCCGTGGCCTTAGCTGT GCTCGCGCTACTCTCTCTTTC	WT	0	0	85.84	0
8329	ATGTCTCGCTCCGTGG-CTTAGCTGT GCTCGCGCTACTCTCTCTTTC	Deletion	1	2	2.64	18.68
3531	ATGTCTCGCTCCGTGGC—TAGCTGT GCTCGCGCTACTCTCTCTTTC	Deletion	2	3	1.12	7.92
2595	ATGTCTCGCTCCGTG-----GCTGTGC TCGCGCTACTCTCTCTTTC	Deletion	6	1	0.82	5.82
2201	ATGTCTCGCTCCGTGGC-----CTC GCGCTACTCTCTCTTTC	Deletion	10	3	0.7	4.94
1902	ATGTCTCGCTCCGTGGCACTTAGC TGTGCTCGCGCTACTCTCTCTTT	Insertion	1	3	0.6	4.27
1262	ATGTCTCGCTCCGTG-----GCTC GCGCTACTCTCTCTTTC	Deletion	11	1	0.4	2.83
1047	ATGTCTCG-----CTTAGCTGTGCT CGCGCTACTCTCTCTTTC	Deletion	9	-6	0.33	2.35
759	ATGTCTC-----GCTCGCGC TACTCTCTCTTTC	Deletion	19	-7	0.24	1.7
730	ATGTCTCGCTCCGTGGC---GCTGT GCTCGCGCTACTCTCTCTTTC	Deletion	4	3	0.23	1.64
654	ATGTCTCGCTCCGTGGC----CTGTG CTCGCGCTACTCTCTCTTTC	Deletion	5	3	0.21	1.47
639	ATGTCTCGCTCCGTGGC---AGCTGT GCTCGCGCTACTCTCTCTTTC	Deletion	3	3	0.2	1.43
548	ATGTCTCGCTCCGTG-----GC GCTACTCTCTCTTTC	Deletion	15	1	0.17	1.23
530	ATGTCTCGCTCCGTGGC-----TGC TCGCGCTACTCTCTCTTTC	Deletion	8	3	0.17	1.19
528	ATGT-----CTCGCGCT ACTCTCTCTTTC	Deletion	23	-10	0.17	1.18
519	ATGTCTCGCTCCGTGGC-----GC TCGCGCTACTCTCTCTTTC	Deletion	9	3	0.16	1.16
470	ATGTCTCGCTCCGTGGCTTCTTAG CTGTGCTCGCGCTACTCTCTCTT	Insertion	2	3	0.15	1.05
456	ATGTCTCGCTCCGTGGC-----GTG CTCGCGCTACTCTCTCTTTC	Deletion	7	3	0.14	1.02
431	ATGTCTC-----GCTGTGCTCG CGCTACTCTCTCTTTC	Deletion	14	-7	0.14	0.97
410	ATGTCTCGCTCCGTGGC—GAGCT GTGCTCGCGCTACTCTCTCTTTC	Deletion	2	3	0.13	0.92
391	ATGTCTCGCTCCGTGGCCGTTT CCCCCTGGAAGCTCCCTCGTGC GCT	Insertion	41	3	0.12	0.88
368	ATGTCTCGCTCCG----- TAGCTGTGCTCGCGCTACTCTC	Deletion	6	-1	0.12	0.83

#Reads	Edited Sequence	Category	Size	INDEL Location	% Reads	% of INDELs
	TCTTTC					
329	ATG----- ----- ----- -----T	Deletion	137	-11	0.1	0.74
328	ATGTCTCGCTCCGTG----- GCTACTCTCTCTTTC	Deletion	17	1	0.1	0.74
310	ATGTCTCGCTCCGTGGC----- CGCGCTACTCTCTCTTTC	Deletion	12	3	0.1	0.7
301	ATGTCTCGCTC----- CCTTAGCTGTGCTCGCGCTACTC TCTCTTTC	Deletion	5	-3	0.1	0.67

Edited alleles that account for >0.1% of overall editing results are shown above. Deletions are shown by dashes. The most frequent editing outcome for this guide was small deletions and insertions.

5

Example 5: Testing different delivery formats

To determine if the RGNs are capable of delivery in different formats, mRNA and RNP nucleofection delivery is tested with primary T-cells. Purified CD3⁺ T-cells or peripheral blood mononuclear cells (PBMCs) are thawed, activated using CD3/CD28 beads (ThermoFisher) for 3 days, then nucleofected using the Lonza 4D-Nucleofector X unit and Nucleocuvette strips. The P3 Primary Cell kit is used for both mRNA and RNP delivery. Cells are transfected using the EO-115 and EH-115 programs for mRNA and RNP delivery respectively. Cells are cultured in CTS OpTimizer T cell expansion medium (ThermoFisher) containing IL-2, IL-7, and IL-15 (Miltenyi Biotec) for 4 days post nucleofection before being harvested using a Nucleospin Tissue genomic DNA isolation kit (Machery Nagel).

10

15

Amplicons surrounding the editing sites are generated by PCR using primers and subjected to NGS sequencing using the Illumina Nextera platform using 2x250bp paired end sequencing following the method in Example 4.

20

Example 6: Identification of Disease Targets

A database of clinical variants was obtained from NCBI ClinVar database, which is available through the world wide web at the NCBI ClinVar website. Pathogenic Single Nucleotide Polymorphisms (SNPs) were identified from this list. Using the genomic locus information, CRISPR targets in the region overlapping and surrounding each SNP were identified. A selection of SNPs that can be corrected using base editing in combination with the RGNs of the invention to target the causal mutation ("Cas1 Mut.") is listed in Table 6. In Table 6, only one alias of each disease is listed. The "RS#" corresponds to the RS accession number through the SNP database at the NCBI website. The

25

AlleleID corresponds to a causal allele accession number. Table 6 also provides genomic target sequence information suitable for the RGN listed for each disease. The target sequence information also provides protospacer sequence for the production of the necessary sgRNA for the corresponding RGN of the invention.

5

Table 6: Disease Targets for RGNs

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Stargardt disease 1	1800553	LPG10134	G>A	22927	ABCA4	85
Stargardt disease 1	1800553	LPG10136	G>A	22927	ABCA4	86
Stargardt disease 1	1800553	LPG10138,LPG10139	G>A	22927	ABCA4	87
Stargardt disease 1	1800553	LPG10145	G>A	22927	ABCA4	88
Stargardt disease 1	1800553	LPG10141	G>A	22927	ABCA4	89
Stargardt disease 1	1800728	LPG10134	T>C	98777	ABCA4	90
Stargardt disease 1	1800728	LPG10138,LPG10139	T>C	98777	ABCA4	91
Stargardt disease 1	1800728	LPG10145	T>C	98777	ABCA4	92
Stargardt disease 1	1800728	LPG10146	T>C	98777	ABCA4	93
Stargardt disease 1	1800728	LPG10150	T>C	98777	ABCA4	94
Stargardt disease 1	1800728	LPG10159	T>C	98777	ABCA4	95
Stargardt disease 1	1800728	LPG10141	T>C	98777	ABCA4	96
Medium-chain acyl-coenzyme A dehydrogenase deficiency	121434274	LPG10138,LPG10139	G>A	18627	ACADM	97
Medium-chain acyl-coenzyme A dehydrogenase deficiency	121434274	LPG10160	G>A	18627	ACADM	98
Very long chain acyl-CoA dehydrogenase deficiency	113994167	LPG10134	T>C	33877	ACADVL	99
Very long chain acyl-CoA dehydrogenase deficiency	113994167	LPG10138,LPG10139	T>C	33877	ACADVL	100
Very long chain acyl-CoA dehydrogenase deficiency	113994167	LPG10145	T>C	33877	ACADVL	101
Very long chain acyl-CoA dehydrogenase deficiency	113994167	LPG10146	T>C	33877	ACADVL	102

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Very long chain acyl-CoA dehydrogenase deficiency	113994167	LPG10141	T>C	33877	ACADVL	103
Adenylosuccinate lyase deficiency	119450941	LPG10138,LPG10139	G>A	17501	ADSL	104
Primary hyperoxaluria, type I	121908529	LPG10134	G>A	38436	AGXT	105
Primary hyperoxaluria, type I	121908529	LPG10136	G>A	38436	AGXT	106
Primary hyperoxaluria, type I	121908529	LPG10138,LPG10139	G>A	38436	AGXT	107
Primary hyperoxaluria, type I	121908529	LPG10145	G>A	38436	AGXT	108
Primary hyperoxaluria, type I	121908529	LPG10141	G>A	38436	AGXT	109
Hypophosphatasia	121918007	LPG10134	G>A	28709	ALPL	110
Hypophosphatasia	121918007	LPG10136	G>A	28709	ALPL	111
Hypophosphatasia	121918007	LPG10138,LPG10139	G>A	28709	ALPL	112
Hypophosphatasia	121918007	LPG10145	G>A	28709	ALPL	113
Metachromatic leukodystrophy	80338815	LPG10134	G>A	18090	ARSA	114
Metachromatic leukodystrophy	80338815	LPG10136	G>A	18090	ARSA	115
Metachromatic leukodystrophy	80338815	LPG10138,LPG10139	G>A	18090	ARSA	116
Metachromatic leukodystrophy	80338815	LPG10145	G>A	18090	ARSA	117
Metachromatic leukodystrophy	80338815	LPG10146	G>A	18090	ARSA	118
Metachromatic leukodystrophy	80338815	LPG10141	G>A	18090	ARSA	119
Breast and/or ovarian cancer	80356962	LPG10134	G>A	70247	BRCA1	120
Breast and/or ovarian cancer	80356962	LPG10134	G>A	70247	BRCA1	121
Breast and/or ovarian cancer	80356962	LPG10136	G>A	70247	BRCA1	122
Breast and/or ovarian cancer	80356962	LPG10138,LPG10139	G>A	70247	BRCA1	123
Breast and/or ovarian cancer	80356962	LPG10145	G>A	70247	BRCA1	124
Breast and/or ovarian cancer	80356962	LPG10146	G>A	70247	BRCA1	125
Breast and/or ovarian cancer	80359003	LPG10134	G>A	67069	BRCA2	126
Breast and/or ovarian cancer	80359003	LPG10145	G>A	67069	BRCA2	127

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Breast and/or ovarian cancer	80359003	LPG10146	G>A	67069	BRCA2	128
Breast and/or ovarian cancer	80359003	LPG10159	G>A	67069	BRCA2	129
Breast and/or ovarian cancer	80359003	LPG10160	G>A	67069	BRCA2	130
Breast and/or ovarian cancer	80359003	LPG10141	G>A	67069	BRCA2	131
Breast and/or ovarian cancer	80359071	LPG10134	G>A	67203	BRCA2	132
Breast and/or ovarian cancer	80359071	LPG10138,LPG10139	G>A	67203	BRCA2	133
Homocystinuria	5742905	LPG10134	T>C	15159	CBS	134
Homocystinuria	5742905	LPG10136	T>C	15159	CBS	135
Homocystinuria	5742905	LPG10138,LPG10139	T>C	15159	CBS	136
Homocystinuria	5742905	LPG10145	T>C	15159	CBS	137
Homocystinuria	5742905	LPG10145	T>C	15159	CBS	138
Homocystinuria	5742905	LPG10150	T>C	15159	CBS	139
Homocystinuria	5742905	LPG10159	T>C	15159	CBS	140
Homocystinuria	5742905	LPG10141	T>C	15159	CBS	141
Homocystinuria	121964962	LPG10134	G>A	15156	CBS	142
Homocystinuria	121964962	LPG10136	G>A	15156	CBS	143
Homocystinuria	121964962	LPG10138,LPG10139	G>A	15156	CBS	144
Homocystinuria	121964962	LPG10145	G>A	15156	CBS	145
Homocystinuria	121964962	LPG10141	G>A	15156	CBS	146
Cystic fibrosis	75527207	LPG10138,LPG10139	G>A	22159	CFTR	147
Cystic fibrosis	75527207	LPG10160	G>A	22159	CFTR	148
Cystic fibrosis	78655421	LPG10134	G>A	22148	CFTR	149
Cystic fibrosis	78655421	LPG10138,LPG10139	G>A	22148	CFTR	150
Cystic fibrosis	78655421	LPG10145	G>A	22148	CFTR	151

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Cystic fibrosis	78655421	LPG10141	G>A	22148	CFTR	152
Familial dysautonomia	111033171	LPG10136	T>C	21124	ELP1	153
Familial dysautonomia	111033171	LPG10138,LPG10139	T>C	21124	ELP1	154
Familial dysautonomia	111033171	LPG10146	T>C	21124	ELP1	155
Tyrosinemia type I	80338901	LPG10134	G>A	26909	FAH	156
Tyrosinemia type I	80338901	LPG10136	G>A	26909	FAH	157
Tyrosinemia type I	80338901	LPG10138,LPG10139	G>A	26909	FAH	158
Tyrosinemia type I	80338901	LPG10145	G>A	26909	FAH	159
Deafness	80338945	LPG10134	T>C	32055	GJB2	160
Deafness	80338945	LPG10136	T>C	32055	GJB2	161
Deafness	80338945	LPG10138,LPG10139	T>C	32055	GJB2	162
Deafness	80338945	LPG10145	T>C	32055	GJB2	163
Deafness	80338945	LPG10146	T>C	32055	GJB2	164
Deafness	80338945	LPG10150	T>C	32055	GJB2	165
Deafness	80338945	LPG10159	T>C	32055	GJB2	166
Deafness	104894396	LPG10138,LPG10139	G>A	32041	GJB2	167
Deafness	104894396	LPG10145	G>A	32041	GJB2	168
Deafness	104894396	LPG10160	G>A	32041	GJB2	169
Deafness	104894396	LPG10141	G>A	32041	GJB2	170
Inclusion body myopathy	28937594	LPG10134	T>C	21064	GNE	171
Inclusion body myopathy	28937594	LPG10138,LPG10139	T>C	21064	GNE	172
Inclusion body myopathy	28937594	LPG10145	T>C	21064	GNE	173
Inclusion body myopathy	28937594	LPG10146	T>C	21064	GNE	174
Inclusion body myopathy	28937594	LPG10141	T>C	21064	GNE	175
Mucopolysaccharidosis type I	121965019	LPG10134	G>A	26947	IDUA	176

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Mucopolysaccharidosis type I	121965019	LPG10136	G>A	26947	IDUA	177
Mucopolysaccharidosis type I	121965019	LPG10138,LPG10139	G>A	26947	IDUA	178
Mucopolysaccharidosis type I	121965019	LPG10145	G>A	26947	IDUA	179
Mucopolysaccharidosis type I	121965019	LPG10150	G>A	26947	IDUA	180
Mucopolysaccharidosis type I	121965019	LPG10141	G>A	26947	IDUA	181
Familial hypercholesterolemia	137929307	LPG10134	G>A	171217	LDLR	182
Familial hypercholesterolemia	137929307	LPG10138,LPG10139	G>A	171217	LDLR	183
Familial hypercholesterolemia	137929307	LPG10145	G>A	171217	LDLR	184
Familial hypercholesterolemia	137929307	LPG10146	G>A	171217	LDLR	185
Familial hypercholesterolemia	137929307	LPG10141	G>A	171217	LDLR	186
Familial Mediterranean fever	28940579	LPG10136	T>C	17579	MEFV	187
Familial Mediterranean fever	28940579	LPG10138,LPG10139	T>C	17579	MEFV	188
Familial Mediterranean fever	28940579	LPG10146	T>C	17579	MEFV	189
Familial Mediterranean fever	28940579	LPG10159	T>C	17579	MEFV	190
Familial Mediterranean fever	28940579	LPG10160	T>C	17579	MEFV	191
Familial Mediterranean fever	104895097	LPG10136	G>A	17588	MEFV	192
Familial Mediterranean fever	104895097	LPG10138,LPG10139	G>A	17588	MEFV	193
Familial Mediterranean fever	104895097	LPG10145	G>A	17588	MEFV	194
Familial Mediterranean fever	104895097	LPG10146	G>A	17588	MEFV	195
Familial Mediterranean fever	104895097	LPG10150	G>A	17588	MEFV	196
Familial Mediterranean fever	104895097	LPG10159	G>A	17588	MEFV	197

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Mevalonic aciduria	28934897	LPG10136	G>A	26968	MVK	198
Mevalonic aciduria	28934897	LPG10138,LPG10139	G>A	26968	MVK	199
Mevalonic aciduria	28934897	LPG10146	G>A	26968	MVK	200
Hypertrophic cardiomyopathy	200411226	LPG10134	G>A	174776	MYBPC3	201
Hypertrophic cardiomyopathy	200411226	LPG10136	G>A	174776	MYBPC3	202
Hypertrophic cardiomyopathy	200411226	LPG10138,LPG10139	G>A	174776	MYBPC3	203
Hypertrophic cardiomyopathy	200411226	LPG10145	G>A	174776	MYBPC3	204
Hypertrophic cardiomyopathy	200411226	LPG10146	G>A	174776	MYBPC3	205
Hypertrophic cardiomyopathy	200411226	LPG10147	G>A	174776	MYBPC3	206
Hypertrophic cardiomyopathy	200411226	LPG10155	G>A	174776	MYBPC3	207
Hypertrophic cardiomyopathy	200411226	LPG10160	G>A	174776	MYBPC3	208
Hypertrophic cardiomyopathy	397516074	LPG10134	G>A	51962	MYBPC3	209
Hypertrophic cardiomyopathy	397516074	LPG10136	G>A	51962	MYBPC3	210
Hypertrophic cardiomyopathy	397516074	LPG10138,LPG10139	G>A	51962	MYBPC3	211
Hypertrophic cardiomyopathy	397516074	LPG10145	G>A	51962	MYBPC3	212
Hypertrophic cardiomyopathy	397516074	LPG10159	G>A	51962	MYBPC3	213
Hypertrophic cardiomyopathy	397516074	LPG10141	G>A	51962	MYBPC3	214
MYH7-related disorder	3218716	LPG10134	G>A	52071	MYH7	215
MYH7-related disorder	3218716	LPG10136	G>A	52071	MYH7	216
MYH7-related disorder	3218716	LPG10138,LPG10139	G>A	52071	MYH7	217
MYH7-related disorder	3218716	LPG10145	G>A	52071	MYH7	218
MYH7-related disorder	3218716	LPG10150	G>A	52071	MYH7	219
MYH7-related disorder	3218716	LPG10159	G>A	52071	MYH7	220
MYH7-related disorder	3218716	LPG10141	G>A	52071	MYH7	221

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
MYH7-related disorder	371898076	LPG10138,LPG10139	G>A	52045	MYH7	222
Hypertrophic cardiomyopathy	104894368	LPG10134	G>A	29104	MYL2	223
Hypertrophic cardiomyopathy	104894368	LPG10138,LPG10139	G>A	29104	MYL2	224
Hypertrophic cardiomyopathy	104894368	LPG10145	G>A	29104	MYL2	225
Hypertrophic cardiomyopathy	104894368	LPG10145	G>A	29104	MYL2	226
Hypertrophic cardiomyopathy	104894368	LPG10160	G>A	29104	MYL2	227
Hypertrophic cardiomyopathy	104894368	LPG10141	G>A	29104	MYL2	228
Niemann-Pick disease type C1	80358259	LPG10136	T>C	18006	NPC1	229
Niemann-Pick disease type C1	80358259	LPG10138,LPG10139	T>C	18006	NPC1	230
Niemann-Pick disease type C1	80358259	LPG10146	T>C	18006	NPC1	231
Niemann-Pick disease type C1	80358259	LPG10150	T>C	18006	NPC1	232
Niemann-Pick disease type C1	80358259	LPG10159	T>C	18006	NPC1	233
Phenylketonuria	5030855	LPG10138,LPG10139	G>A	15646	PAH	234
Phenylketonuria	5030855	LPG10146	G>A	15646	PAH	235
Phenylketonuria	62508698	LPG10134	G>A	15619	PAH	236
Phenylketonuria	62508698	LPG10136	G>A	15619	PAH	237
Phenylketonuria	62508698	LPG10138,LPG10139	G>A	15619	PAH	238
Phenylketonuria	62508698	LPG10145	G>A	15619	PAH	239
Phenylketonuria	62508698	LPG10146	G>A	15619	PAH	240
Phenylketonuria	62508698	LPG10150	G>A	15619	PAH	241
Phenylketonuria	62516152	LPG10134	G>A	108520	PAH	242
Phenylketonuria	62516152	LPG10138,LPG10139	G>A	108520	PAH	243
Phenylketonuria	62516152	LPG10145	G>A	108520	PAH	244
Phenylketonuria	62516152	LPG10146	G>A	108520	PAH	245
Phenylketonuria	62516152	LPG10160	G>A	108520	PAH	246

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Phenylketonuria	62516152	LPG10141	G>A	108520	PAH	247
Phenylketonuria	62644499	LPG10134	G>A	15656	PAH	248
Phenylketonuria	62644499	LPG10136	G>A	15656	PAH	249
Phenylketonuria	62644499	LPG10138,LPG10139	G>A	15656	PAH	250
Phenylketonuria	62644499	LPG10145	G>A	15656	PAH	251
Phenylketonuria	62644499	LPG10159	G>A	15656	PAH	252
Zellweger syndrome	61750420	LPG10134	G>A	22555	PEX1	253
Zellweger syndrome	61750420	LPG10136	G>A	22555	PEX1	254
Zellweger syndrome	61750420	LPG10138,LPG10139	G>A	22555	PEX1	255
Zellweger syndrome	61750420	LPG10145	G>A	22555	PEX1	256
Zellweger syndrome	61750420	LPG10146	G>A	22555	PEX1	257
Zellweger syndrome	61750420	LPG10150	G>A	22555	PEX1	258
Zellweger syndrome	61750420	LPG10141	G>A	22555	PEX1	259
Immunodeficiency 14	397518423	LPG10134	G>A	94255	PIK3CD	260
Immunodeficiency 14	397518423	LPG10136	G>A	94255	PIK3CD	261
Immunodeficiency 14	397518423	LPG10138,LPG10139	G>A	94255	PIK3CD	262
Immunodeficiency 14	397518423	LPG10145	G>A	94255	PIK3CD	263
Immunodeficiency 14	397518423	LPG10146	G>A	94255	PIK3CD	264
Immunodeficiency 14	397518423	LPG10150	G>A	94255	PIK3CD	265
Immunodeficiency 14	397518423	LPG10159	G>A	94255	PIK3CD	266
Immunodeficiency 14	397518423	LPG10141	G>A	94255	PIK3CD	267
POLG-related condition	113994095	LPG10138,LPG10139	G>A	28535	POLG	268
POLG-related condition	113994095	LPG10146	G>A	28535	POLG	269
POLG-related condition	113994098	LPG10134	G>A	28541	POLG	270
POLG-related condition	113994098	LPG10138,LPG10139	G>A	28541	POLG	271
POLG-related condition	113994098	LPG10145	G>A	28541	POLG	272

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
POLG-related condition	113994098	LPG10141	G>A	28541	POLG	273
Cardiomyopathy	121908987	LPG10134	G>A	21885	PRKAG2	274
Cardiomyopathy	121908987	LPG10136	G>A	21885	PRKAG2	275
Cardiomyopathy	121908987	LPG10138,LPG10139	G>A	21885	PRKAG2	276
Cardiomyopathy	121908987	LPG10145	G>A	21885	PRKAG2	277
Cardiomyopathy	121908987	LPG10146	G>A	21885	PRKAG2	278
Cardiomyopathy	121908987	LPG10159	G>A	21885	PRKAG2	279
Cardiomyopathy	121908987	LPG10141	G>A	21885	PRKAG2	280
Shwachman syndrome	113993993	LPG10136	T>C	18235	SBDS	281
Shwachman syndrome	113993993	LPG10138,LPG10139	T>C	18235	SBDS	282
Brugada syndrome	137854601	LPG10134	G>A	24416	SCN5A	283
Brugada syndrome	137854601	LPG10136	G>A	24416	SCN5A	284
Brugada syndrome	137854601	LPG10138,LPG10139	G>A	24416	SCN5A	285
Brugada syndrome	137854601	LPG10145	G>A	24416	SCN5A	286
Brugada syndrome	137854601	LPG10146	G>A	24416	SCN5A	287
Brugada syndrome	137854601	LPG10150	G>A	24416	SCN5A	288
Alpha-1-antitrypsin deficiency	28929474	LPG10134	G>A	33006	SERPINA1	289
Alpha-1-antitrypsin deficiency	28929474	LPG10136	G>A	33006	SERPINA1	290
Alpha-1-antitrypsin deficiency	28929474	LPG10138,LPG10139	G>A	33006	SERPINA1	291
Alpha-1-antitrypsin deficiency	28929474	LPG10138,LPG10139	G>A	33006	SERPINA1	292
Alpha-1-antitrypsin deficiency	28929474	LPG10145	G>A	33006	SERPINA1	293
Alpha-1-antitrypsin deficiency	28929474	LPG10141	G>A	33006	SERPINA1	294
Mucopolysaccharidosis, MPS-III-A	104894635	LPG10134	G>A	20146	SGSH	295
Mucopolysaccharidosis, MPS-III-A	104894635	LPG10138,LPG10139	G>A	20146	SGSH	296
Mucopolysaccharidosis, MPS-III-A	104894635	LPG10145	G>A	20146	SGSH	297

Disease	RS#	RGN	CasI Mut.	AlleleID	Gene Symbol	Target (SEQ ID NO.)
Mucopolysaccharidosis, MPS-III-A	104894635	LPG10141	G>A	20146	SGSH	298
Tuberous sclerosis syndrome	28934872	LPG10134	G>A	27436	TSC2	299
Tuberous sclerosis syndrome	28934872	LPG10138,LPG10139	G>A	27436	TSC2	300
Tuberous sclerosis syndrome	28934872	LPG10145	G>A	27436	TSC2	301
Tuberous sclerosis syndrome	28934872	LPG10141	G>A	27436	TSC2	302
Amyloidogenic transthyretin amyloidosis	76992529	LPG10134	G>A	28465	TTR	303
Amyloidogenic transthyretin amyloidosis	76992529	LPG10138,LPG10139	G>A	28465	TTR	304
Amyloidogenic transthyretin amyloidosis	76992529	LPG10145	G>A	28465	TTR	305
Amyloidogenic transthyretin amyloidosis	76992529	LPG10150	G>A	28465	TTR	306
Amyloidogenic transthyretin amyloidosis	76992529	LPG10160	G>A	28465	TTR	307
Amyloidogenic transthyretin amyloidosis	76992529	LPG10141	G>A	28465	TTR	308
Von Willebrand disease	41276738	LPG10134	G>A	15335	VWF	309
Von Willebrand disease	41276738	LPG10136	G>A	15335	VWF	310
Von Willebrand disease	41276738	LPG10138,LPG10139	G>A	15335	VWF	311
Von Willebrand disease	41276738	LPG10145	G>A	15335	VWF	312
Von Willebrand disease	41276738	LPG10146	G>A	15335	VWF	313
Von Willebrand disease	41276738	LPG10150	G>A	15335	VWF	314
Von Willebrand disease	41276738	LPG10141	G>A	15335	VWF	330

Example 7: Targeting mutations responsible for Hurler Syndrome

The following describes a potential treatment for Hurler Syndrome, also referred to as MPS-1, using an RNA directed base editing system that corrects a mutation responsible for Hurler syndrome in a large proportion of patients with the disease. This approach utilizes a base editing fusion protein that is RNA guided and that can be packaged into a single AAV vector for delivery to a wide range of

tissue types. Depending on the exact regulatory elements and base editor domain used, it may also be possible to engineer a single vector that encodes for both the base editing fusion protein and a single guide RNA to target the diseased locus.

5 *Example 7.1: Identifying RGN with ideal PAM*

The genetic disease MPS-1 is a lysosomal storage disease characterized at the molecular level by the accumulation of dermatan sulfate and heparan sulfate in lysosomes. This disease is generally an inherited genetic disorder caused by mutations in the IDUA gene (NCBI Reference sequence NG_008103.1), which encodes α -L-iduronidase. The disease is a result of a deficiency of α -L-iduronidase. The most common IDUA mutations found in studies of individuals of Northern European background are W402X and Q70X, each nonsense mutation resulting in premature termination of translation (Bunge et al. (1994), Hum. Mol. Genet, 3(6): 861-866, herein incorporated by reference). Reversion of a single nucleotide would restore the wild-type coding sequence and result in protein expression controlled by the endogenous regulatory mechanisms of the genetic locus.

The W402X mutation of the human Idua gene accounts for a high proportion of MPS-1H cases. Base editors can target a narrow sequence window relative to the binding site of the protospacer component of the guide RNA and thus the presence of a PAM sequence a specific distance from the target locus is essential for the success of the strategy. Given the constraints that the target mutation must be on the exposed non-target strand (NTS) during the interaction of the base editing protein and that the footprint of the RGN domain will block access to the region near the PAM, an accessible locus is thought to be 10-30 bp from the PAM. To avoid editing and mutagenesis of other nearby adenosine bases in this window, different linkers are screened. The ideal window is 12-16 bp from the PAM.

A PAM sequence compatible with LPG10134, LPG10136, LPG10139 and LPG10145 is readily apparent at the genetic locus. These nucleases have a PAM sequence of 5'-nGG-3' (SEQ ID NO: 73), 5'-nnnnCC-3' (SEQ ID NO: 74), 5'-nnnnC-3' (SEQ ID NO: 76), and 5'-nnGG-3' (SEQ ID NO: 78) respectively, and are compact in size – potentially allowing delivery via a single AAV vector. This delivery approach bestows multiple advantages relative to others, such as access to a wide range of tissues (liver, muscle, CNS) and well-established safety profile and manufacturing techniques.

Cas9 from *S. pyogenes* (SpyCas9) requires a PAM sequence of NGG (SEQ ID NO: 331), which is present near the W402X locus, but the size of SpyCas9 prevents packaging into a single AAV vector, and thus forgoes the aforementioned advantages of this approach. While a dual delivery strategy may be employed (for example, Ryu et al, (2018), Nat. Biotechnol., 36(6): 536-539, herein incorporated by reference), it would add significant manufacturing complexity and cost. Additionally, dual viral vector delivery significantly decreases the efficiency of gene correction, since a successful edit in a given cell requires infection with both vectors and assembly of the fusion protein in the cell.

A commonly used Cas9 ortholog from *S. aureus* (SauCas9) is considerably smaller in size relative to SpyCas9 but has a more complex PAM requirement – NGRRT (SEQ ID NO: 332). This sequence is not within a range expected to be useful for base editing of the causative locus.

5 Example 7.2: RGN fusion constructs and sgRNA sequences

A DNA sequence encoding a fusion protein with the following domains is produced using standard molecular biology techniques: 1) an RGN domain with mutations that inactivate the DNA cleavage activity (“dead” or “nickase”); 2) an adenine deaminase useful for base editing. All constructs described in Table 7 comprise a fusion protein with the base editing active domain, in this example LPG50148 (SEQ ID NO: 333), operably fused to the N-terminal end of a dead RGN LPG10134, LPG10136, LPG10139, or LPG10145. Other adenine deaminases useful for base editing DNA may also be used (see for example International Publ. No. WO 2020/139873, U.S. Provisional Appl. Nos. 63/077,089 filed September 11, 2020, 63/146,840 filed February 8, 2021, and 63/164,273 filed March 22, 2021, and International Appl. No. PCT/US2021/049853 filed September 10, 2021, each of which is herein incorporated by reference in its entirety). It is known in the art that a fusion protein could also be made with the base-editing enzyme at the C-terminal end of the RGN. Additionally, the RGN and the base editor of the fusion protein are typically separated by a linker amino acid sequence. It is known in the art that lengths of standard linkers range from 15-30 amino acids.

20

Table 7: Constructs for RNA-targeted base editing

SEQ ID NO.	Construct	RGN	Dead (D)or Nickase (N)	Base editor
334	SV40-LPG50148-Linker-d LPG10134 -Linker-Nuc	LPG10134	D	ADAT
335	SV40-LPG50148-Linker-d LPG10145 -Linker-Nuc	LPG10145	D	ADAT
336	SV40-LPG50148-Linker-d LPG10136 -Linker-Nuc	LPG10136	D	ADAT
337	SV40-LPG50148-Linker-d LPG10139 -Linker-Nuc	LPG10139	D	ADAT

The accessible editing sites of an RGN are determined by the PAM sequence. When combining an RGN with a base editing domain, the target residue for editing must reside on the non-target strand (NTS), since the NTS is single stranded while the RGN is associated with the locus. Evaluating a number of nucleases and corresponding guide RNAs enables the selection of the most appropriate gene editing tool for this particular locus. Several potential PAM sequences that can be targeted by the constructs described above in the human *Idua* gene are in the proximity of the mutant nucleotide responsible for the W402X mutation. A sequence encoding a guide RNA transcript containing 1) a “spacer” that is complementary to the non-coding DNA strand at the disease locus;

30

and 2) RNA sequence required for association of the guide RNA with the RGN is also produced. Such a sgRNA may be, for example, SEQ ID NOs: 338-341 for LPG10134, LPG10145, LPG10136, and LPG10139, respectively. These sgRNA molecules, and similar sgRNAs that may be devised by one of skill in the art, can be evaluated for their efficiency in directing the base editors above to the locus of interest.

Example 7.3: Assay for activity in cells from Hurler disease patients

To verify the genotype strategy and evaluate the constructs described above, fibroblasts from Hurler disease patients are used. A vector is designed containing appropriate promoters upstream of the fusion protein coding sequence and the sgRNA encoding sequence for expression of these in human cells, similar to those vectors described in Example 4. It is recognized that promoters and other DNA elements (for example enhancers, or terminators) which either are known for high levels of expression in human cells or may specifically express well in fibroblast cells may also be used. The vector is transfected into the fibroblasts using standard techniques, for example transfection similar to what is described in Example 4. Alternatively, electroporation may be used. The cells are cultured for 1 - 3 days. Genomic DNA (gDNA) is isolated using standard techniques. The editing efficiency is determined by performing a qPCR genotyping assay and/or next generation sequencing on the purified gDNA, as described further below.

Taqman™ qPCR analysis utilizes probes specific for the wild-type and mutant allele. These probes bear fluorophores which are resolved by their spectral excitation and/or emission properties using a qPCR instrument. A genotyping kit containing PCR primers and probes can be obtained commercially (i.e. Thermo Fisher Taqman™ SNP genotyping assayID C__27862753_10 for SNP ID rs121965019) or designed. An example of a designed primer and probe set is shown in Table 8.

Table 8: RT-PCR primers and probes

Description	Sequence	SEQ ID NO.
Forward Amplification Primer	5'-GACTCCTTCACCAAG-3'	342
Reverse Amplification Primer	5'-GTAGATCAGCACCG-3'	343
Wild Type Probe	5'-CTCTG <u>GG</u> CCGAAGT-3'	344
W402X Probe	5'-CTCTA <u>G</u> GGCCGAAGT-3'	345

Following the editing experiment, the gDNA is subjected to qPCR analysis using standard methods and the primers and probes described above. Expected results are shown in Table 9. This *in vitro* system can be used to expediently evaluate constructs and choose one with high editing efficiency for further studies. The systems will be evaluated in comparison with cells with and without the W402X mutation, and preferably with some that are heterozygous for this mutation. The Ct values will be compared to either a reference gene or the total amplification of the locus using a dye such as Sybr green.

Table 9: Expected qPCR results

Genotype	Transfected with base editor	Expected PCR result
Idua ^{WT/WT}	No	Homozygous WT
Idua ^{WT/W402X}	No	Heterozygous: 50% WT, 50% W402X
Idua ^{W402X/W402X}	No	Homozygous W402X
Idua ^{W402X/W402X}	Yes	Variable

The tissues can also be analyzed by next generation sequencing. Primer binding sites such as the ones shown below (Table 10), or other suitable primer binding sites that can be identified by a person of skill in the art, can be used. Following PCR amplification, products containing Illumina Nextera XT overhang sequences undergo library preparation following the Illumina 16S Metagenomic Sequencing Library protocol. Deep sequencing is performed on an Illumina Mi-Seq platform. Typically, 200,000 of 250 bp paired-end reads (2 x 100,000 reads) are generated per amplicon. The reads are analyzed using CRISPResso (Pinello et al., 2016) to calculate the rates of editing. Output alignments are hand-curated to confirm insertion and deletion sites as well as identify microhomology sites at the recombination sites.

Table 10: NGS primer binding sites

Direction	Sequence	SEQ ID NO.
Forward	5'-ACTTCCTCCAGCC-3'	346
Reverse	5'-GAACCCCGGCTTA-3'	347

Western blotting of cell lysate of transfected cells and control cells using an anti-IDUA antibody is performed to verify expression of the full-length protein and an enzyme activity assay on the cell lysate using substrate 4-methylumbelliferyl α-L-iduronide verifies that the enzyme is catalytically active (Hopwood et al., Clin.Chim. Acta (1979), 92(2): 257-265, incorporated by reference herein). These experiments are performed in comparison with the original Idua^{W402X/W402X} cell line (without transfection), the Idua^{W402X/W402X} cell line transfected with the base editing construct and a random guide sequence, and a cell line expressing wild-type IDUA.

Example 7.4: Disease treatment validation in a murine model

To verify the efficacy of this therapeutic approach, a mouse model with a nonsense mutation in the analogous amino acid is used. The mouse strain bears a W392X mutation in its Idua gene (Gene ID: 15932) which corresponds to the homologous mutation in Hurler syndrome patients (Bunge et al., (1994), Hum. Mol. Genet. 3(6): 861-866, incorporated by reference herein). This locus comprises a distinct nucleotide sequence relative to that in humans, which lacks the PAM sequence necessary for correction with the base editors described in the previous examples, and thus necessitates design of a distinct fusion protein to perform the nucleotide correction. Amelioration of

the disease in this animal can validate the therapeutic approach of correcting the mutation in tissues accessible by a gene delivery vector.

Mice homozygous for this mutation display a number of phenotypic characteristics similar to Hurler syndrome patients. A base editing-RGN fusion protein as described above (Table 7) along with an RNA guide sequence are incorporated into an expression vector that allows protein expression and RNA transcription in mice. A study design is shown below in Table 11. The study includes groups that are treated with a high dose of the expression vector comprising the base-editing fusion protein and RNA guide sequence, a low dose of same expression vector, control which is the model mouse treated with an expression vector that does not comprise the base editing fusion protein or the guide RNA, and a second control which is a wild type mouse treated with the same empty vector.

Table 11: Genome editing experiment in murine model

Group	Mouse strain	N	Treatment
1	Idua-W392X	≥ 5	Low dose of vector
2	Idua-W392X	≥ 5	High dose of vector
3	Idua-W392X	≥ 5	Vehicle
4	129/Sv (WT)	5	Vehicle

Endpoints to evaluate include body weight, urine GAG excretion, serum IDUA enzymatic activity, IDUA activity in tissues of interest, tissue pathology, genotyping of tissues of interest to verify correction of the SNP, and behavioral and neurological evaluation. Since some endpoints are terminal, additional groups may be added for evaluation of, for example, tissue pathology and tissue IDUA activities before the end of the study. Additional examples of endpoints can be found in published papers establishing Hurler syndrome animal models (Shull et al. (1994), Proc. Natl. Acad. Sci. U.S.A., 91(26): 12937-12941; Wang et al. (2010), Mol. Genet. Metab., 99(1): 62-71; Hartung et al. (2004), Mol. Ther., 9(6): 866-875; Liu et al. (2005), Mol. Ther., 11(1): 35-47; Clarke et al. (1997), Hum. Mol. Genet. 6(4): 503-511; all herein incorporated by reference).

One possible delivery vector utilizes the adeno associated virus (AAV). A vector is produced to include a base editor-dRGN fusion protein coding sequence (for example, Nuc-ADAT-Linker-dAPG19748-Linker-SV40, as described above) preceded by a CMV enhancer (SEQ ID NO: 328) and promoter (SEQ ID NO: 327), or other suitable enhancer and promoter combination), optionally a Kozak sequence, and operably fused at the 3' end to a terminator sequence and a poly-adenylation sequence such as the minimal sequence described in Levitt, N.; Briggs, D.; Gil, A.; Proudfoot, N. J. Definition of an Efficient Synthetic Poly(A) Site. Genes Dev. 1989, 3 (7), 1019–1025. The vector may further comprise an expression cassette encoding for a single guide RNA operably linked at its 5' end to a human U6 promoter (SEQ ID NO: 329) or another promoter suitable for production of small non-coding RNAs, and further comprising inverted terminal repeat (ITR) sequences necessary and

well-known in the art for packaging into the AAV capsid. Production and viral packaging is performed by standard methods, such as those described in U.S. Patent No. 9,587,250, herein incorporated by reference.

Other possible viral vectors include adenovirus and lentivirus vectors, which are commonly used and would contain similar elements, with different packaging capabilities and requirements. Non-viral delivery methods also be used, such as mRNA and sgRNA encapsulated by lipid nanoparticles (Cullis, P. R. and Allen, T. M. (2013), *Adv. Drug Deliv. Rev.* 65(1): 36-48; Finn et al. (2018), *Cell Rep.* 22(9): 2227-2235, both incorporated by reference) hydrodynamic injection of plasmid DNA (Suda T and Liu D, 2007) *Mol. Ther.* 15(12): 2063-2069, herein incorporated by reference), or ribonucleoprotein complexes of sgRNA and associated with gold nanoparticles (Lee, K.; Conboy, M.; Park, H. M.; Jiang, F.; Kim, H. J.; Dewitt, M. A.; Mackley, V. A.; Chang, K.; Rao, A.; Skinner, C.; et al. Nanoparticle Delivery of Cas9 Ribonucleoprotein and Donor DNA in Vivo Induces Homology-Directed DNA Repair. *Nat. Biomed. Eng.* 2017, 1 (11), 889–90).

Example 7.5: Disease correction in a murine model with a humanized locus

To evaluate the efficacy of an identical base editor construct as would be used for human therapy, a mouse model in which the nucleotides near W392 are altered to match the sequence in humans around W402 is needed. This can be accomplished by a variety of techniques, including use of an RGN and an HDR template to cut and replace the locus in mouse embryos.

Due to the high degree of amino acid conservation, most nucleotides in the mouse locus can be altered to those of the human sequence with silent mutations as shown in Table 12. The only base changes resulting in altered coding sequence in the resulting engineered mouse genome occur after the introduced stop codon.

Table 12: Nucleotide mutations to generate a humanized mouse locus

	Human (W402X)		Mouse (W392X)		Humanized Mouse	
Feature	Nucleotide (SEQ ID NO: 548)	Encoded AA	Nucleotide (SEQ ID NO: 549)	Encoded AA	Nucleotide (SEQ ID NO: 550)	Encoded AA
Protospacer	G	E	A	G	G	G
	G	E	G	E	G	E
	A		A		A	
	G		A		G	
	C	Q	C	Q	C	Q
	A		A		A	
	G		A		G	
	C	L	C	L	C	L

	Human (W402X)		Mouse (W392X)		Humanized Mouse	
Feature	Nucleotide (SEQ ID NO: 548)	Encoded AA	Nucleotide (SEQ ID NO: 549)	Encoded AA	Nucleotide (SEQ ID NO: 550)	Encoded AA
	T		T		T	
	C		C		C	
	T	STOP	T	STOP	T	STOP
	A		A		A	
	G		G		G	
	G	A	G	A	G	A
	C		C		C	
	C		A		C	
	G	E	G	E	G	E
	A		A		A	
	A		G		A	
	G	V	G	V	G	V
	T		T		T	
	G		C		G	
	T	S	T	S	T	S
	C		C		C	
	G		A		G	
PAM, non-critical	C	Q	A	K	C	Q
	A		A		A	
	G		G		G	
	G	A	G	A	G	A
PAM, critical	C		C		C	
	C		T		C	

Upon engineering of this mouse strain, similar experiments will be performed as described in Example 7.4.

5 **Example 8: Targeting mutations responsible for Friedreich's Ataxia**

The expansion of the trinucleotide repeat sequence causing Friedreich's Ataxia (FRDA) occurs in a defined genetic locus within the FXN gene, referred to as the FRDA instability region. RNA guided nucleases (RGNs) may be used for excising the instability region in FRDA patient cells. This approach requires 1) an RGN and guide RNA sequence that can be programmed to target the allele in the human genome; and 2) a delivery approach for the RGN and guide sequence. Many nucleases used for genome editing, such as the commonly used Cas9 nuclease from *S. pyogenes* (SpCas9), are too large to be packaged into adeno-associated viral (AAV) vectors, especially when

considering the length of the SpCas9 gene and the guide RNA in addition to other genetic elements required for functional expression cassettes. This makes a viable approach using SpCas9 unlikely.

Compact RNA guided nucleases of the invention, for example LPG10134, LPG10145, LPG10136, and LPG10139, are uniquely well suited for the excision of the FRDA instability region.

- 5 LPG10134, LPG10145, LPG10136, and LPG10139 have a PAM requirement that is in the vicinity of the FRDA instability region. Additionally, LPG10134, LPG10145, LPG10136, or LPG10139 can be packaged into an AAV vector along with a guide RNA.

Table 13 shows the location of genomic target sequences suitable for targeting LPG10134, LPG10145, LPG10136, or LPG10139 to the 5' and 3' flanks of the FRDA instability region. Once at
10 the locus, the RGN would excise the FA instability region. Excision of the region can be verified with Illumina sequencing of the locus.

Table 13: Genomic target sequences for RGN systems

RGN	Location relative to FRDA instability region	Genome target sequence (SEQ ID NO.)
LPG10134	5'	348
LPG10134	5'	349
LPG10134	3'	350
LPG10134	3'	351
LPG10145	5'	352
LPG10145	5'	353
LPG10145	3'	354
LPG10145	3'	355
LPG10136	5'	356
LPG10136	5'	357
LPG10136	3'	358
LPG10136	3'	359
LPG10139	5'	360
LPG10139	5'	361
LPG10139	3'	362
LPG10139	3'	363

15

Example 9: Targeting mutations responsible for Sickle Cell Diseases

Targeting sequences within the BCL11A enhancer region (SEQ ID NO: 364) may provide a mechanism for increasing fetal hemoglobin (HbF) to either cure or alleviate the symptoms of sickle cell diseases. For example, genome wide association studies have identified a set of genetic variations
20 at BCL11A that are associated with increased HbF levels. These variations are a collection of SNPs found in non-coding regions of BCL11A that function as a stage-specific, lineage-restricted enhancer region. Further investigation revealed that this BCL11A enhancer is required in erythroid cells for BCL11A expression (Bauer et al, (2013) Science 343:253-257, incorporated by reference herein). The enhancer region was found within intron 2 of the BCL11A gene, and three areas of DNaseI

hypersensitivity (often indicative of a chromatin state that is associated with regulatory potential) in intron 2 were identified. These three areas were identified as “+62”, “+58” and “+55” in accordance with the distance in kilobases from the transcription start site of BCL11A. These enhancer regions are roughly 350 (+55); 550 (+58); and 350 (+62) nucleotides in length (Bauer et al., 2013).

5

Example 9.1: Identifying preferred RGN systems

Here we describe a potential treatment for beta-hemoglobinopathies using an RGN system that disrupts BCL11A binding to its binding site within the HBB locus, which is the gene responsible for making beta-globin in adult hemoglobin. This approach uses NHEJ which is more efficient in mammalian cells. In addition, this approach uses a nuclease of sufficiently small size that can be packaged into a single AAV vector for *in vivo* delivery.

10

The GATA1 enhancer motif in the human BCL11A enhancer region (SEQ ID NO: 364) is an ideal target for disruption using RNA guided nucleases (RGNs) to reduce BCL11A expression with concurrent re-expression of HbF in adult human erythrocytes (Wu et al. (2019) Nat Med 387:2554). Several PAM sequences compatible with LPG10134, LPG10145, LPG10136, and LPG10139 are readily apparent at the genetic locus surrounding this GATA1 site. These nucleases have a PAM sequence of 5'-nGG-3' (SEQ ID NO:73), 5'-nnGG-3 (SEQ ID NO: 78)', 5'-nnnnCC-3' (SEQ ID NO: 74), and 5'-nnnnC-3' (SEQ ID NO: 76), respectively, and are compact in size, potentially allowing their delivery along with an appropriate guide RNA in a single AAV or adenoviral vector. This delivery approach bestows multiple advantages relative to others, such as access to hematopoietic stem cells and a well-established safety profile and manufacturing techniques.

15

20

The commonly used Cas9 nuclease from *S. pyogenes* (SpyCas9) requires a PAM sequence of 5'-NGG-3', (SEQ ID NO: 331) several of which are present near the GATA1 motif. However, the size of SpyCas9 prevents packaging into a single AAV or adenoviral vector and thus forgoes the aforementioned advantages of this approach. While a dual delivery strategy may be employed, it would add significant manufacturing complexity and cost. Additionally, dual viral vector delivery significantly decreases the efficiency of gene correction, since a successful edit in a given cell requires infection with both vectors.

25

An expression cassette encoding a human codon optimized LPG10134, LPG10145, LPG10136, or LPG10139 is produced, similar to those described in Example 4. Expression cassettes which express guide RNAs for RGNs LPG10134, LPG10145, LPG10136, and LPG10139 are also produced. These guide RNAs comprise: 1) a protospacer sequence that is complementary to either the non-coding or coding DNA strand within the BCL11A enhancer locus (the target sequence) and 2) an RNA sequence required for association of the guide RNA with the RGN. Because several potential PAM sequences for targeting by LPG10134, LPG10145, LPG10136, and LPG10139 surround the BCL11A GATA1 enhancer motif, several potential guide RNA constructs are produced to determine the best protospacer sequence that produces robust cleavage and NHEJ mediated

30

35

disruption of the BCL11A GATA1 enhancer sequence. The target genomic sequences in Table 14 are evaluated to direct the RGN to this locus.

Table 14: Target Sequences for BCL11A GATA1 enhancer locus using LPG10134, LPG10145, LPG10136 or LPG10139

Guide	RGN	Target genomic sequence (SEQ ID NO.)
1	LPG10134	365
2	LPG10134	366
3	LPG10134	367
4	LPG10145	368
5	LPG10145	369
6	LPG10145	370
7	LPG10136	371
8	LPG10136	372
9	LPG10136	373
10	LPG10139	374
11	LPG10139	375
12	LPG10139	376

To evaluate the efficiency with which LPG10134, LPG10145, LPG10136, or LPG10139 generates insertions or deletions that disrupt the BCL11A enhancer region, human cell lines such as human embryonic kidney cells (HEK cells) are used. A DNA vector comprising an RGN expression cassette (for example, as described in Example 4) is produced. A separate vector comprising an expression cassette comprising a coding sequence for a guide RNA sequence is also produced. Such an expression cassette may further comprise a human RNA polymerase III U6 promoter (SEQ ID NO: 329), as described in Example 4. Alternatively, a single vector comprising expression cassettes of both the RGN and guide RNA may be used. The vector is introduced into HEK cells using standard techniques such as those described in Example 4, and the cells are cultured for 1-3 days. Following this culture period, genomic DNA is isolated and the frequency of insertions or deletions is determined by using T7 Endonuclease I digestion and/or direct DNA sequencing, as described in Example 4.

A region of DNA encompassing the target BCL11A region is amplified by PCR with primers containing Illumina Nextera XT overhang sequences. These PCR amplicons are either examined for NHEJ formation using T7 Endonuclease I digestion, or undergo library preparation following the Illumina 16S Metagenomic Sequencing Library protocol or a similar Next Generation Sequencing (NGS) library preparation. Following deep sequencing, the reads generated are analyzed by CRISPResso to calculate rates of editing. Output alignments are hand-curated to confirm insertion and deletion sites. This analysis identifies the preferred RGN and the corresponding preferred guide

RNA (sgRNA). The analysis may result in any of LPG10134, LPG10145, LPG10136, and LPG10139 being equally preferred. Additionally, the analysis may determine there is more than one preferred guide RNA, or that all target genomic sequences in Table 14 are equally preferred.

5 *Example 9.2: Assay for expression of fetal hemoglobin*

In this example, LPG10134, LPG10145, LPG10136, or LPG10139 generated insertions or deletions disrupting the BCL11A enhancer region are assayed for expression of fetal hemoglobin. Healthy human donor CD34⁺ hematopoietic stem cells (HSCs) are used. These HSCs are cultured and vector(s) comprising expression cassettes comprising the coding regions of the preferred RGN and the preferred sgRNA are introduced using methods similar to those described in Example 8.1. Following electroporation, these cells are differentiated *in vitro* into erythrocytes using established protocols (for example, Giarratana et al. (2004) Nat Biotechnology 23:69-74, herein incorporated by reference). The expression of HbF is then measured using western blotting with an anti-human HbF antibody, or quantified via High Performance Liquid Chromatography (HPLC). It is expected that successful disruption of the BCL11A enhancer locus will lead to an increase in HbF production when compared to HSCs electroporated with only the RGN but no guide.

Example 9.3: Assay for decreased sickle cell formation

In this example, LPG10134, LPG10145, LPG10136, or LPG10139-generated insertions or deletions disrupting the BCL11A enhancer region are assayed for decreased sickle-cell formation. Donor CD34⁺ hematopoietic stem cells (HSCs) from patients afflicted with sickle cell disease are used. These HSCs are cultured and vector(s) comprising expression cassettes comprising the coding regions of preferred RGN and the preferred sgRNA are introduced using methods similar to those described in Example 8.1. Following electroporation, these cells are differentiated *in vitro* into erythrocytes using established protocols (Giarratana et al. (2004) Nat Biotechnology 23:69-74). The expression of HbF is then measured using western blotting with an anti-human HbF antibody, or quantified via High Performance Liquid Chromatography (HPLC). It is expected that successful disruption of the BCL11A enhancer locus will lead to an increase in HbF production when compared to HSCs electroporated with only the RGN but no guide.

Sickle cell formation is induced in these differentiated erythrocytes by the addition of metabisulfite. The numbers of sickled vs normal erythrocytes are counted using a microscope. It is expected that the numbers of sickled cells are less in cells treated with LPG10134, LPG10145, LPG10136, or LPG10139 plus sgRNAs than with cells untreated, or treated with RGNs alone.

35 *Example 9.4: Disease treatment validation in a murine model*

To evaluate the efficacy of using LPG10134, LPG10145, LPG10136, or LPG10139 for disruption of the BCL11A locus, suitable humanized mouse models of sickle cell anemia are used.

Expression cassettes encoding for the preferred RGN and for the preferred sgRNA are packaged into AAV vectors or adenovirus vectors. In particular, adenovirus type Ad5/35 is effective at targeting HSCs. A suitable mouse model containing a humanized HBB locus with sickle cell alleles is chosen, such as B6;FVB-Tg(LCR-HBA2,LCR-HBB*E26K)53Hhb/J or B6.Cg-Hbatm1Paz Hbbtm1Tow

5 Tg(HBA-HBBs)41Paz/HhbJ. These mice are treated with granulocyte colony-stimulating factor alone or in combination with plerixafor to mobilize HSCs into circulation. AAVs or adenoviruses carrying the RGN and guide plasmid are then injected intravenously, and the mice are allowed to recover for a week. Blood obtained from these mice is tested in an *in vitro* sickling assay using metabisulfite, and the mice are followed longitudinally to monitor mortality rates and hematopoietic
10 function. It is expected that treatment with AAVs or adenoviruses carrying an RGN and guide RNA will reduce sickling, mortality, and improve hematopoietic function when compared to mice treated with viruses lacking both expression cassettes, or with viruses carrying the RGN expression cassette alone.

15 **Example 10: Protein purification and biochemical testing**

The presently disclosed RGNs were expressed, purified, and tested for *in vitro* cleavage of a target sequence. The cut site was subsequently determined using an *in vitro* cleavage assay for LPG10145.

20 *Example 10.1: Recombinant Expression and Purification of RNA-guided nucleases and biochemical cleavage assay*

Plasmids containing the bacterial codon-optimized, HIS-tagged RGN coding sequences were synthesized and cloned into a pET-29b(+) vector backbone. Transformation of the RGN bacterial expression plasmid was carried out with One Shot™ BL21 Star™ (DE3) Chemically Competent *E.*
25 *coli* cells using heat shock. RGNs were expressed at a 0.5 L scale using MagicMedia™ *E. coli* Expression Medium (Invitrogen) supplemented with 50 µg/mL Kanamycin. After seeding with a starter culture, expression cultures were incubated for 5 hours at 30 °C shaking at 300 rpm, then dropped to 18 °C for an additional 24 hours. The cells were then harvested by centrifugation and frozen at -80 °C. Cell pellets from expression cultures were thawed at room temperature, resuspended
30 in lysis buffer, homogenized, then lysed with an EmulsiFlex-C3 cell disruptor (Avestin). The crude lysate solution was then clarified using high speed centrifugation. Clarified lysates were then purified using immobilized metal affinity chromatography (IMAC) using an ÄKTA Pure25 Fast Protein Liquid Chromatography system (Cytiva). LPG10136, LPG10138, and LPG10139 were further purified using cation exchange chromatography. Purified RGN proteins were then concentrated
35 and exchanged into a formulation buffer containing 20 mM sodium phosphate, 300 mM sodium chloride, 1 mM DTT, pH 7.4, and 20 % glycerol then flash frozen using liquid nitrogen. Purity of

purified RGNs was determined using sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

Ribonucleoprotein complexes (comprising nuclease and an sgRNA) were formed by incubation of nuclease and the RNA in a buffered solution for 20 min at room temperature. The complex was transferred to a tube containing digestion buffer and a PCR amplified target, directly linked at its 3' end to the corresponding PAM sequence for each RGN. Each RGN as a ribonucleoprotein complex was incubated with its respective target (library 1 or library 2; SEQ ID NOs: 459 and 460, respectively) polynucleotide at 37° C for 120 mins. The digestion reaction was quenched using ethylenediaminetetraacetic acid (EDTA) and analyzed using fragment analysis to quantify cleavage products.

Ten of the twelve presently disclosed RGNs were solubly expressed and isolated from *E. coli*. The yield from recombinant expression and subsequent purification varied greatly depending on the identity of the RGN, ranging from several milligrams to greater than one-hundred milligrams. Of the ten RGN proteins that were successfully expressed and purified, eight were active in a biochemical DNA cleavage assay when tested against two different target sequences and several compatible PAM contexts. Inactivity in these *in vitro* assays with purified protein could be due to several factors specific to these particular expression, purification, and/or cleavage conditions and may not necessarily reflect the activity of the RGNs under other conditions or within *in vivo* settings.

Table 15: Purification purity and *in vitro* cleavage of dsDNA

RGN	Isolated Yield mg/L culture	Purity (%)	Max Target Strand Cleavage Observed (%)
LPG10134	15	78	0
LPG10136	34 (14)	66	31
LPG10138	67 (6)	75	18
LPG10139	79 (36)	75	7
LPG10141	0	n/a	n/a
LPG10145	148	90	100
LPG10146	127	87	58
LPG10147	0	n/a	n/a
LPG10150	148	70	32

RGN	Isolated Yield mg/L culture	Purity (%)	Max Target Strand Cleavage Observed (%)
LPG10155	15	77	33
LPG10159	62	83	2.6
LPG10160	3	35	0

Isolated yield from IMAC purification
(isolated yield from CEX)

Table 16: Sequences for *in vitro* cleavage and perfect target cleavage

RGN ID	Target Sequence	PAM Context	PAM SEQ ID NO	Cleavage of Target Strand (%)	Cleavage of Non-target Strand (%)
LPG10134	Library 1	AGGACCTC	461	0	0
LPG10134	Library 1	AGGAATTC	462	0	0
LPG10134	Library 1	AGGAAAGC	463	0	0
LPG10134	Library 2	AGGACCTC	461	0	0
LPG10134	Library 2	AGGAATTC	462	0	0
LPG10134	Library 2	AGGAAAGC	463	0	0
LPG10136	Library 1	AGGACCTC	461	5.0	3.3
LPG10136	Library 1	AGGACTTC	464	0	0
LPG10136	Library 2	AGGACCTC	461	30.9	19.7
LPG10136	Library 2	AGGACTTC	464	11.3	7.5
LPG10138	Library 1	AGGACCTC	461	1.4	0.5
LPG10138	Library 1	AGGAATTC	462	0	0
LPG10138	Library 1	AGGACTTC	464	5.5	3.7
LPG10138	Library 2	AGGACCTC	461	4.7	1.5
LPG10138	Library 2	AGGAATTC	462	0	0
LPG10138	Library 2	AGGACTTC	464	18.0	9.4
LPG10139	Library 1	AGGACCTC	461	4.4	2.4
LPG10139	Library 2	AGGACCTC	461	7.3	4.5
LPG10145	Library 1	ACGGATTC	465	92.9	95.3
LPG10145	Library 2	ACGGATTC	465	100	100
LPG10146	Library 1	AGGAAACC	466	3.9	2.8
LPG10146	Library 1	GGATAACC	467	0	0
LPG10146	Library 1	GAGTAACC	468	1.5	1.0
LPG10146	Library 1	CAATAACC	469	0	0
LPG10146	Library 2	AGGAAACC	466	48.9	48.6
LPG10146	Library 2	GGATAACC	467	39.7	27.2
LPG10146	Library 2	GAGTAACC	468	57.7	48.2
LPG10146	Library 2	CAATAACC	469	32.7	25.9
LPG10150	Library 1	AGGACCTC	461	1.4	0.9
LPG10150	Library 1	AGGACTTC	464	2.3	1.7
LPG10150	Library 2	AGGACCTC	461	25.1	16.5
LPG10150	Library 2	AGGACTTC	464	31.8	26.1

RGN ID	Target Sequence	PAM Context	PAM SEQ ID NO	Cleavage of Target Strand (%)	Cleavage of Non-target Strand (%)
LPG10155	Library 1	AGAAATTC	470	32.7	20.1
LPG10155	Library 2	AGAAATTC	470	7.6	3.5
LPG10159	Library 2	AGAAATTC	470	2.5	1.2
LPG10160	Library 1	AAATATTC	471	0	0
LPG10160	Library 2	AAATATTC	471	0	0

Example 10.2 In vitro cleavage site determination

Cleavage sites were determined using RNP (ribonucleoprotein) and an appropriate plasmid substrate. *E. coli* expression plasmids coding for an RGN fused to a His10 N-terminal tag were constructed and transformed into BL21 (DE3) Star *E. coli* (Invitrogen) for protein expression. RGN expression was performed using autoinduction MagicMedia (Thermo). After lysis and clarification, proteins were purified with a 3-step purification method which included immobilized metal affinity chromatography, cation exchange chromatography, and anion exchange chromatography. RNP complexes were formed by incubation of the RGN with its RNA guide (SEQ ID NO: 473 for Library 1 and SEQ ID NO: 474 for Library 2) in a buffered solution for 15 min at room temperature.

The cleavage reaction was comprised of the RNP, digestion buffer and the plasmid target. The plasmid target (SEQ ID NO: 472) sequence contained two target nucleotide sequences, described as Library 1 and Library 2, (SEQ ID NO: 459 and SEQ ID NO: 460, respectively), -5' to the RGN PAM sequence. Incubation of the cleavage reaction at 37 °C for 90 min resulted in cleaved products. Cleaved products were visualized via agarose gel electrophoresis. The total cleavage reaction was cleaned up using a magnetic-bead DNA purification method with no size selection, and this clean-up was repeated after each enzymatic reaction. The cleaned DNA was end-repaired with T4 DNA polymerase (NEB) and A-tailed using the Klenow Fragment (3'-5' exo-) (NEB). Adapter oligos (SEQ ID NOs: 475 and 476) were annealed by mixing in equimolar amounts, heating to 95 °C and cooling slowly to room temperature. Adapters were annealed to A-tailed cleavage products using T4 DNA ligase in combination with T4 polynucleotide kinase. The final cleaned ligation products served as PCR templates.

PCRs to amplify the adapter-ligated cleavage products were performed using the appropriate primer pairs complementary to the adapter sequence and the plasmid backbone upstream and downstream of the anticipated cleavage site. Specifically, the PCR reactions included 2x Ultra II Q5 Master Mix (NEB) with 50-100 ng of template DNA and 0.5 μM of each primer. The PCR cycling conditions were as follows: 98 °C for 1 min, followed by 30 cycles of 98 °C for 10 sec, 62 °C for 10 sec, 72 °C for 10 sec, followed by a final step at 72 °C for 1 min, holding at 10 °C forever. PCR products were visualized by agarose gel electrophoresis and sequence verified by Sanger sequencing.

The cleavage site was determined to be blunt if there was no sequence absent or repeated in the Sanger sequence. If the cut site had a 5'-overhang, the overhang sequence would be present in both sequenced PCR products. A 3'-overhang would yield a sequence missing in both PCR products relative to the uncut plasmid substrate.

- 5 It was determined that LPG10145 has a cleavage site at the +3 position relative to the PAM, i.e., a blunt cleavage is introduced between the third and fourth nucleotides upstream (5') of the PAM sequence.

Example 11: Delivery of RNPs and mRNA to PBMCs

- 10 To determine if the RGNs are capable of delivery in different formats, RNP nucleofection delivery was tested with peripheral blood mononuclear cells (PBMCs). PBMCs were thawed, activated using CD3/CD28 beads (ThermoFisher) for 3 days, then nucleofected using the Lonza 4D-Nucleofector X unit and Nucleocuvette strips. The P3 Primary Cell kit was used for both mRNA and RNP delivery. Cells were transfected using the EO-115 and EH-115 programs for mRNA and RNP
15 delivery, respectively. Cells were cultured in CTS OpTimizer T cell expansion medium (ThermoFisher) containing IL-2, IL-7, and IL-15 (Miltenyi Biotec) for 4 days post nucleofection before being harvested using a Nucleospin Tissue genomic DNA isolation kit (Machery Nagel).

- To determine the editing efficiency, the nucleofected PBMCs were incubated with an appropriate fluorophore-conjugated antibody followed by flow cytometry or NGS. Editing efficiency
20 by flow cytometry is reported as percent knockout of the gene of interest. An unedited control was included to ensure staining efficiency was complete. Amplicons surrounding the editing sites were generated by PCR and subjected to NGS sequencing using the Illumina Nextera platform using 2x250bp paired end sequencing following the method in Example 4.

- Using RNP delivery of LPG10136, RNPs were formed to test 10 different guides (see Figure 2
25 and Table 17). Of the 9 guides tested, only one guide, SGN002661, showed high levels of editing as measured by protein knockout via flow cytometry. SGN002661 showed over 75% protein knockout as measured by flow cytometry.

Table 17: sgRNAs used for RNP delivery of LPG10136

sgRNA name	sgRNA target sequence SEQ ID NO
SGN002654	505
SGN002655	506
SGN002656	507

sgRNA name	sgRNA target sequence SEQ ID NO
SGN002657	508
SGN002658	509
SGN002659	510
SGN002660	511
SGN002661	512
SGN002662	513
SGN002663	514

Example 11.1 Optimization of target length

For delivery of LPG10145 as ribonucleoproteins (RNP: RNA-guided nuclease complexed with single guide RNAs) in PBMCs, nucleofection was utilized, which is an electroporation-based method that allows for the transfer of DNA, RNA, and/or protein into the cell nucleus. The TRAC and B2M genes were targeted due to their clinical relevance and because these genes control cell surface proteins, which provided the convenience of utilizing high throughput flow cytometry-based analysis. For this experiment, the length of the spacer sequence was shortened from 25 to 20 nucleotides to determine the effects of spacer length on editing efficiency for two targets of interest. Isolated peripheral blood mononuclear cells (PBMC) were thawed, activated with CD3/CD28 beads, and incubated at 37 °C with 5% CO₂. After 3 days, the beads were removed from the cells. The cells were then concentrated via centrifugation and resuspended in nucleofection buffer (P3 Solution Lonza) so that 1x10⁶ cells could be used for each reaction. The RNP (60 pmol RGN and 120 pmol guide) incubated at room temperature for at least 10 minutes prior to addition of the PBMC. The cells+LPG10145+sgRNA reactions were nucleofected according to the manufacturer's instructions using Program EH-115 (Lonza). After nucleofection, the cells rested for 10 minutes, followed by incubation in media for 1-4 days. To determine the editing efficiency, the nucleofected cells were incubated with an appropriate fluorophore-conjugated antibody followed by flow cytometry. Editing efficiency is reported as percent knockout of the gene of interest. An unedited control was included to ensure staining efficiency was complete.

In addition, spacer length optimization was confirmed by mRNA delivery of LPG10145 while expanding the length of the spacers from 27 to 17 nucleotides using the same guides that targeted TRAC and B2M. For delivery of LPG10145 as mRNA, 2 µg of LPG10145 mRNA and 4 µg of sgRNA was resuspended in nucleofection buffer (P3 solution) along with 3.0x10⁴ cells per reaction. The cells were added to the reaction, and nucleofected according to the manufacturer's instructions using program EO-

115 (Lonza). After nucleofection, cells were transferred to culture vessel and incubated in media for 4 days. Evaluation of editing efficiency by flow cytometry was conducted as described above.

Table 18: RNP delivery of LPG10145 to cells testing effects of target length on editing

Nuclease	SGN	Spacer length	Target SEQ ID NO	Editing Rate by flow cytometry (Replicate #1)	Editing Rate by flow cytometry (Replicate #2)	Editing Rate by flow cytometry (Replicate #3)
None	Unedited Control			10.3	18.1	
LPG10145	SGN002702	25	516	77.1	68.8	80.7
	SGN005121	24	491	90.01	89.3	76.2
	SGN005122	23	492	88.9	90	87.4
	SGN005123	22	493	90.1	91.38	85.2
	SGN005124	21	494	92.61	91.26	85.5
	SGN003018	20	481	83.2	83.6	55.2
LPG10145	SGN002707	25	517	50.4	53	20.6
	SGN005117	24	487	50.1	52.5	19.9
	SGN005118	23	488	50.5	58	22.8
	SGN005119	22	489	NT	NT	21.7
	SGN005120	21	490	NT	NT	19.2
	SGN003023	20	486	57.3	51.5	15.7

5 NT: not tested

Table 19: mRNA delivery of LPG10145 to cells testing effects of target length on editing

Nuclease	SGN	Spacer Length	Target SEQ ID NO	Editing Rate by FLOW Cytometry (Replicate 1)	Editing Rate by FLOW Cytometry (Replicate 2)
None	Unedited			1.1	.8
LPG10145	SGN007076	17	495	1.1	1.3
	SGN007077	18	496	1.1	1.3

Nuclease	SGN	Spacer Length	Target SEQ ID NO	Editing Rate by FLOW Cytometry (Replicate 1)	Editing Rate by FLOW Cytometry (Replicate 2)
	SGN007078	19	497	18.1	22.8
	SGN003018	20	481	84.8	91.0
	SGN005124	21	494	94.1	89.5
	SGN005123	22	493	93.58	94.72
	SGN005122	23	492	93.61	92.61
	SGN005121	24	491	91.85	95.83
	SGN002702	25	557	93.40	94.81
	SGN007079	26	498	86.8	89.7
	SGN007080	27	499	82.3	87.2
None	Unedited			1.4	.8
LPG10145	SGN007081	17	500	1.3	1.6
	SGN007082	18	501	1.3	1.9
	SGN007083	19	502	23.7	27.7
	SGN003023	20	486	51.4	56.8
	SGN005120	21	490	55.0	58.4
	SGN005119	22	489	56.7	61.6
	SGN005118	23	488	69.8	73.7
	SGN005117	24	487	69.7	58.9
	SGN002707	25	558	55.1	56.9
	SGN007084	26	503	56.1	63.8
	SGN007085	27	504	49.1	57.7

Analysis

Using RNP delivery and testing the spacer lengths from 20 to 25 nucleotides, all spacer lengths demonstrated similar levels of editing for each target. The best editing, although slight, was seen with spacer lengths of 21–24 nucleotides. Because there were small differences in editing between 20–25 nucleotides, the spacer lengths tested for each target were expanded and tested with mRNA. These data corroborated the RNP data and helped to define that the highest editing was when using spacer lengths between 21–24 nucleotides.

Example 11.2 RNP dose dependence

To understand if increasing concentration of RGN can effectively improve editing, different concentrations of RNP were provided in a PBMC cell editing experiment. The RNP concentrations tested were 60 pmole, 90 pmole and 120 pmole, with a protein:RNA ratio of 1:2. The results showed that with a working gRNA, the editing rate on the desired target can be improved with higher amounts of RGN (see Table 20 and Figures 3A and 3B).

Table 20: sgRNAs used for RNP dose dependence experiments

SGN name	SGN target sequence SEQ ID NO
SGN002699	515
SGN003014	477
SGN003015	478
SGN003016	479
SGN003017	480
SGN003018	481
SGN002707	517
SGN003019	482
SGN003020	483
SGN003021	484
SGN003022	485
SGN003023	486

Example 12: Off target analysis

To assess the specificity of the nucleases, off target editing was determined at potential sites identified via bioinformatics. Potential off target sites for LPG10145 were identified by targets with less than five mismatches in the target sequence and at least one residue match in the PAM sequence.

The same methods as those described in Example 11.1 for RNP delivery to mammalian cells and amplicon sequencing were used to test the specificity and off target editing of LPG10145. In samples with high editing rates for SGN003017 and SGN003023, the potential off target locations in Table 21 were assayed for potential editing. The primers in Table 22 were used to amplify potential off target sites with sequence similarity to the on target site to look for off target editing.

Table 21: Off target sequences assayed

SGN	Off target Number	Off target seq	SEQ ID
SGN003017	3017-1	TGTCCACGGAGCGAGACAGGGAGG	518
SGN003023	3023-1	ATAGGCAGACAACTTGTATAGG	519
SGN003023	3023-2	ATAGGCAGACAGACTTGCAGAGG	520
SGN003023	3023-3	ACAGGCAGACAGATTTGTCAGAGG	521
SGN003023	3023-4	AAAGGCAGACAGACATGTCAGTGG	522
SGN003023	3023-5	CTAGGCAGACAGACTTCCTTCCTAGG	523
SGN003023	3023-6	ATGGGGCAGACAGACTTGTACAGG	524
SGN003023	3023-7	ACAGGCAGACAGACTTGCATTTGG	525
SGN003023	3023-8	ATAGGCAGACAGACTTGTTAGAAG	526
SGN003023	3023-9	ATAGGTAGACAGACTTGTGTCAGTGA	527

Table 22: Primers used to amplify off target regions

Description	Primer sequence	SEQ ID
3017-1 FWD	TCTTCGCCTGTGATCTCTGA	528
3023-1 FWD	GCTAGTTCCAGCTGCCTAGG	530
3023-2 FWD	TGAGCCCTTCTTCTGTGCTG	532
3023-3 FWD	AGTGCTAGAGTGATGTGGGA	534
3023-4 FWD	ATCTCCCTCAGTCCAGTCCC	536
3023-5 FWD	CCAGAACATCAGCAGCAAGC	538
3023-6 FWD	AAGGTGGGACTCACTCTGAA	540
3023-7 FWD	CCCTCAGCTCTGACTCCTCT	542
3023-8 FWD	CCTGTCAAGGGAGTGTTTCT	544
3023-9 FWD	ATGCTCCGCTCCTTGATCTG	546
3017-1 REV	TTGGATGGGATGTCCTGAGG	529
3023-1 REV	CAGTGCGTTTCTCTGGTCCT	531
3023-2 REV	CCTCCAGATCCCCACTACCA	533
3023-3 REV	AGGTCACCTTTGTTGCCATC	535
3023-4 REV	CCATCTCATCCAGTGCCCTC	537
3023-5 REV	CCTGGGTCACCTCCTGTCAC	539
3023-6 REV	ATTTTACTCAAGGCCAGGC	541
3023-7 REV	TGAACTCAGGACCACATGGC	543

Description	Primer sequence	SEQ ID
3023-8 REV	ATCCTTGCAATCCTCTGAAA	545
3023-9 REV	TCATTCCCTCCCCACTTTCTC	547

Using RNP delivery, there was no detectable off target editing at the two guides tested. Two off target locations showed low levels of background indels that were also seen in amplicons from unedited control cells. These off target locations were 3023-5 and 3023-9; denoted with an asterisks in

5 Table 23.

Table 23: Off target editing for SGN003017 and SGN003023

Delivery	Guide	On-Target Efficiency	Off-target Site	Off-target Editing
RNP	SGN003017 - B2M	59%	1	0%
RNP	SGN003023 - TRAC	54%	1	0%
			2	0%
			3	0%
			4	0.11%
			5	0.07%*
			6	0.49%
			7	0%
			8	0%
			9	0.14*

10 **Example 13: Glycine scanning of LPG10145**

Determination of Glycine Mutations and Insertions

The protein sequence of LPG10145 was run through the DynaMine webserver which provided an S2 prediction score for each residue, estimating rigidity and flexibility of that residue's backbone. Scores range from 1(rigid) to 0 (highly dynamic). Residues with a score of < 0.72 were

15 mutated to glycine unless a nearby residue was a glycine rich region (defined as two glycines next to each other). Insertion sites for glycine were chosen as flexible regions with a score higher than 0.72

but less than 0.75 and that were adjacent to a glycine. These insertion sites were also mapped onto a LPG10145 homology model to check if they were predicted to be in flexible regions.

Screening Activity of LPG10145 Glycine Mutants in Mammalian Cells

5 Glycine mutants were compared with parental LPG10145 in their ability to edit exon 1 of beta-2-microglobulin (B2M) in HEK293T cells using two different guides (SGN003014 and SGN003018). These guides were chosen for their moderate to low levels of editing with the parental LPG10145 and were tested on saturating (optimal) editing conditions as well as non-saturating (sub-optimal) conditions. Optimal editing conditions were performed with plasmid lipofection using
10 Lipofectamine 3000 of cells seeded the previous day at 10,000 cells and using 160 ng of plasmid encoding LPG10145 or LPG10145 variant and 40 ng of guide-encoding plasmid. Sub-optimal editing conditions were performed with plasmid lipofection of cells seeded the previous day at 10,000 cells using 40 ng of plasmid DNA encoding LPG10145 or LPG10145 variant and 40 ng of guide-encoding plasmid. Cells were incubated at 37°C and 5% CO₂ for 2 days, genomic DNA extracted, and the target
15 region amplified by PCR and submitted for NGS sequencing.

Table 24: Activity of LPG10145 Glycine Mutants

LPG10145 Construct	Editing Normalized to WT (WT = 1)		% Editing	
	SGN003014	SGN003018	SGN003014	SGN003018
pLEM145v3.1	1	1	48.1*	47.99*
S44G	0.417464	0.760913	20.08	36.52
S46G	0.533056	0.715908	25.64	34.36
A47G	0.582952	0.86384	28.04	41.46
S48G	0.470686	0.784665	22.64	37.66
R49G	0.427651	0.663611	20.57	31.85
N50G	0.486071	0.823627	23.38	39.53
E51G	0.437006	0.816543	21.02	39.19
E52G	0.497089	0.779039	23.91	37.39
F82G	0.356133	0.97531	17.13	46.81
P83G	0.588773	0.879675	28.32	42.22
F84G	0.363825	0.711741	17.5	34.16
P85G	0.530977	0.590895	25.54	28.36
N87G	0.512266	0.661527	24.64	31.75
T88G	0.848233	1.050526	40.8	50.42
A90G	0.809979	1.05636	38.96	50.7
N91G	0.613929	0.94864	29.53	45.53
S133G	0.728067	0.943223	35.02	45.27
N138G	0.59106	0.89926	28.43	43.16
L176G	0.735759	0.831128	35.39	39.89
E178G	0.681289	0.979685	32.77	47.02

LPG10145 Construct	Editing Normalized to WT (WT = 1)		% Editing	
	SGN003014	SGN003018	SGN003014	SGN003018
P234G	0.499376	1.005521	24.02	48.26
S236G	0.641372	0.921763	30.85	44.24
E237G	0.66736	0.874883	32.1	41.99
K238G	0.449688	0.653401	21.63	31.36
S239G	0.434719	0.699865	20.91	33.59
S334G	0.642204	0.965934	30.89	46.36
P335G	0.571102	0.891134	27.47	42.77
A336G	0.567775	0.996562	27.31	47.83
P349G	0.81684	1.158871	39.29	55.62
V428G	0.892931	1.282217	42.95	61.54
K544G	0.645946	0.936973	31.07	44.97
Q623G	0.72578	1.020106	34.91	48.96
N624G	0.645114	0.765496	31.03	36.74
S647G	0.707069	0.950099	34.01	45.6
N740G	0.798753	0.892385	38.42	42.83
K741G	0.124116	0.379623	5.97	18.22
S742G	0.57131	0.806126	27.48	38.69
R743G	0.44657	0.729243	21.48	35
E744G	0.975468	1.079487	46.92	51.81
T745G	0.66736	0.931972	32.1	44.73
H746G	0.646778	0.87905	31.11	42.19
M827G	0.804366	1.009063	38.69	48.43
N828G	0.573181	0.736118	27.57	35.33
V844G	0.811019	1.010314	39.01	48.49
P910G	0.778794	1.091572	37.46	52.39
N911G	0.862162	1.035733	41.47	49.71
N939G	0.69605	0.981561	33.48	47.11
N940G	0.478378	0.624857	23.01	29.99
P942G	0.418295	0.652985	20.12	31.34
N1044G	0.632848	1.013647	30.44	48.65
N1058G	0.980873	0.905928	47.18	43.48
P1059G	0.597713	0.925721	28.75	44.43
A1060G	0.755094	1.068236	36.32	51.27
G429	0.822661	1.020523	39.57	48.98
G473	0.707692	1.057819	34.04	50.77
G592	0.729314	0.777164	35.08	37.3
G845	0.834096	0.945515	40.12	45.38
G930	0.797089	1.009689	38.34	48.46

*Editing for the parental WT control is an average of two replicates

Example 14: Robustness Testing of LPG10145

Example 14.1: Screening LPG10145 Editing at Multiple Target Loci in Mammalian Cells by Plasmid Delivery

Guides targeting several genes were designed for robustness testing in HEK293T cells by plasmid delivery. These guides were tested under optimal editing conditions for HEK293T cells in a 96-well plate which involved seeding 10,000 cells on day 1, lipofection using Lipofectamine 3000 on day 2, and genomic DNA extraction on day 4. Lipofections were performed by mixing 160 ng of LPG10145-encoding plasmid and 40 ng of guide-encoding plasmid, and 0.4 µl of p3000 in Opti-MEM. Then, 0.3 µl of Lipofectamine 3000 diluted in Opti-MEM was added to the plasmid mixture and incubated for 15 mins before adding to cells. Regions around the editing site for each guide are amplified from the extracted genomic DNA and sequenced by NGS as described in Example 4. The editing efficiency of LPG10145 with each guide is reported as percent editing (percent of INDELS at the target site). Out of 32 guides tested, LPG10145 exhibited editing greater than 20% with 43.7 % of the guides (14/32 guides) and had editing over 10% at 53% of guides tested (17/32 guides).

Table 25: Robust editing by LPG10145 by plasmid delivery in HEK293T cells

Guide	Gene Name	% Editing	Replicates per guide
SGN006164	Gene A	0.6	1
SGN006165	Gene A	1.07	1
SGN006166	Gene A	17.83	1
SGN006167	Gene A	4.86	1
SGN006168	Gene A	0.78	1
SGN006169	Gene A	6.315	2
SGN006170	Gene A	40.59	2
SGN002707	TRAC	34.87	2
SGN002703	TRAC	6.555	2
SGN006172	TRAC	29.745	2
SGN006173	TRAC	31.86	2
SGN006174	TRAC	26.595	2
SGN006175	TRAC	20.83	2
SGN006176	B2M	9.61	2
SGN002700	B2M	10.615	2
SGN006178	B2M	23.975	2
SGN006179	B2M	45.445	2
SGN006180	B2M	0.895	2
SGN006181	B2M	4.465	2
SGN006182	B2M	32.365	2
SGN006183	Gene B	5.595	2
SGN006184	Gene B	11.065	2
SGN006185	Gene B	9.09	2
SGN006186	Gene B	22.7	2
SGN006187	Gene C	31.87	2
SGN006188	Gene C	0.065	2

Guide	Gene Name	% Editing	Replicates per guide
SGN006189	Gene C	35.725	2
SGN006190	Gene C	4.325	2
SGN006192	Gene C	3.4	2
SGN006193	Gene C	2.24	1
SGN003014	B2M	34.41	2
SGN003018	B2M	56.51	2

Example 15: LPG10145 Reproducibility Screening

5 To evaluate LPG10145 editing reproducibility, LPG10145 was delivered as a ribonucleoprotein complex in T cells through nucleofection. Methods for RNP delivery and experimental read out through amplicon sequencing were carried out as described in Example 11. Here, multiple sgRNA targeting different genes were utilized to show the reproducibility of LPG10145 editing with all guides returning a coefficient of variation (CV) value of less than 50% (Figure 4).

THAT WHICH IS CLAIMED:

1. A nucleic acid molecule comprising a polynucleotide encoding an RNA-guided nuclease (RGN) polypeptide, wherein said polynucleotide comprises a nucleotide sequence encoding an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs:1-12;

wherein said RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence.

2. The nucleic acid molecule of claim 1, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

3. The nucleic acid molecule of claim 1 or 2, wherein said polynucleotide encoding an RGN polypeptide is operably linked to a promoter heterologous to said polynucleotide.

4. The nucleic acid molecule of any one of claims 1-3, wherein said RGN polypeptide is capable of cleaving said target DNA sequence upon binding.

5. The nucleic acid molecule of claim 4, wherein said RGN polypeptide is capable of generating a double-stranded break.

6. The nucleic acid molecule of claim 4, wherein said RGN polypeptide is capable of generating a single-stranded break.

7. The nucleic acid molecule of any one of claims 1-3, wherein said RGN polypeptide is nuclease inactive or is a nickase.

8. The nucleic acid molecule of any one of claims 1-7, wherein the RGN polypeptide is operably linked to a prime editing polypeptide.

9. The nucleic acid molecule of claim 8, wherein said prime editing polypeptide comprises a DNA polymerase.

10. The nucleic acid molecule of claim 8, wherein said prime editing polypeptide comprises a reverse transcriptase.

11. The nucleic acid molecule of any one of claims 1-7, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

12. The nucleic acid molecule of claim 11, wherein the base-editing polypeptide is a deaminase.

13. The nucleic acid molecule of claim 12, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

14. The nucleic acid molecule of claim 12, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

15. The nucleic acid molecule of claim 12, wherein the deaminase has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

16. The nucleic acid molecule of any one of claims 1-15, wherein the RGN polypeptide comprises one or more nuclear localization signals.

17. The nucleic acid molecule of any one of claims 1-16, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

18. The nucleic acid molecule of any one of claims 1-17, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

19. A vector comprising the nucleic acid molecule of any one of claims 1-18.

20. The vector of claim 19, further comprising at least one nucleotide sequence encoding said gRNA capable of hybridizing to said target DNA sequence.

21. The vector of claim 20, wherein the guide RNA is selected from the group consisting of:

a) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;

b) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;

c) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;

d) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;

e) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;

f) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;

g) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;

h) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;

i) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

j) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 10;

k) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

l) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24; and

ii) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36;

wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

22. The vector of claim 20, wherein the guide RNA is selected from the group consisting of:

a) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13; and

ii) a tracrRNA having 1000% sequence identity to SEQ ID NO: 25;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1;

b) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2;

c) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3;

d) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 4;

e) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17; and

5 ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 5;

10 f) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18; and

15 ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6;

g) a guide RNA comprising:

20 i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 19; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 31;

25 wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 7;

h) a guide RNA comprising:

30 i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 20; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32;

35 wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 8;

i) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9;

j) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 10;

k) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 11; and

l) a guide RNA comprising:

i) a CRISPR RNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24; and

ii) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36;

wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12.

23. The vector of claim 20 or 21, where said gRNA is a single guide RNA.

24. The vector of embodiment 23, wherein said sgRNA further comprises an extension comprising an edit template for prime editing.

25. The vector of claim 20 or 21, wherein said gRNA is a dual-guide RNA.

26. A cell comprising the nucleic acid molecule of any one of claims 1-18 or the vector of any one of claims 19-25.

27. A method for making an RGN polypeptide comprising culturing the cell of claim 26 under conditions in which the RGN polypeptide is expressed.

28. A method for making an RGN polypeptide comprising introducing into a cell a heterologous nucleic acid molecule comprising a nucleotide sequence encoding an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12;

wherein said RGN polypeptide is capable of binding a target DNA sequence in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence;

and culturing said cell under conditions in which the RGN polypeptide is expressed.

29. The method of claim 28, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

30. The method of any one of claims 27-29, further comprising purifying said RGN polypeptide.

31. The method of any one of claims 27-29, wherein said cell further expresses one or more guide RNAs capable of binding to said RGN polypeptide to form an RGN ribonucleoprotein complex.

32. The method of claim 31, further comprising purifying said RGN ribonucleoprotein complex.

33. An RNA-guided nuclease (RGN) polypeptide, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; and

wherein said RGN polypeptide is capable of binding a target DNA sequence of a DNA molecule in an RNA-guided sequence specific manner when bound to a guide RNA (gRNA) capable of hybridizing to said target DNA sequence.

34. The RGN polypeptide of claim 33, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

35. The RGN polypeptide of claim 33 or 34, wherein said RGN polypeptide is an isolated RGN polypeptide.

36. The RGN polypeptide of any one of claims 33-35, wherein said RGN polypeptide is capable of cleaving said target DNA sequence upon binding.

37. The RGN polypeptide of claim 36, wherein cleavage by said RGN polypeptide generates a double-stranded break.

38. The RGN polypeptide of claim 36, wherein cleavage by said RGN polypeptide generates a single-stranded break.

39. The RGN polypeptide of any one of claims 33-35, wherein said RGN polypeptide is nuclease inactive or a nickase.

40. The RGN polypeptide of any one of claims 33-39, wherein said RGN polypeptide is operably linked to a prime editing polypeptide.

41. The RGN polypeptide of claim 40, wherein said prime editing polypeptide comprises a DNA polymerase.

42. The RGN polypeptide of claim 40, wherein said prime editing polypeptide comprises a reverse transcriptase.

43. The RGN polypeptide of any one of claims 33-39, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

44. The RGN polypeptide of claim 43, wherein the base-editing polypeptide is a deaminase.

45. The RGN polypeptide of claim 44, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

46. The RGN polypeptide of claim 44, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

47. The RGN polypeptide of claim 44, wherein the deaminase has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

48. The RGN polypeptide of any one of claims 33-47, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

49. The RGN polypeptide of any one of claims 33-48, wherein the RGN polypeptide comprises one or more nuclear localization signals.

50. A ribonucleoprotein (RNP) complex comprising the RGN polypeptide of any one of claims 33-49 and the guide RNA bound to the RGN polypeptide.

51. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12 or a polynucleotide comprising a nucleotide sequence encoding the RGN polypeptide;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

52. The system of claim 51, wherein at least one of said nucleotide sequences encoding the one or more guide RNAs and said nucleotide sequence encoding the RGN polypeptide is operably linked to a promoter heterologous to said nucleotide sequence.

5 53. The system of claim 51 or 52, wherein the nucleotide sequences encoding the one or more guide RNAs and the nucleotide sequence encoding the RGN polypeptide are located on one vector.

10 54. A system for binding a target DNA sequence of a DNA molecule, said system comprising:

a) one or more guide RNAs capable of hybridizing to said target DNA sequence or one or more polynucleotides comprising one or more nucleotide sequences encoding the one or more guide RNAs (gRNAs); and

15 b) an RNA-guided nuclease (RGN) polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12;

wherein the one or more guide RNAs are capable of hybridizing to the target DNA sequence, and

20 wherein the one or more guide RNAs are capable of forming a complex with the RGN polypeptide in order to direct said RGN polypeptide to bind to said target DNA sequence of the DNA molecule.

25 55. The system of any one of claims 51-54, wherein the RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

56. The system of any one of claims 51-55, wherein at least one of said nucleotide sequences encoding the one or more guide RNAs is operably linked to a promoter heterologous to said nucleotide sequence.

30 57. The system of any one of claims 51-56, wherein said RGN polypeptide and said one or more guide RNAs are not found complexed to one another in nature.

58. The system of any one of claims 51-57, wherein said target DNA sequence is a eukaryotic target DNA sequence.

35 59. The system of any one of claims 51-58, wherein said gRNA is a single guide RNA (sgRNA).

60. The system of claim 59, wherein said sgRNA further comprises an extension comprising an edit template for prime editing.

61. The system of any one of claims 51-58, wherein said gRNA is a dual-guide RNA.

62. The system of any one of claims 51-61, wherein said gRNA is selected from the group consisting of:

a) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 1;

b) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 2;

c) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 4;

e) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 5;

f) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 6;

g) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 7;

h) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 8;

5 i) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 9;

10 j) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NOs: 10;

15 k) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 11; and

20 l) a gRNA comprising a CRISPR repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide comprises an amino acid sequence having at least 90% sequence identity to SEQ ID NO: 12.

63. The system of any one of claims 51-61, wherein said gRNA is selected from the group consisting of:

25 a) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1;

30 b) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2;

35 c) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15 and a tracrRNA

having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3;

d) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:

4;

e) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:

5;

f) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:

6;

g) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 31, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:

7;

h) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO:

8;

i) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity

to SEQ ID NO: 33, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9;

j) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NOs:10;

k) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 11; and

l) a gRNA comprising a CRISPR repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12.

64. The system of any one of claims 51-63, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

65. The system of any one of claims 51-64, wherein the target DNA sequence is within a cell.

66. The system of any one of claims 51-65, wherein the one or more guide RNAs is capable of hybridizing to the target DNA sequence and the guide RNA is capable of forming a complex with the RGN polypeptide to direct cleavage of the target DNA sequence.

67. The system of claim 66, wherein the cleavage generates a double-stranded break.

68. The system of claim 66, wherein the cleavage generates a single-stranded break.

69. The system of any one of claims 51-65, wherein said RGN polypeptide is nuclease inactive or is a nickase.

70. The system of any one of claims 51-69, wherein the RGN polypeptide is operably linked to a prime editing polypeptide.

71. The system of claim 70, wherein the prime editing polypeptide comprises a DNA polymerase.

72. The system of claim 70, wherein the prime editing polypeptide comprises a reverse transcriptase.

73. The system of any one of claims 51-69, wherein the RGN polypeptide is operably linked to a base-editing polypeptide.

74. The system of claim 73, wherein the base-editing polypeptide is a deaminase.

75. The system of claim 74, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

76. The system of claim 74, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

77. The system of claim 74, wherein the deaminase has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

78. The system of any one of claims 51-77, wherein the RGN polypeptide comprises one or more nuclear localization signals.

79. The system of any one of claims 51-78, wherein the RGN polypeptide is codon optimized for expression in a eukaryotic cell.

80. The system of any one of claims 51-79, wherein said system further comprises one or more donor polynucleotides.

81. A cell comprising the system of any one of claims 51-80.

82. A pharmaceutical composition comprising the nucleic acid molecule of any one of claims 1-18, the vector of any one of claims 19-25, the cell of claim 26 or 81, the RGN polypeptide of any one of claims 33-49, the RNP complex of claim 50, or the system of any one of claims 51-80, and a pharmaceutically acceptable carrier.

83. A method for binding a target DNA sequence of a DNA molecule comprising delivering a system according to any one of claims 51-80, to said target DNA sequence or a cell comprising the target DNA sequence.

84. The method of claim 83, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

85. The method of claim 83, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby modulating expression of said target DNA sequence or a gene under transcriptional control by said target DNA sequence.

86. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule comprising delivering a system according to any one of claims 36-57 to said target DNA sequence or a cell comprising the DNA molecule, wherein cleavage or modification of said target DNA sequence occurs.

87. The method of claim 86, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

88. The method of claim 86, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

89. The method of claim 86, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

90. A method for binding a target DNA sequence of a DNA molecule comprising:

a) assembling an RNA-guided nuclease (RGN) ribonucleotide complex by combining:

i) one or more guide RNAs capable of hybridizing to the target DNA sequence;

and

ii) an RGN polypeptide comprising an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs:1-12;

under conditions suitable for formation of the RGN ribonucleotide complex; and
b) contacting said target DNA sequence or a cell comprising said target DNA sequence with the assembled RGN ribonucleotide complex;

wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence.

91. The method of claim 90, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

92. The method of claim 90 or 91, wherein said method is performed *in vitro*, *in vivo*, or *ex vivo*.

93. The method of any one of claims 90-92, wherein said RGN polypeptide or said guide RNA further comprises a detectable label, thereby allowing for detection of said target DNA sequence.

94. The method of any one of claims 90-92, wherein said guide RNA or said RGN polypeptide further comprises an expression modulator, thereby allowing for the modulation of expression of said target DNA sequence.

95. The method of any one of claims 90-92, wherein said RGN polypeptide further comprises a prime editing polypeptide, thereby allowing for the modification of said target DNA sequence.

96. The method of claim 95, wherein said prime editing polypeptide comprises a DNA polymerase.

97. The method of claim 95, wherein said prime editing polypeptide comprises a reverse transcriptase.

98. The method of any one of claims 90-92, wherein said RGN polypeptide further comprises a base-editing polypeptide, thereby allowing for the modification of said target DNA sequence.

99. The method of claim 98, wherein said base-editing polypeptide comprises a deaminase.

100. The method of claim 99, wherein said deaminase is a cytosine deaminase or an adenine deaminase.

5 101. The method of any one of claims 90-92, wherein said RGN polypeptide is capable of cleaving said target DNA sequence, thereby allowing for the cleaving and/or modifying of said target DNA sequence.

10 102. A method for cleaving and/or modifying a target DNA sequence of a DNA molecule, comprising contacting the DNA molecule with:

a) an RNA-guided nuclease (RGN) polypeptide, wherein said RGN comprises an amino acid sequence having at least 90% sequence identity to any one of SEQ ID NOs: 1-12; and

b) one or more guide RNAs capable of targeting the RGN of (a) to the target DNA sequence;

15 wherein the one or more guide RNAs hybridize to the target DNA sequence, thereby directing said RGN polypeptide to bind to said target DNA sequence and cleavage and/or modification of said target DNA sequence occurs.

20 103. The method of claim 102, wherein said RGN polypeptide comprises an amino acid sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 1-12.

25 104. The method of claim 102 or 103, wherein cleavage by said RGN polypeptide generates a double-stranded break.

105. The method of claim 102 or 103, wherein cleavage by said RGN polypeptide generates a single-stranded break.

30 106. The method of claim 102 or 103, wherein said RGN polypeptide is a nickase and is operably linked to a prime editing polypeptide.

107. The method of claim 106, wherein said prime editing polypeptide comprises a DNA polymerase.

35 108. The method of claim 106, wherein said prime editing polypeptide comprises a reverse transcriptase.

109. The method of claim 102 or 103, wherein said RGN polypeptide is nuclease inactive or a nickase and is operably linked to a base-editing polypeptide.

110. The method of claim 109, wherein the base-editing polypeptide is a deaminase.

111. The method of claim 110, wherein the deaminase is a cytosine deaminase or an adenine deaminase.

112. The method of claim 110, wherein the deaminase has at least 90% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

113. The method of claim 110, wherein the deaminase has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to an amino acid sequence of any one of SEQ ID NOs: 377-448.

114. The method of claim 102 or 103, wherein said modified target DNA sequence comprises insertion of heterologous DNA into the target DNA sequence.

115. The method of claim 102 or 103, wherein said modified target DNA sequence comprises deletion of at least one nucleotide from the target DNA sequence.

116. The method of claim 102 or 103, wherein said modified target DNA sequence comprises mutation of at least one nucleotide in the target DNA sequence.

117. The method of any one of claims 83-116, wherein said target DNA sequence is located adjacent to a protospacer adjacent motif (PAM).

118. The method of any one of claims 83-117, wherein said target DNA sequence is a eukaryotic target DNA sequence.

119. The method of any one of claims 83-118, wherein said gRNA is a single guide RNA (sgRNA).

120. The method of claim 119, wherein said sgRNA further comprises an extension comprising an edit template for prime editing.

121. The method of any one of claims 83-118, wherein said gRNA is a dual-guide RNA.

122. The method of any one of claims 83-121, wherein:

a) said RGN has at least 90% sequence identity to SEQ ID NO: 1, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25;

b) said RGN has at least 90% sequence identity to SEQ ID NO: 2, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26;

c) said RGN has at least 90% sequence identity to SEQ ID NO: 3, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27;

d) said RGN has at least 90% sequence identity to SEQ ID NO: 4, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28;

e) said RGN has at least 90% sequence identity to SEQ ID NO: 5, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29;

f) said RGN has at least 90% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30;

g) said RGN has at least 90% sequence identity to SEQ ID NO: 7, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31;

h) said RGN has at least 90% sequence identity to SEQ ID NO: 8, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32;

i) said RGN has at least 90% sequence identity to SEQ ID NO: 9, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33;

j) said RGN has at least 90% sequence identity to SEQ ID NO: 10, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34;

k) said RGN has at least 90% sequence identity to SEQ ID NO: 11, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35; or

l) said RGN has at least 90% sequence identity to SEQ ID NO: 12, said guide RNA comprises a crRNA repeat sequence having at least 90% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36.

123. The method of any one of claims 83-121, wherein:

a) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25;

b) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26;

c) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27;

d) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 4, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28;

e) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 5, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29;

f) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 6, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30;

g) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 7, said guide RNA comprises a crRNA repeat sequence

having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 19 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 31;

h) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 8, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 20 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32;

i) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 9, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33;

j) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 10, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34;

k) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 11, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35; or

l) said RGN has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12, said guide RNA comprises a crRNA repeat sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24 and a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36.

124. The method of any one of claims 83-123, wherein the target DNA sequence is within a cell.

125. The method of claim 124, further comprising culturing the cell under conditions in which the RGN polypeptide is expressed and cleaves and modifies the target DNA sequence to produce a DNA molecule comprising a modified target DNA sequence; and selecting a cell comprising said modified target DNA sequence.

126. A cell comprising a modified target DNA sequence according to the method of claim 125.

127. A pharmaceutical composition comprising the cell of any one of claims 26, 81, and 126, and a pharmaceutically acceptable carrier.

128. A method of treating a disease, disorder, or condition, said method comprising administering to a subject in need thereof an effective amount of a pharmaceutical composition of claim 82 or 127.

10

129. The method of claim 128, wherein said disease is associated with a causal mutation and said effective amount of said pharmaceutical composition corrects said causal mutation.

130. The method of claim 128 or 129, wherein said subject is at risk of developing said disease, disorder, or condition.

15

131. A nucleic acid molecule comprising a CRISPR RNA (crRNA) or a polynucleotide encoding a crRNA, wherein said crRNA comprises a spacer sequence and a CRISPR repeat sequence, wherein said CRISPR repeat sequence comprises a nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 13-24;

20

wherein a guide RNA comprising:

a) said crRNA; and

b) a trans-activating CRISPR RNA (tracrRNA) hybridized to said CRISPR repeat sequence of said crRNA;

25

is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of said crRNA when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide.

132. The nucleic acid molecule of claim 131, wherein said polynucleotide encoding a crRNA is operably linked to a promoter heterologous to said polynucleotide.

30

133. The nucleic acid molecule of claim 131 or 132, wherein said CRISPR repeat sequence comprises a nucleotide sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs: 13-24.

35

134. A vector comprising the nucleic acid molecule comprising said polynucleotide encoding said crRNA of any one of claims 131-133.

135. The vector of claim 134, wherein said vector further comprises a polynucleotide encoding said tracrRNA.

136. The vector of claim 135, wherein said tracrRNA is selected from the group consisting of:

a) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 25, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13;

b) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 26, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 14;

c) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 27, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15;

d) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 28, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16;

e) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 29, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17;

f) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 30, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18;

g) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 31, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19;

h) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 32, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20;

i) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 33, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21;

j) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 34, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22;

k) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 35, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23; and

l) a tracrRNA having at least 90% sequence identity to SEQ ID NO: 36, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24.

137. The vector of claim 135, wherein said tracrRNA is selected from the group consisting of:

a) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13;

b) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14;

5 c) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15;

10 d) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 28, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 16;

15 e) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 29, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 17;

20 f) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 30, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 18;

g) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 31, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 19;

25 h) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 32, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 20;

30 i) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 33, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 21;

35 j) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 34, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 22;

k) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 35, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 23; and

l) a tracrRNA having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24.

138. The vector of any one of claims 134-137, wherein said vector further comprises a polynucleotide encoding said RGN polypeptide.

139. The vector of claim 138, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 1, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 2, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 3, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 4, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 16 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 28;

e) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 5, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 17 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 29;

f) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 6, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 18 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 30;

g) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 7, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 19 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 31;

h) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 8, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 20 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 32;

i) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 9, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 21 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 33;

j) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 10, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 22 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 34;

k) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 11, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 23 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 35; and

l) a RGN polypeptide having at least 90% sequence identity to SEQ ID NO: 12, wherein said CRISPR repeat sequence has at least 90% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 90% sequence identity to SEQ ID NO: 36.

140. The vector of claim 138, wherein said RGN polypeptide is selected from the group consisting of:

a) a RGN polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 1, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 13 and said tracrRNA has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 25;

b) a RGN polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14 and said tracrRNA has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 26;

c) a RGN polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 3, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 15 and said tracrRNA has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27;

d) a RGN polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 4, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ

1) a RGN polypeptide having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 12, wherein said CRISPR repeat sequence has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 24 and said tracrRNA has at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 36.

141. A nucleic acid molecule comprising a trans-activating CRISPR RNA (tracrRNA) or a polynucleotide encoding a tracrRNA comprising a nucleotide sequence having at least 90% sequence identity to any one of SEQ ID NOs: 25-36;

wherein a guide RNA comprising:

a) said tracrRNA; and

b) a crRNA comprising a spacer sequence and a CRISPR repeat sequence, wherein said tracrRNA hybridizes with said CRISPR repeat sequence of said crRNA;

is capable of hybridizing to a target DNA sequence in a sequence specific manner through the spacer sequence of said crRNA when said guide RNA is bound to an RNA-guided nuclease (RGN) polypeptide.

142. The nucleic acid molecule of claim 141, wherein said polynucleotide encoding a tracrRNA is operably linked to a promoter heterologous to said polynucleotide.

143. The nucleic acid molecule of claim 141 or 142, wherein said tracrRNA comprises a nucleotide sequence having at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any one of SEQ ID NOs:25-36.

144. A vector comprising the nucleic acid molecule comprising said polynucleotide encoding said tracrRNA of any one of claims 141-143.

145. A single guide RNA comprising the nucleic acid molecule comprising said crRNA of any one of claims 131-133 and the nucleic acid molecule comprising said tracrRNA of any one of claims 141-143.

146. A dual guide RNA comprising the nucleic acid molecule comprising said crRNA of any one of claims 131-133 and the nucleic acid molecule comprising said tracrRNA of any one of claims 141-143.

147. A cell comprising the nucleic acid molecule of any one of claims 131-133 and 141-143, the vector of any one of claims 134-140 and 144, the single guide RNA of claim 145, or the dual guide RNA of claim 146.

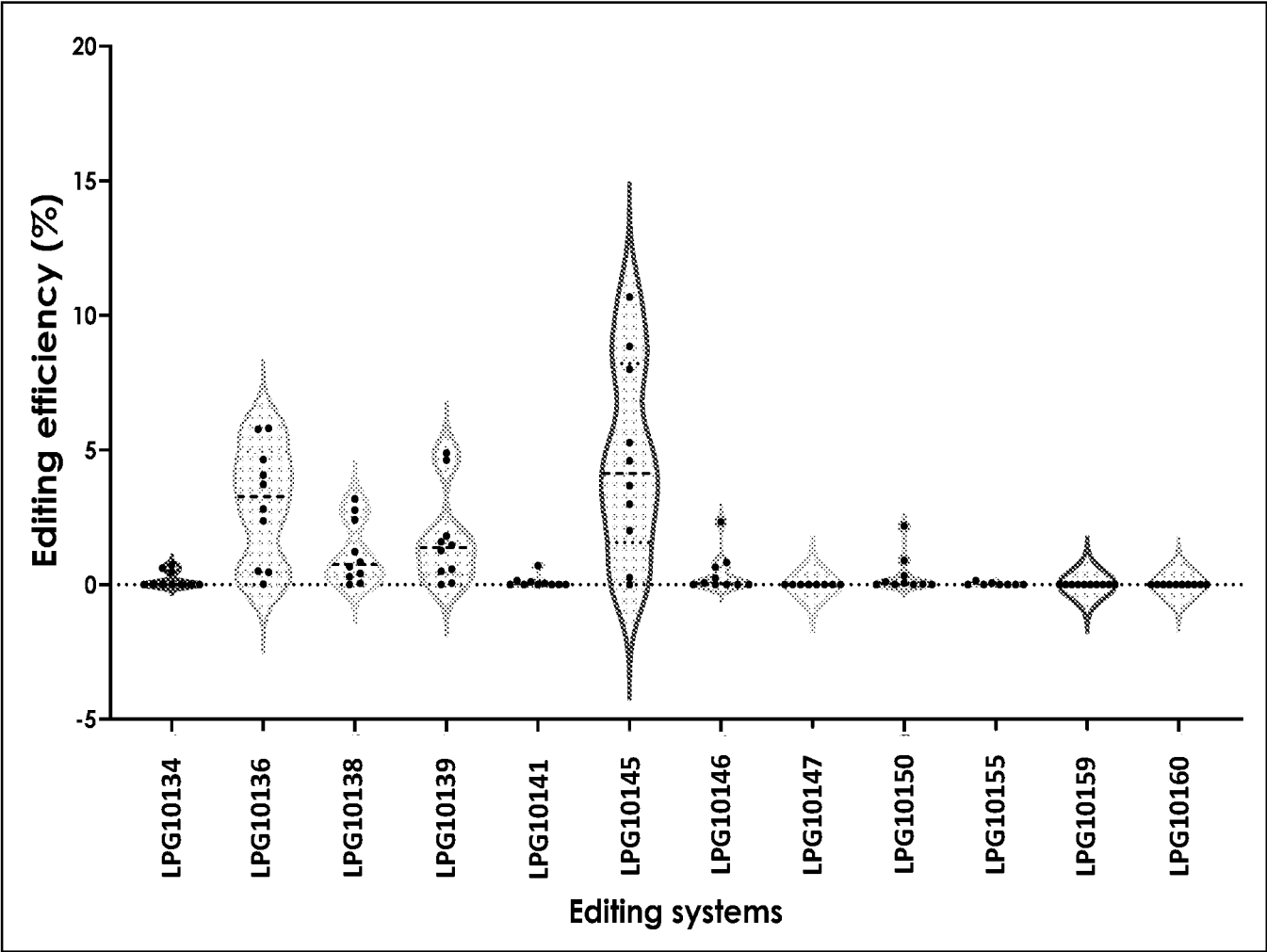


FIGURE 1

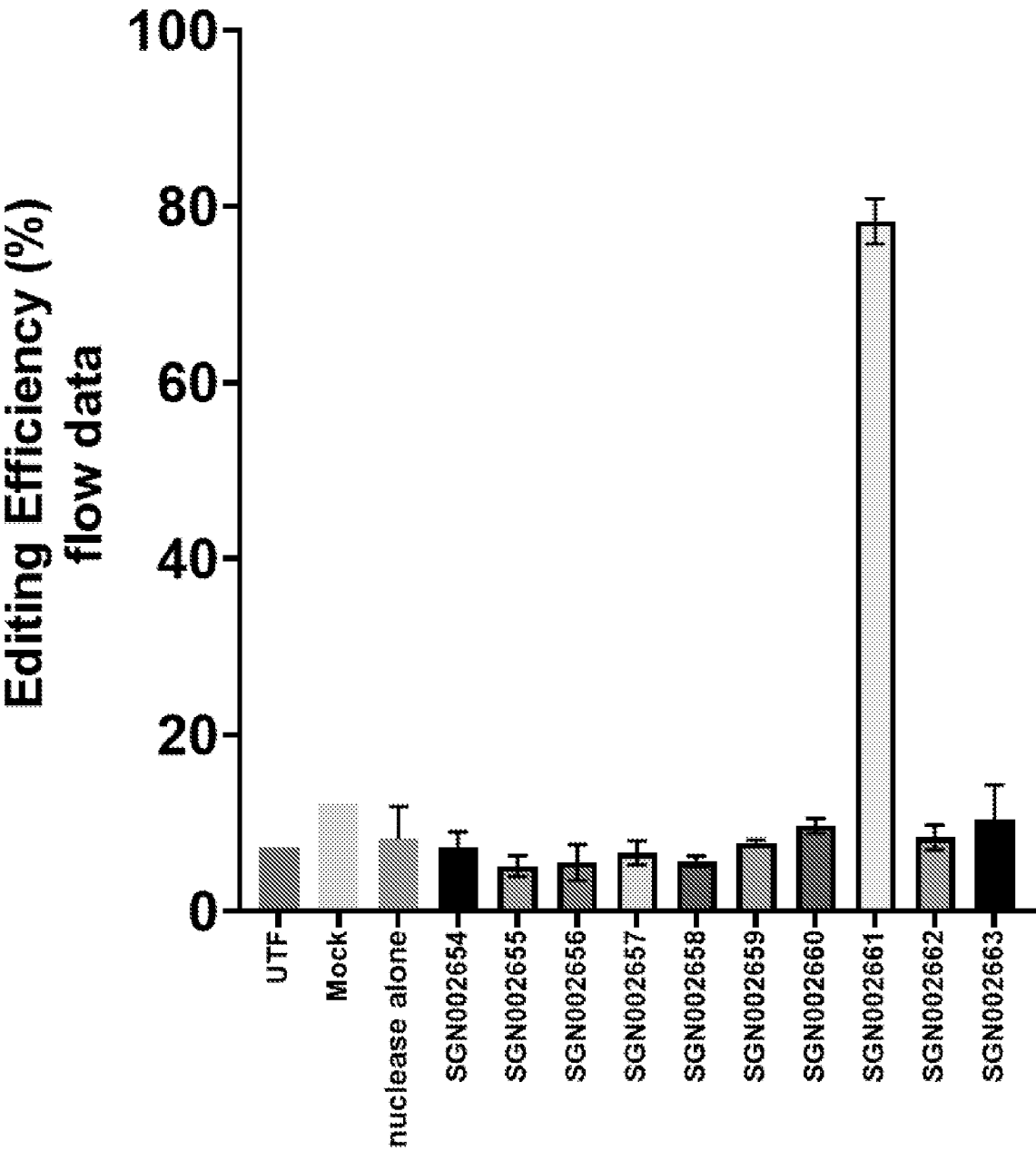


FIGURE 2

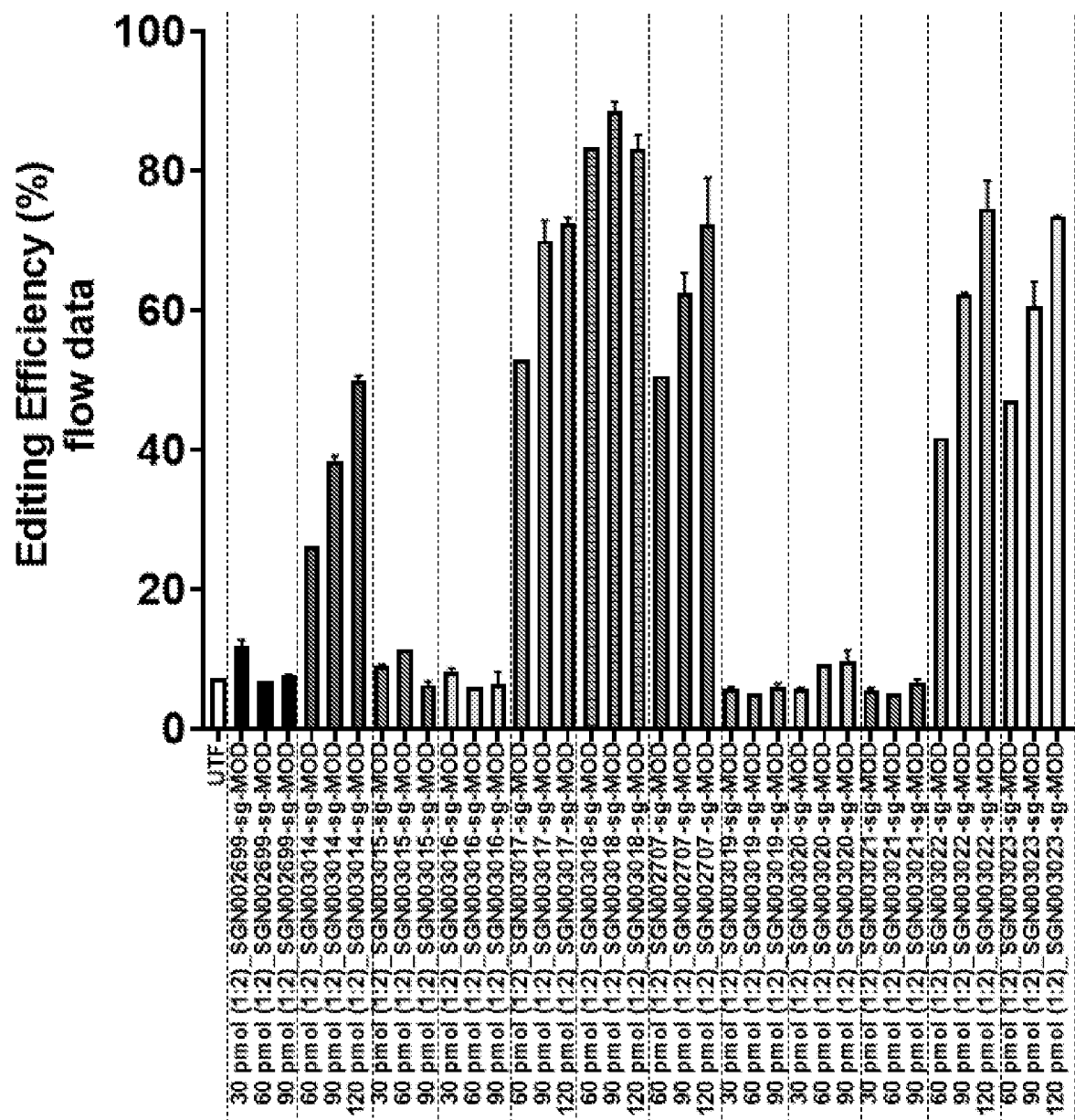


FIGURE 3A

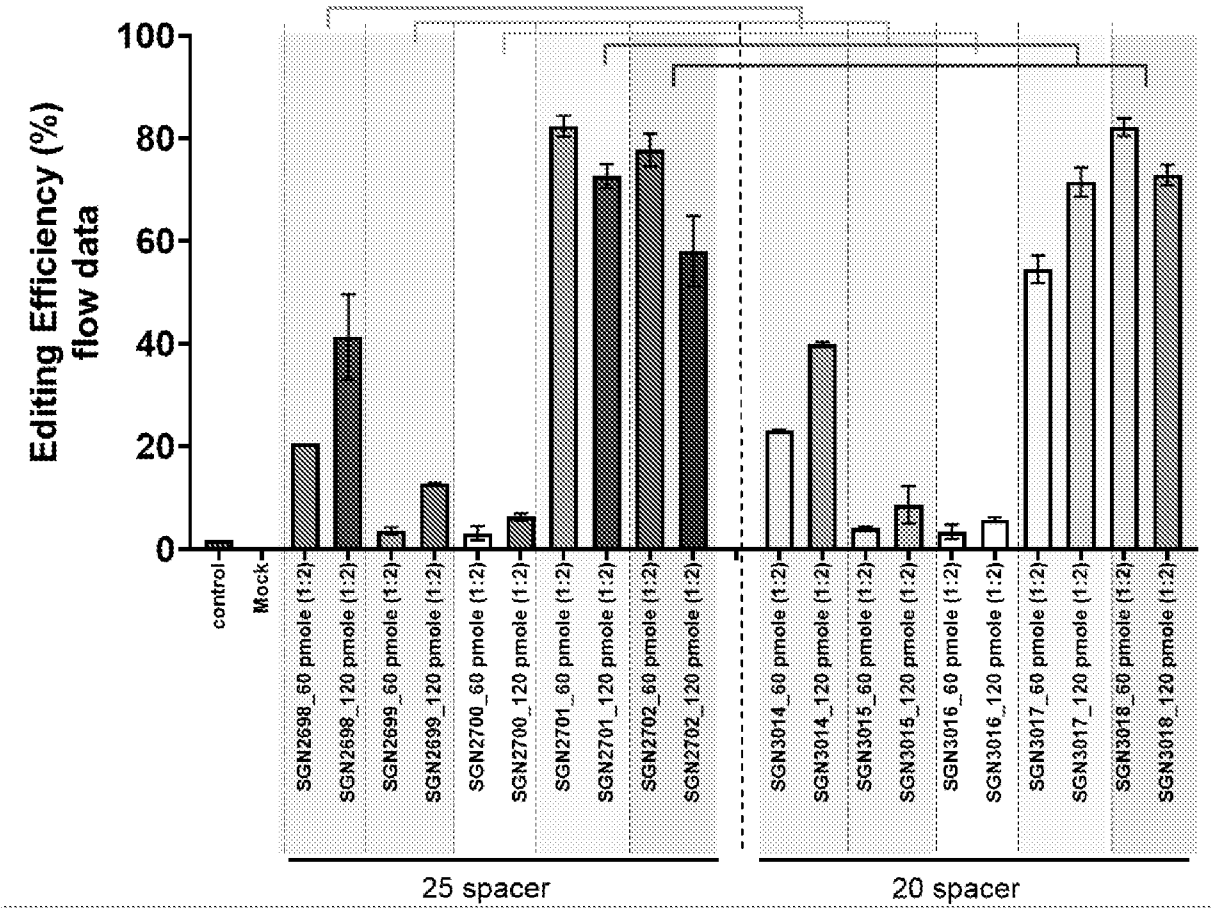


FIGURE 3B

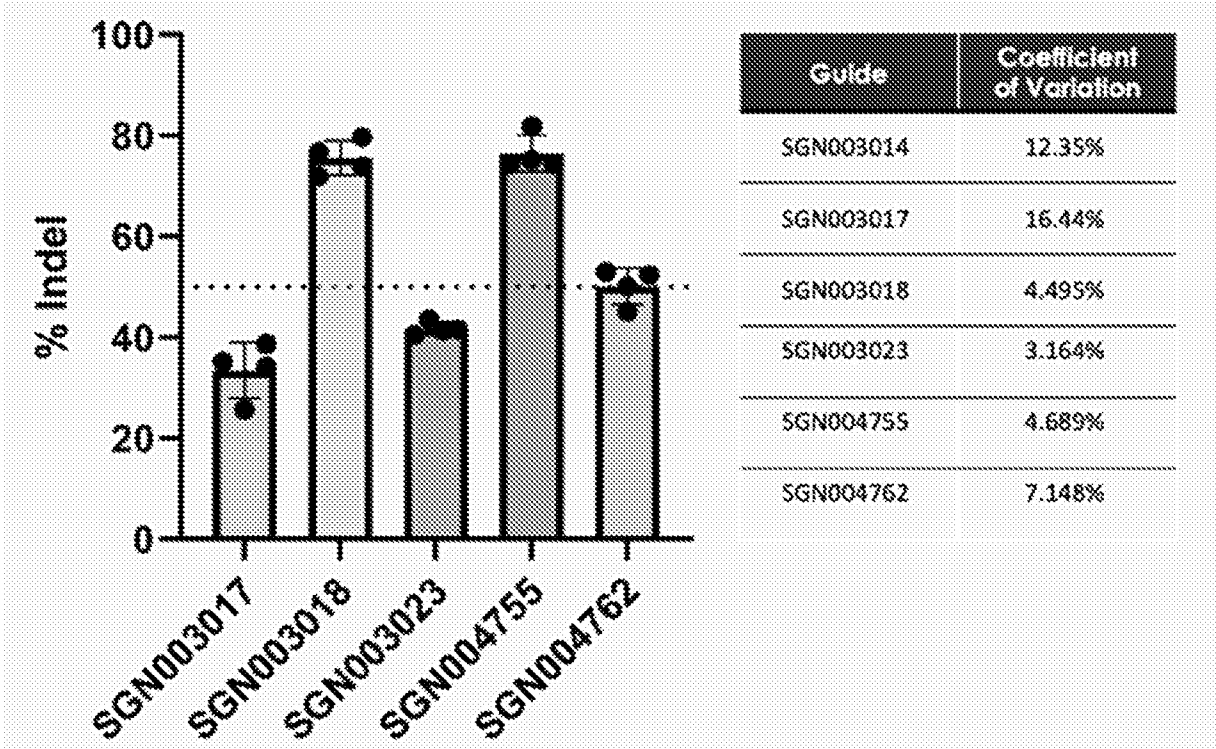


FIGURE 4

INTERNATIONAL SEARCH REPORT

International application No
PCT/IB2023/050560

A. CLASSIFICATION OF SUBJECT MATTER INV. C12N15/10 C12N9/22 A61P3/00 A61P7/00 A61P21/00 A61P25/28 ADD. According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) C12N A61P Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) EPO-Internal		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	LIU LINA ET AL: "Genome-Based Taxonomy of Brevundimonas with Reporting Brevundimonas huaxiensis sp. nov.", MICROBIOLOGY SPECTRUM, vol. 9, no. 1, 3 September 2021 (2021-09-03), XP093034790, DOI: 10.1128/Spectrum.00111-21 --/--	1, 2, 4-7, 18, 26, 27, 31, 33, 34, 36-39, 48, 50, 51, 54, 55, 58, 61-69, 80, 81, 83, 85, 86, 88-92, 94, 101-105, 115-118, 121-124, 126, 131, 133, 141,
☒ Further documents are listed in the continuation of Box C. ☒ See patent family annex.		
* Special categories of cited documents : "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family		
Date of the actual completion of the international search 15 June 2023		Date of mailing of the international search report 29/06/2023
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016		Authorized officer Salminen, Aaro

INTERNATIONAL SEARCH REPORT

International application No.

PCT/IB2023/050560

Box No. I Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:
 - a. ☒ forming part of the international application as filed.
 - b. ☐ furnished subsequent to the international filing date for the purposes of international search (Rule 13*ter*.1(a)).

☐ accompanied by a statement to the effect that the sequence listing does not go beyond the disclosure in the international application as filed.
2. ☐ With regard to any nucleotide and/or amino acid sequence disclosed in the international application, this report has been established to the extent that a meaningful search could be carried out without a WIPO Standard ST.26 compliant sequence listing.
3. Additional comments:

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB2023/050560

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

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

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

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

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

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
1-147 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims;; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☒ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No

PCT/IB2023/050560

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	figure 1 -----	143, 146, 147
X	US 2010/192451 A1 (PONNUSAMY LOGANATHAN [US] ET AL) 5 August 2010 (2010-08-05)	1, 2, 4-7, 18, 26, 27, 31, 33, 34, 36-39, 48, 50, 51, 54, 55, 58, 61-69, 80-83, 85, 86, 88-92, 94, 101-105, 115-118, 121-124, 126, 127, 131, 133, 141, 143, 146, 147
	examples 5, 10-12; table 1 -----	
X	DATABASE UniProtKB [Online] 8 May 2019 (2019-05-08), N/a: "CRISPR-associated endonuclease Cas9 (Enterococcus asini)", XP093053981, Database accession no. A0A413AJC9 the whole document	1-125, 127-147
A	SCHMIDT MORITZ J. ET AL: "Improved CRISPR genome editing using small highly active and specific engineered RNA-guided nucleases", NATURE COMMUNICATIONS, vol. 12, no. 1, 9 July 2021 (2021-07-09), pages 1-12, XP93034439, DOI: 10.1038/s41467-021-24454-5 the whole document	1-147
A	WO 2021/248016 A2 (EMENDOBIO INC [US]; IZHAR LIOR [IL] ET AL.) 9 December 2021 (2021-12-09) the whole document	1-147
A	US 2021/403925 A1 (CHEVESSIER-TÜNNESSEN FRÉDÉRIC [DE] ET AL) 30 December 2021 (2021-12-30) the whole document ----- -/--	1-147

INTERNATIONAL SEARCH REPORT

International application No

PCT/IB2023/050560

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CAROLIN ANDERS ET AL: "Structural basis of PAM-dependent target DNA recognition by the Cas9 endonuclease", EUROPE PMC FUNDERS GROUP AUTHOR MANUSCRIPT, vol. 513, no. 7519, 27 July 2014 (2014-07-27), pages 1-22, XP055538018, DOI: 10.1038/nature13579 the whole document -----	1-147
A	DANIEL H. HAFT ET AL: "A Guild of 45 CRISPR-Associated (Cas) Protein Families and Multiple CRISPR/Cas Subtypes Exist in Prokaryotic Genomes", PLOS COMPUTATIONAL BIOLOGY, vol. 1, no. 6, 1 January 2005 (2005-01-01), page e60, XP055445295, US ISSN: 1553-734X, DOI: 10.1371/journal.pcbi.0010060 the whole document	1-147
A,P	& DATABASE RefSeq [Online] 1 May 2022 (2022-05-01), Haft D H: "type II CRISPR RNA-guided endonuclease Cas9 [Enterococcus asini]", XP93054269, Database accession no. WP_231453593.1 the whole document -----	1-147

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10134 (SEQ ID NO: 1) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 13 and 25)

2. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10136 (SEQ ID NO: 2) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 14 and 26)

3. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10138 (SEQ ID NO: 3) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 15 and 27)

4. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10139 (SEQ ID NO: 4) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 16 and 28)

5. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10141 (SEQ ID NO: 5) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 17 and 29)

6. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10145 (SEQ ID NO: 6) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 18 and 30)

7. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10146 (SEQ ID NO: 7) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 19 and 31)

8. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10147 (SEQ ID NO: 8) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 20 and 32)

9. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10150 (SEQ ID NO: 9) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 21 and 33)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10155 (SEQ ID NO: 10) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 22 and 34)

11. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10159 (SEQ ID NO: 11) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 23 and 35)

12. claims: 1-147 (partially)

RNA-guided nuclease labeled LPG10160 (SEQ ID NO: 12) and
related crRNA and tracrRNA sequences (SEQ ID NOs: 24 and 36)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/IB2023/050560

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 2010192451 A1	05-08-2010	NONE	
WO 2021248016 A2	09-12-2021	AU 2021285983 A1	02-02-2023
		CA 3179130 A1	09-12-2021
		CN 116157514 A	23-05-2023
		EP 4162039 A2	12-04-2023
		IL 298706 A	01-02-2023
		KR 20230056630 A	27-04-2023
		US 2023122086 A1	20-04-2023
		WO 2021248016 A2	09-12-2021
US 2021403925 A1	30-12-2021	AU 2018240515 A1	01-08-2019
		BR 112019015244 A2	14-04-2020
		CA 3050616 A1	27-09-2018
		CN 110914433 A	24-03-2020
		EP 3601576 A1	05-02-2020
		JP 2020513824 A	21-05-2020
		KR 20190133699 A	03-12-2019
		RU 2019132890 A	26-04-2021
		SG 10202110491P A	29-11-2021
		SG 11201906297Q A	30-10-2019
		US 2021403925 A1	30-12-2021
		WO 2018172556 A1	27-09-2018