COMPOSITIONS AND METHODS FOR EFFICIENT GENOME EDITING

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 63/218,744, filed July 06, 2021 and U.S. Provisional Application No. 63/219,623, filed July 08, 2021, each of which applications are incorporated herein by reference in their entirety.

BACKGROUND

[0002] Prime editing technology is a gene editing technology that can make targeted insertions, deletions, and all transversion and transition point mutations in a target genome. This disclosure provides improved prime editing methods and compositions that allow for efficient and precise editing of target genes.

SUMMARY OF THE INVENTION

[0003] Provided herein, in some embodiments, are methods and compositions for efficient prime editing of alterations in a target sequence in a target DNA, *e.g.*, a target gene.

[0004] Without wishing to be bound by any particular theory, the prime editing process may search and replace endogenous sequences in a target polynucleotide. As exemplified in **FIG. 3**, the spacer sequence of a prime editing guide RNA (PEgRNA) recognizes and anneals with a search target sequence in a target strand of a double stranded target polynucleotide, *e.g.*, a double stranded target DNA. A prime editing complex may generate a nick in the target DNA on the edit strand which is the complementary strand of the target strand. The prime editing complex may then use a free 3' end formed at the nick site of the edit strand to initiate DNA synthesis, where a primer binding site sequence (PBS) of the PEgRNA complexes with the free 3' end, and a single stranded DNA is synthesized using an editing template of the PEgRNA as a template. The editing template may comprise one or more intended nucleotide edits compared to the endogenous double stranded target DNA sequence. Accordingly, the newly synthesized single stranded DNA also comprises the nucleotide edit(s) encoded by the editing template. Through removal of the editing target sequence on the edit strand of the double stranded target DNA and DNA repair mechanism, the newly synthesized single stranded DNA replaces the editing target sequence, and the desired nucleotide edit(s) are incorporated into the double stranded target DNA.

[0005] Provided herein, in some embodiments, are modified prime editor (PE) polypeptides, modified PEgRNAs that can associate with each other and efficiently incorporate intended nucleotide edits in the double stranded target DNA, and methods of using the same for editing target DNA in specific cell types, *e.g.*, hematopoietic stem cells.

[0006] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos. 289, 291, 293, 294, 295, 301, 302, 303, 306, 309, 310, and 311.

[0007] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos. 286-411.

[0008] In some embodiments, the amino acid sequence of the peptide linker has at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to the selected sequence. In some embodiments, the selected sequence is SEQ ID NO: 302. In some embodiments, the selected sequence is SEQ ID NO: 309.

[0009] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises at least 4 contiguous SGGS motifs.

[0010] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises 4 to 10 contiguous SGGS motifs.

[0011] In some embodiments, the peptide linker comprises 4, 5, 6, 8, or 10 contiguous SGGS motifs.

[0012] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises at least 2 contiguous EAAAK motifs.

[0013] In one aspect, provided herein is a prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises 2 to 8 contiguous EAAAK motifs.

[0014] In some embodiments, the peptide linker comprises 2, 3, 4, 6, or 8 contiguous EAAAK motifs. In some embodiments, the DNA polymerase domain comprises a reverse transcriptase (RT) domain. In some embodiments, the RT domain is a Moloney murine leukemia virus (M-MLV) RT domain. In some embodiments, the M-MLV RT domain comprises an amino acid having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 5. In some embodiments, the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1. In some embodiments, the M-MLV RT domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 36.

[0015] In some embodiments, the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ

ID NO: 1. In some embodiments, the M-MLV RT domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 54.

[0016] In one aspect, the present disclosure provides a prime editing composition comprising: a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1.

[0017] In one aspect, provided herein is a prime editing composition comprising a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain is truncated at C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1.

[0018] In some embodiments, the M-MLV RT domain comprises an amino acid substitution D200N, T306K, W313F, T330P, or any combination thereof as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1. In some embodiments, the DNA binding domain is connected to the M-MLV RT domain in a fusion protein. In some embodiments, the DNA binding domain and the M-MLV RT domain are connected by a peptide linker. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos 286-411.

[0019] In some embodiments, the DNA binding domain comprises a CRISPR associated (Cas) protein. In some embodiments, the Cas protein is a Type II Cas protein. In some embodiments, the Cas protein is Cas9. In some embodiments, the Cas9 protein is a nickase that comprises a mutation in a HNH domain. In some embodiments, the Cas9 protein comprises a H840A mutation compared to SEQ ID NO: 2. In some embodiments, the DNA binding domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 7.

[0020] In some embodiments, the Cas protein is a Type V Cas protein. In some embodiments, the Cas protein is a Cas12a, Cas12b, Cas12c, Cas12d, or Cas12e. In some embodiments, the fusion protein comprises the DNA polymerase domain and the DNA binding domain from N-terminus to C-terminus. In some embodiments, the fusion protein comprises the DNA polymerase domain and the DNA binding domain from C-terminus to N-terminus. In some embodiments, the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 78, 105, 117, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, and 227. In some embodiments, the selected sequence is SEQ ID NO 78.

[0021] In some embodiments, the selected sequence is SEQ ID NO 105. In some embodiments, the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 86, 111, 122, 128, 134, 140, 146, 152, 158, 164, 170, 176, 182, 188, 194, 200, 206, 212, 218, 224, and 230. In some embodiments, the selected sequence is SEQ ID NO: 86. In some embodiments, the selected sequence is SEQ ID NO: 111. In some embodiments, the fusion protein comprises an amino acid sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the selected sequence. In some embodiments, the fusion protein comprises one or more nuclear localization signals (NLSs). In some embodiments, the one or more NLSs comprises an amino acid sequence selected from the group consisting of SEQ ID Nos 8-15 or 621.

[0022] In some embodiments, the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 77, 93, 104, 116, and 620. In some embodiments, the selected sequence is SEQ ID NO: 77 or SEQ ID NO: 620. In some embodiments, the selected sequence is SEQ ID NO: 93. In some embodiments, the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 85, 96, 110, and 622. In some embodiments, the selected sequence is SEQ ID NO: 85 or SEQ ID NO: 622.

[0023] In some embodiments, the selected sequence is SEQ ID NO: 110. In some embodiments, the fusion protein comprises an amino acid sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the selected sequence. In some embodiments, the prime editing composition of any one of aspects above, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, and 229.

[0024] In some embodiments, the selected sequence is SEQ ID NO 81 or 82. In some embodiments, the prime editing composition of any one of aspects above, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232. In some embodiments, the selected sequence is SEQ ID NO 89 or 90.

[0025] In some embodiments, the prime editing composition of any one of aspects above, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 94, 95, 106, 107, 118, and 119. In some embodiments, the prime editing composition of any one of aspects above, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 87, 88, 97, 98, 100, 101, 112, and 113. In some embodiments, the selected sequence is SEQ ID NO 79 or 80. In some embodiments, the selected sequence is SEQ ID NO 87 or 88. In some embodiments, the polynucleotide encoding the fusion protein further comprises a stop codon at the 3' end.

[0026] In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 276-279. In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 282-285. In some embodiments, the prime editing composition further comprising a 5' untranslated region (UTR) and/or a 3' UTR. In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 274, 275, 592, or 593. In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 280, 281, 594, or 595. In some embodiments, the polynucleotide comprises DNA. In some embodiments, the polynucleotide comprises mRNA. In some embodiments, the prime editing composition further comprises a regulatory element sequence, optionally wherein the regulatory element sequence is a promoter.

[0027] In one aspect, provided herein is a prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to a sequence corresponding to nucleotides 100-2130 of a sequence selected from the group consisting of SEQ ID Nos 412-555.

[0028] In one aspect, provided herein is a prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 83 or 84.

[0029] In some embodiments, the second polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO 83 or 84.

[0030] In one aspect, provided herein is a prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises the sequence of SEQ ID No 83 or 84.

[0031] In one aspect, provided herein is a prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 91 or 92.

[0032] In some embodiments, the second polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO 91 or 92.

[0033] In one aspect, provided herein is a prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises the sequence of SEQ ID No 91 or 92.

[0034] In some embodiments, the first polynucleotide encodes a CRISPR associated (Cas) protein. In some embodiments, the Cas protein is a Type II Cas protein. In some embodiments, the Cas protein is Cas9. In some embodiments, the Cas9 protein is a nickase that comprises a mutation in a HNH domain, optionally wherein the Cas9 protein comprises a H840A mutation compared to SEQ ID NO: 2. In some embodiments, the Cas protein is a Type V Cas protein. In some embodiments, the Cas protein is a Cas12a, Cas12b, Cas12c, Cas12d, or Cas12e. In some embodiments, the first polynucleotide and the second polynucleotide are connected in a fusion polynucleotide. In some embodiments, the first polynucleotide and the second polynucleotide are connected by a sequence that encodes a peptide linker. In some embodiments, the polynucleotide encoding the peptide linker comprises the sequence of SEQ ID No 235, 236 or 633-636.

[0035] In some embodiments, the first polynucleotide is connected to the 5' end of the second polynucleotide. In some embodiments, the first polynucleotide is connected to the 3' end of the second polynucleotide. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, 229, 241, and 242. In some embodiments, the selected sequence is SEQ ID NO 81 or 82. In some embodiments, the selected sequence is SEQ ID NO 241 or 242.

[0036] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, , 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232. In some embodiments, the selected sequence is SEQ ID NO 89 or 90. In some embodiments, the selected sequence is SEQ ID NO 102 or 103. In some embodiments, the selected sequence is SEQ ID NO 114 or 115. In some embodiments, the first polynucleotide, the second polynucleotide, or both further comprises a sequence encoding a nuclear localization signal (NLS).

[0037] In some embodiments, the NLS comprises the sequence of SEQ ID No 239 or 240 and is connected to the 3' end of the second polynucleotide. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 94, 95, 106,107, 118, 119, 233, and 234. In some embodiments, the selected sequence is SEQ ID NO: 79 or 80.

[0038] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 87, 88, 97,98, 100, 101, 112, and 113. In some embodiments, the selected sequence is SEQ ID NO: 87 or 88. In some embodiments, the fusion polynucleotide further comprises a stop codon at the 3' end.

[0039] In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO 276-279. In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO 282-285. In some embodiments, the fusion polynucleotide comprises a 5' untranslated region (UTR) and/or a 3' UTR. In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 274, 275, 592, or 593. In some embodiments, the polynucleotide comprises the sequence of SEQ ID NO 280, 281, 594, or 595. In some embodiments, the first polynucleotide, the second polynucleotide, and/or the fusion polynucleotide comprises DNA. In some embodiments, the first polynucleotide, the second polynucleotide, and/or the fusion polynucleotide comprises mRNA. In some embodiments, the fusion polynucleotide further comprises a regulatory element sequence, optionally wherein the regulatory element sequence is a promoter.

[0040] In some embodiments, the sequence identities are determined by Needleman-Wunsch alignment of two sequences with Gap Costs set to Existence: 11 Extension: 1 where percent identity is calculated by dividing the number of identities by the length of the alignment. In some embodiments, the prime editing composition further comprises a prime editing guide RNA (PEgRNA) or a polynucleotide encoding the PEgRNA. In some embodiments, the prime editing composition further comprises a nick guide RNA (ngRNA) or a polynucleotide encoding the ngRNA.

[0041] In one aspect, provided herein is a vector comprising one or more of the polynucleotides of the prime editing composition of any one of aspects above.

[0042] In some embodiments, the vector is a AAV vector. In some embodiments, the vector is a lipid nanoparticle (LNP).

[0043] In one aspect, provided herein is a pharmaceutical composition comprising the prime editing composition of any one of aspects above or the vector of any one of aspects above, and a pharmaceutically acceptable excipient.

[0044] In one aspect, provided herein is a method of editing a target gene, the method comprising contacting the target gene with the prime editing composition of any one of aspects above.

[0045] In some embodiments, the target gene is in a cell. In some embodiments, the cell is a human cell. In some embodiments, the cell is a (CD34+) hematopoietic stem cell or a hematopoietic stem progenitor cell. In some embodiments, the contacting is ex vivo. In some embodiments, the cell is in a subject.

INCORPORATION BY REFERENCE

[0046] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0047] The novel features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings of which:

[0048] **FIG. 1** is a schematic representation of an exemplary prime editor fusion protein comprising a Cas9 nickase, a reverse transcriptase, and a linker.

[0049] **FIG. 2** depicts a prime editing guide RNA (PEgRNA) architectural overview in an exemplary schematic of PEgRNA designed for a prime editor.

[0050] **FIG. 3** depicts a schematic of a prime editing guide RNA (PEgRNA) binding to a double stranded target DNA sequence.

[0051] **FIG. 4** is a schematic showing the spacer and gRNA core part of an exemplary guide RNA, in two separate molecules. The rest of the PEgRNA structure is not shown.

[0052] **FIG. 5** depicts prime editing efficiency of prime editors having engineered RT domains. “pegRNA only” (top bar for each prime editor) refers to editing efficiency achieved with a pegRNA not paired with a ngRNA; “pegRNA+ngRNA” (bottom bar for each prime editor) refers to editing efficiency achieved with a pegRNA and a ngRNA.

DETAILED DESCRIPTION OF THE INVENTION

[0053] Provided herein, in some embodiments, are compositions and editing methods for advanced prime editing of target DNA polynucleotides in target cells. Compositions provided herein can comprise prime editors (PEs) that can use engineered guide polynucleotides, *e.g.*, CRISPR-Cas guide RNAs termed prime editing guide RNAs (PEgRNAs) that target PEs to specific DNA loci in the target DNA polynucleotides and can encode DNA edits that can serve a variety of functions, including direct correction of disease-causing mutations.

[0054] The following description and examples illustrate embodiments of the present disclosure in detail. It is to be understood that this disclosure is not limited to the particular embodiments described herein and as such can vary. Those of skill in the art will recognize that there are numerous variations and modifications of this disclosure, which are encompassed within its scope. Although various features of the present disclosure can be described in the context of a single embodiment, the features can also be provided separately or in any suitable combination. Conversely, although the present disclosure can be described herein in the context of separate embodiments for clarity, the present disclosure can also be implemented in a single embodiment.

Definitions

[0055] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art.

[0056] The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. As used herein, the singular forms “a”, “an” and “the” are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms “including”, “includes”, “having”, “has”, “with”, or variants thereof as used herein mean “comprising”.

[0057] Unless otherwise specified, the words “comprising”, “comprise”, “comprises”, “having”, “have”, “has”, “including”, “includes”, “include”, “containing”, “contains” and “contain” are inclusive or open-ended and do not exclude additional, unrecited elements or method steps.

[0058] Reference to “some embodiments”, “an embodiment”, “one embodiment”, or “other embodiments” means that a particular feature or characteristic described in connection with the embodiments is included in at least one or more embodiments, but not necessarily all embodiments, of the present disclosure.

[0059] The term “about” or “approximately” means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *i.e.*, the limitations of the measurement system. For example, “about” can mean within 1 standard deviation, per the practice in the art. Alternatively, “about” can mean a range of up to 20%, up to 10%, up to 5%, or up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, preferably within 5-fold, and more preferably within 2-fold, of a value. Where particular values are described in the application and claims, unless otherwise stated, the term “about” meaning within an acceptable error range for the particular value should be assumed.

[0060] As used herein, a “cell” can generally refer to a biological cell. A cell can be the basic structural, functional and/or biological unit of a living organism. A cell can originate from any organism having one or more cells. Some non-limiting examples include: a prokaryotic cell, eukaryotic cell, a bacterial cell, an archaeal cell, a cell of a single-cell eukaryotic organism, a protozoa cell, a cell from a plant, an animal cell, a cell from an invertebrate animal (*e.g.* fruit fly, cnidarian, echinoderm, nematode, etc.), a cell from a vertebrate animal (*e.g.*, fish, amphibian, reptile, bird, mammal), a cell from a mammal (*e.g.*, a pig, a cow, a goat, a sheep, a rodent, a rat, a mouse, a non-human primate, a human, etc.), et cetera. Sometimes a cell may not originate from a natural organism (*e.g.,* a cell can be synthetically made, sometimes termed an artificial cell).

[0061] In some embodiments, the cell is a mammalian cell. In some embodiments, the cell is a human cell. A cell can be of or derived from different tissues, organs, and/or cell types. In some embodiments, the cell is a primary cell. As used herein, the term “primary cell”, means a cell isolated from an organism, *e.g.*, a mammal, which is grown in tissue culture (*i.e.*, *in vitro*) for the first time before subdivision and transfer to a subculture. In some embodiments, the cell is a stem cell. In some non-limiting examples, mammalian cells including primary cells and stem cells, can be modified through introduction of one or more polynucleotides, polypeptides, and/or prime editing compositions (e.g., through transfections, transduction, electroporation, and the like) and further passaged. Such modified cells may include hematopoietic stem cells (HSCs), hematopoietic progenitor cells, (HSPCs), hepatocytes, fibroblasts, keratinocytes, epithelial cells (*e.g.*, mammary epithelial cells, intestinal epithelial cells), endothelial cells, glial cells, neural cells, formed elements of the blood (*e.g.*, lymphocytes, bone marrow cells, hematopoietic stem progenitor cells), muscle cells and precursors of these somatic cell types. In some embodiments, the cell is a primary hepatocyte. In some embodiments, the cell is a primary human hepatocyte. In some embodiments, the cell is a stem cell. In some embodiments, the cell is a progenitor cell. In some embodiments, the cell is a pluripotent cell (e.g., a pluripotent stem cell) In some embodiments, the cell (e.g., a stem cell) is an embryonic stem cell, tissue-specific stem cell, mesenchymal stem cell, or an induced pluripotent stem cell. In some embodiments, the cell is an induced pluripotent stem cell (iPSC). In some embodiments, the cell is an embryonic stem cell (ESC). In some embodiments, the cell is a primary human hepatocyte derived from an induced human pluripotent stem cell (iPSC). In some embodiments, the cell is a neuron. In some embodiments, the cell is a neuron from basal ganglia. In some embodiments, the cell is a neuron from basal ganglia of a human subject. In some embodiments, the cell is an epithelial cell from lung, liver, stomach, or intestine. In some embodiments, the cell is an epithelial cell from lung, liver, stomach, or intestine of a human subject. In some embodiments, the cell is a retinal cell. In some embodiments, the cell is a retinal cell from a human subject.

[0062] In some embodiments, the cell is a human stem cell. In some embodiments, the cell is a human pluripotent stem cell. In some embodiments, the cell is a human fibroblast. In some embodiments, the cell is an induced human pluripotent stem cell. In some embodiments, the cell is a human stem cell. In some embodiments, the cell is a human embryonic stem cell.

[0063] In some embodiments, the cell is a CD34+ cell. In some embodiments, the cell is a hematopoietic stem cell (HSC). In some embodiments, the cell is a hematopoietic progenitor cell (HPC). In some embodiments, hematopoietic stem cells and hematopoietic progenitor cells are referred to as hematopoietic stem or progenitor cells (HSPCs). In some embodiments, the cell is a human HSC. In some embodiments, the cell is a human HPC. In some embodiments, the cell is a human HSPC. In some embodiments, the cell is a long term (LT)-HSC. In some embodiments, the cell is a short-term (ST)-HSC. In some embodiments, the cell is a myeloid progenitor cell. In some embodiments, the cell is a lymphoid progenitor cell. In some embodiments, the cell is a granulocyte monocyte progenitor cell. In some embodiments, the cell is a megakaryocyte erythroid progenitor cell. In some embodiments, the cell is a multipotent progenitor cell (MPP).

[0064] In some embodiments, the cell is a stem cell. In some embodiments, the cell is a human stem cell. In some embodiments, the cell is a hematopoietic stem cell (HSC) or a hematopoietic stem and progenitor cell. In some embodiments, the HSC is from bone marrow or mobilized peripheral blood. In some embodiments the human stem cell is an induced pluripotent stem cell (iPSC). In some embodiments, the cell is a human HSC. In some embodiments, the cell is a human CD34+ cell. In some embodiments, the cell is a hematopoietic stem and progenitor cell (HSPC). In some embodiments, the cell is a human hematopoietic stem and progenitor cell (HSPC). In some embodiments, the cell is a hematopoietic progenitor cell, multipotent progenitor cell, lymphoid progenitor cell, a myeloid progenitor cell, a megakaryocyte-erythroid progenitor cell, a granulocyte-megakaryocyte progenitor cell, a granulocyte, a promyelocyte, a neutrophil, an eosinophil, a basophil, an erythrocyte, a reticulocyte, a thrombocyte, a megakaryoblast, a platelet-producing megakaryocyte, a monocyte, a macrophage, a dendritic cell, a microglia, an osteoclast, a lymphocyte, a NK cell, a B-cell, or a T-cell. In some embodiments, the cell edited by prime editing can be differentiated into, or give rise to recovery of a population of cells, e.g., common lymphoid progenitor cells, common myeloid progenitor cells, megakaryocyte-erythroid progenitor cells, granulocyte-megakaryocyte progenitor cells, granulocytes, promyelocytes, neutrophils, eosinophils, basophils, erythrocytes, reticulocytes, thrombocytes, megakaryoblasts, platelet-producing megakaryocytes, platelets, monocytes, macrophages, dendritic cells, microglia, osteoclasts, lymphocytes, such as NK cells, B-cells or T-cells. In some embodiments, the cell edited by prime editing can be differentiated into or give rise to recovery of a population of cells, e.g., neutrophils, platelets, red blood cells, monocytes, macrophages, antigen-presenting cells, microglia, osteoclasts, dendritic cells, inner ear cell, inner ear support cell, cochlear cell and/or lymphocytes. In some embodiments, the cell is in a subject, e.g., a human subject.

[0065] In some embodiments, a cell is not isolated from an organism but forms part of a tissue or organ of an organism, e.g., a mammal. In some non-limiting examples, mammalian cells include formed elements of the blood (e.g., lymphocytes, bone marrow cells), precursors of any of these somatic cell types, and stem cells.

[0066] In some embodiments, a cell is isolated from an organism. In some embodiments, a cell is derived from an organism. In some embodiments, a cell is a differentiated cell. In some embodiments, the cell is a fibroblast. In some embodiments, the cell is differentiated from an induced pluripotent stem cell. In some embodiments, the cell is differentiated from an HSC or an HPSC. In some embodiments, the cell is differentiated from an induced pluripotent stem cell (iPSC). In some embodiments, the cell is differentiated from an embryonic stem cell (ESC).

[0067] In some embodiments, the cell is a differentiated human cell. In some embodiments, cell is a human fibroblast. In some embodiments, the cell is differentiated from an induced human pluripotent stem cell. In some embodiments, the cell is differentiated from a human iPSC or a human ESC.

[0068] In some embodiments, the cell comprises a prime editor, a PEgRNA, or a prime editing composition disclosed herein. In some embodiments, the cell is from a human subject. In some embodiments, the human subject has a disease or condition, or is at a risk of developing a disease or a condition associated with a mutation to be corrected by prime editing. In some embodiments, the cell is from a human subject, and comprises a prime editor or a prime editing composition for correction of the mutation. In some embodiment, the cell comprises a mutation in a double stranded target DNA. In some embodiments, the cell comprises a mutation in a target gene. In some embodiments, the cell comprises a mutation that is associated with a a disease, disorder, or a condition. In some embodiments, the cell is in a human subject. In some embodiments, the cell comprises a prime editor or a prime editing composition for correction of the mutation. In some embodiments, the cell is in a human subject, and comprises a prime editor, a PEgRNA, or a prime editing composition disclosed herein for correction of the mutation. In some embodiments, the cell is from a human subject. In some embodiments, the cell is from a human subject and the mutation has been edited or corrected by prime editing.

[0069] The term “substantially” as used herein can refer to a value approaching 100% of a given value. In some embodiments, the term can refer to an amount that can be at least about 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.9%, or 99.99% of a total amount. In some embodiments, the term can refer to an amount that may be about 100% of a total amount.

[0070] The terms “protein” and “polypeptide” can be used interchangeably to refer to a polymer of two or more amino acids joined by covalent bonds (*e.g.*, an amide bond) that can adopt a three-dimensional conformation. In some embodiments, a protein or polypeptide comprises at least 10 amino acids, 15 amino acids, 20 amino acids, 30 amino acids or 50 amino acids joined by covalent bonds (*e.g.*, amide bonds). In some embodiments, a protein comprises at least two amide bonds. In some embodiments, a protein comprises multiple amide bonds. In some embodiments, a protein comprises at least 10 amide bonds, 15 amide bonds, 20 amide bonds, 30 amide bonds, or 50 amide bonds. In some embodiments, a protein comprises an enzyme, enzyme precursor protein, regulatory protein, structural protein, cytokine, chemokine, growth factor, receptor, nucleic acid binding protein, a biomarker, a member of a specific binding pair (*e.g.*, a ligand or aptamer), or an antibody. In some embodiments, a protein can be a full-length protein (*e.g.*, a fully processed protein having certain biological function). In some embodiments, a protein can be a variant or a fragment of a full-length protein. For example, in some embodiments, a Cas9 protein domain comprises an H840A amino acid substitution compared to a naturally occurring *S. pyogenes* Cas9 protein. A variant of a protein or enzyme, for example a variant reverse transcriptase, comprises a polypeptide having an amino acid sequence that is about 60% identical, about 70% identical, about 80% identical, about 90% identical, about 95% identical, about 96% identical, about 97% identical, about 98% identical, about 99% identical, about 99.5% identical, or about 99.9% identical to the amino acid sequence of a reference protein.

[0071] In some embodiments, a protein comprises one or more protein domains or subdomains. As used herein, the term “polypeptide domain”, “protein domain”, or “domain” when used in the context of a protein or polypeptide, refers to a polypeptide chain that has one or more biological functions, *e.g.*, a catalytic function, a protein-protein binding function, or a protein-DNA function. In some embodiments, a protein comprises multiple protein domains. In some embodiments, a protein comprises multiple protein domains that are naturally occurring. In some embodiments, a protein comprises multiple protein domains from different naturally occurring proteins. For example, in some embodiments, a prime editor can be a fusion protein comprising a Cas9 protein domain of S. pyogenes or a fragment, mutant, or variant thereof and a reverse transcriptase protein domain of a retrovirus (e.g., Moloney murine leukemia virus) or a mutant, fragment, or variant of the retrovirus. A protein that comprises amino acid sequences from different origins or naturally occurring proteins can be referred to as a fusion, or a chimeric protein.

[0072] In some embodiments, a protein comprises a functional variant or functional fragment of a full-length wild-type protein. A “functional fragment” or “functional portion”, as used herein, refers to any portion of a reference protein (*e.g.*, a wild-type protein) that encompasses less than the entire amino acid sequence of the reference protein while retaining one or more of the functions, *e.g.*, catalytic or binding functions. For example, a functional fragment of a reverse transcriptase can encompass less than the entire amino acid sequence of a wild-type reverse transcriptase but retains the ability under at least one set of conditions to catalyze the polymerization of a polynucleotide. When the reference protein is a fusion of multiple functional domains, a functional fragment thereof can retain one or more of the functions of at least one of the functional domains. For example, a functional fragment of a Cas9 can encompass less than the entire amino acid sequence of a wild-type Cas9 but retains its DNA binding ability and lack its nuclease activity partially or completely.

[0073] A “functional variant” or “functional mutant”, as used herein, refers to any variant or mutant of a reference protein (*e.g.,* a wild-type protein) that encompasses one or more alterations to the amino acid sequence of the reference protein while retaining one or more of the functions, *e.g.*, catalytic or binding functions. In some embodiments, the one or more alterations to the amino acid sequence comprises amino acid substitutions, insertions or deletions, or any combination thereof. In some embodiments, the one or more alterations to the amino acid sequence comprises amino acid substitutions. For example, a functional variant of a reverse transcriptase can comprise one or more amino acid substitutions compared to the amino acid sequence of a wild-type reverse transcriptase but retains the ability under at least one set of conditions to catalyze the polymerization of a polynucleotide. When the reference protein is a fusion of multiple functional domains, a functional variant thereof can retain one or more of the functions of at least one of the functional domains. For example, in some embodiments, a functional fragment of a Cas9 can comprise one or more amino acid substitutions in a nuclease domain, *e.g.*, an H840A amino acid substitution, compared to the amino acid sequence of a wild-type Cas9, but retains the DNA binding ability and lacks the nuclease activity partially or completely.

[0074] The term “function” and its grammatical equivalents as used herein may refer to a capability of operating, having, or serving an intended purpose. Functional can comprise any percent from baseline to 100% of an intended purpose. For example, functional can comprise or comprise about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or up to about 100% of an intended purpose. In some embodiments, the term functional can mean over or over about 100% of normal function, for example, 125%, 150%, 175%, 200%, 250%, 300%, 400%, 500%, 600%, 700% or up to about 1000% of an intended purpose.

[0075] In some embodiments, a protein or polypeptides includes naturally occurring amino acids (*e.g.*, one of the twenty amino acids commonly found in peptides synthesized in nature, and known by the one letter abbreviations A, R, N, C, D, Q, E, G, H, I, L, K, M, F, P, S, T, W, Y and V). In some embodiments, a protein or polypeptides includes non-naturally occurring amino acids (*e.g.*, amino acids which is not one of the twenty amino acids commonly found in peptides synthesized in nature, including synthetic amino acids, amino acid analogs, and amino acid mimetics). In some embodiments, a protein or polypeptide is modified.

[0076] In some embodiments, a protein comprises an isolated polypeptide. The term "isolated" means free or removed to varying degrees from components which normally accompany it as found in the natural state or environment. For example, a polypeptide naturally present in a living animal is not isolated, and the same polypeptide partially or completely separated from the coexisting materials of its natural state is isolated.

[0077] In some embodiments, a protein is present within a cell, a tissue, an organ, or a virus particle. In some embodiments, a protein is present within a cell or a part of a cell (*e.g.*, a bacteria cell, a plant cell, or an animal cell). In some embodiments, the cell is in a tissue, in a subject, or in a cell culture. In some embodiments, the cell is a microorganism (*e.g.*, a bacterium, fungus, protozoan, or virus). In some embodiments, a protein is present in a mixture of analytes (*e.g.*, a lysate). In some embodiments, the protein is present in a lysate from a plurality of cells or from a lysate of a single cell.

[0078] The terms "homologous," "homology," or "percent homology" as used herein refer to the degree of sequence identity between an amino acid and a corresponding reference amino acid sequence, or a polynucleotide sequence and a corresponding reference polynucleotide sequence. "Homology" can refer to polymeric sequences, *e.g.,* polypeptide or DNA sequences that are similar. Homology can mean, for example, nucleic acid sequences with at least about: 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 100% identity. In other embodiments, a "homologous sequence" of nucleic acid sequences can exhibit at least 93%, 95%, 98% or 99% sequence identity to the reference nucleic acid sequence. For example, a "region of homology to a genomic region" can be a region of DNA that has a similar sequence to a given genomic region in the genome. A region of homology can be of any length that is sufficient to promote binding of, e.g., a spacer or a primer binding sitesequence to the genomic region. For example, the region of homology can comprise at least 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100 or more bases in length such that the region of homology has sufficient homology to undergo binding with the corresponding genomic region.

[0079] When a percentage of sequence homology or identity is specified, in the context of two nucleic acid sequences or two polypeptide sequences, the percentage of homology or identity generally refers to the alignment of two or more sequences across a portion of their length when compared and aligned for maximum correspondence. When a position in the compared sequence can be occupied by the same base or amino acid, then the molecules can be homologous at that position. Unless stated otherwise, sequence homology or identity is assessed over the specified length of the nucleic acid, polypeptide or portion thereof. In some embodiments, the homology or identity is assessed over a functional portion or specified portion of the length.

[0080] Alignment of sequences for assessment of sequence homology can be conducted by algorithms known in the art, such as the Basic Local Alignment Search Tool (BLAST) algorithm, which is described in Altschul et al, J. Mol. Biol. 215:403- 410, 1990. A publicly available, internet interface, for performing BLAST analyses is accessible through the National Center for Biotechnology Information. Additional known algorithms include those published in: Smith & Waterman, “Comparison of Biosequences”, Adv. Appl. Math. 2:482, 1981; Needleman & Wunsch, “A general method applicable to the search for similarities in the amino acid sequence of two proteins” J. Mol. Biol. 48:443, 1970; Pearson & Lipman “Improved tools for biological sequence comparison”, Proc. Natl. Acad. Sci. USA 85:2444, 1988; or by automated implementation of these or similar algorithms. Global alignment programs can also be used to align similar sequences of roughly equal size. Examples of global alignment programs include NEEDLE (available at www.ebi.ac.uk/Tools/psa/emboss_needle/) which is part of the EMBOSS package (Rice P et al., Trends Genet., 2000; 16: 276-277), and the GGSEARCH program https://fasta.bioch.virginia.edu/fasta_www2/, which is part of the FASTA package (Pearson W and Lipman D, 1988, Proc. Natl. Acad. Sci. USA, 85: 2444-2448). Both of these programs are based on the Needleman-Wunsch algorithm which is used to find the optimum alignment (including gaps) of two sequences along their entire length. A detailed discussion of sequence analysis can also be found in Unit 19.3 of Ausubel et al ("Current Protocols in Molecular Biology" John Wiley & Sons Inc, 1994-1998, Chapter 15, 1998). In some embodiments, an alignment between a query sequence and a reference sequence is performed with Needleman-Wunsch alignment with Gap Costs set to Existence: 11 Extension: 1 where percent identity is calculated by dividing the number of identities by the length of the alignment, as further described in Altschul et al.("Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402, 1997) and Altschul et al, ("Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109, 2005).

[0081] A skilled person understands that amino acid (or nucleotide) positions may be determined in homologous sequences based on alignment, for example, “H840” in a reference Cas9 sequence may correspond to H839, or another corresponding position in a Cas9 homolog when the Cas9 homolog is aligned against the reference Cas9 sequence. The term “homolog” as used herein refers to a gene or a protein that is related to another gene or protein by a common ancestral DNA sequence. A homolog can be an ortholog or a paralog. An ortholog refers to a gene or protein that is related to another gene or protein by a speciation event. A paralog refers to a gene or protein that is related to another gene or protein by a duplication event within a genome. A paralog may be within the same species of the gene or protein it is related to. A paralog may also be in a different species of the gene or protein it is related to. In some embodiments, an ortholog may retain the same function. In some embodiments, a paralog may evolve a new function.

[0082] The term “polynucleotide” or “nucleic acid molecule” can be any polymeric form of nucleotides, including DNA, RNA, a hybridization thereof, or RNA-DNA chimeric molecules. In some embodiments, a polynucleotide comprises cDNA, genomic DNA, mRNA, tRNA, rRNA, or microRNA. In some embodiments, a polynucleotide is double stranded, *e.g.*, a double-stranded DNA in a gene. In some embodiments, a polynucleotide is single-stranded or substantially single-stranded, *e.g.*, single-stranded DNA or an mRNA. In some embodiments, a polynucleotide is a cell-free nucleic acid molecule. In some embodiments, a polynucleotide circulates in blood. In some embodiments, a polynucleotide is a cellular nucleic acid molecule. In some embodiments, a polynucleotide is a cellular nucleic acid molecule in a cell circulating in blood.

[0083] Polynucleotides can have any three-dimensional structure. The following are nonlimiting examples of polynucleotides: a gene or gene fragment (for example, a probe, primer, EST or SAGE tag), an exon, an intron, intergenic DNA (including, without limitation, heterochromatic DNA), messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), a ribozyme, cDNA, a recombinant polynucleotide, a branched polynucleotide, a plasmid, a vector, isolated DNA, isolated RNA, sgRNA, guide RNA, a nucleic acid probe, a primer, an snRNA, a long non-coding RNA, a snoRNA, a siRNA, a miRNA, a tRNA-derived small RNA (tsRNA), an antisense RNA, an shRNA, or a small rDNA-derived RNA (srRNA).

[0084] In some embodiments, a polynucleotide comprises deoxyribonucleotides, ribonucleotides or analogs thereof. In some embodiments, a polynucleotide comprises modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure can be imparted before or after assembly of the polynucleotide. The sequence of nucleotides can be interrupted by non-nucleotide components. A polynucleotide can be further modified after polymerization, such as by conjugation with a labeling component.

[0085] In some embodiments, a polynucleotide is composed of a specific sequence of four nucleotide bases: adenine (A); cytosine (C); guanine (G); thymine (T); and uracil (U) for thymine when the polynucleotide is RNA. In some embodiments, the polynucleotide can comprise one or more other nucleotide bases, such as inosine (I), which is read by the translation machinery as guanine (G).

[0086] In some embodiments, a polynucleotide can be modified. As used herein, the terms “modified” or “modification” refers to chemical modification with respect to the A, C, G, T and U nucleotides. In some embodiments, modifications can be on the nucleoside base and/or sugar portion of the nucleosides that comprise the polynucleotide. In some embodiments, the modification can be on the internucleoside linkage (*e.g.*, phosphate backbone). In some embodiments, multiple modifications are included in the modified nucleic acid molecule. In some embodiments, a single modification is included in the modified nucleic acid molecule.

[0087] The term "complement", "complementary", or “complementarity” as used herein, refers to the ability of two polynucleotide molecules to base pair with each other. Complementary polynucleotides may base pair via hydrogen bonding, which can be Watson Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding. For example, an adenine on one polynucleotide molecule will base pair to a thymine or uracil on a second polynucleotide molecule and a cytosine on one polynucleotide molecule will base pair to a guanine on a second polynucleotide molecule. Two polynucleotide molecules are complementary to each other when a first polynucleotide molecule comprising a first nucleotide sequence can base pair with a second polynucleotide molecule comprising a second nucleotide sequence. For instance, the two

DNA molecules 5’-ATGC-3’ and 5'-GCAT-3’ are complementary, and the complement of the DNA molecule 5’-ATGC-3’ is 5’-GCAT-3’. A percentage of complementarity indicates the percentage of nucleotides in a polynucleotide molecule which can base pair with a second polynucleotide molecule (*e.g.*, 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary, respectively). “Perfectly complementary” means that all the contiguous nucleotides of a polynucleotide molecule will base pair with the same number of contiguous nucleotides in a second polynucleotide molecule. "Substantially complementary" as used herein refers to a degree of complementarity that can be at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% over all or a portion of two polynucleotide molecules. In some embodiments, the portion of complementarity may be a region of 10, 15, 20, 25, 30, 35, 40, 45, 50, or more nucleotides. “Substantially complementary” can also refer to a 100% complementarity over a portion or region of two polynucleotide molecules. In some embodiments, the portion or region of complementarity between the two polynucleotide molecules is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% of the length of at least one of the two polynucleotide molecules or a functional or defined portion thereof.

[0088] As used herein, “expression” refers to the process by which polynucleotides, *e.g.*, DNA, are transcribed into mRNA and/or the process by which polynucleotides, *e.g.*, the transcribed mRNA, translated into peptides, polypeptides, or proteins. If the polynucleotide is derived from genomic DNA, expression can include splicing of the mRNA in a eukaryotic cell. In some embodiments, expression of a polynucleotide, *e.g.*, a gene or a DNA encoding a protein, is determined by the amount of the protein encoded by the gene after transcription and translation of the gene. In some embodiments, expression of a polynucleotide, *e.g.*, a gene or a DNA encoding a protein, is determined by the amount of a functional form of the protein encoded by the gene after transcription and translation of the gene. In some embodiments, expression of a gene is determined by the amount of the mRNA, or transcript, that is encoded by the gene after transcription the gene. In some embodiments, expression of a polynucleotide, *e.g.*, an mRNA, is determined by the amount of the protein encoded by the mRNA after translation of the mRNA. In some embodiments, expression of a polynucleotide, *e.g.*, a mRNA or coding RNA, is determined by the amount of a functional form of the protein encoded by the polypeptide after translation of the polynucleotide.

[0089] The term “sequencing” as used herein, can comprise capillary sequencing, bisulfite-free sequencing, bisulfite sequencing, TET-assisted bisulfite (TAB) sequencing, ACE-sequencing, high-throughput sequencing, Maxam-Gilbert sequencing, massively parallel signature sequencing, Polony sequencing, 454 pyrosequencing, Sanger sequencing, Illumina sequencing, SOLiD sequencing, Ion Torrent semiconductor sequencing, DNA nanoball sequencing, Heliscope single molecule sequencing, single molecule real time (SMRT) sequencing, nanopore sequencing, shot gun sequencing, RNA sequencing, or any combination thereof.

[0090] The terms “equivalent” or “biological equivalent” are used interchangeably when referring to a particular molecule, or biological or cellular material, and means a molecule having minimal homology to another molecule while still maintaining a desired structure or functionality.

[0091] The term “encode” as it is applied to polynucleotides refers to a polynucleotide which is said to “encode” another polynucleotide, a polypeptide, or an amino acid if, in its native state or when manipulated by methods well known to those skilled in the art, it can be used as polynucleotide synthesis template, *e.g.*, transcribed into an RNA, reverse transcribed into a DNA or cDNA, and/or translated to produce an amino acid, or a polypeptide or fragment thereof. In some embodiments, a polynucleotide comprising three contiguous nucleotides form a codon that encodes a specific amino acid. In some embodiments, a polynucleotide comprises one or more codons that encode a polypeptide. In some embodiments, a polynucleotide comprising one or more codons comprises a mutation in a codon compared to a wild-type reference polynucleotide. In some embodiments, the mutation in the codon encodes an amino acid substitution in a polypeptide encoded by the polynucleotide as compared to a wild-type reference polypeptide.

[0092] The term “mutation” as used herein refers to a change and/or alteration in an amino acid sequence of a protein or nucleic acid sequence of a polynucleotide. Such changes and/or alterations can comprise the substitution, insertion, deletion and/or truncation of one or more amino acids, in the case of an amino acid sequence, and/or nucleotides, in the case of nucleic acid sequence, compared to a reference amino acid or a reference nucleic acid sequence. In some embodiments, the reference sequence is a wild-type sequence. In some embodiments, a mutation in a nucleic acid sequence of a polynucleotide encodes a mutation in the amino acid sequence of a polypeptide. In some embodiments, the mutation in the amino acid sequence of the polypeptide or the mutation in the nucleic acid sequence of the polynucleotide is a mutation associated with a disease state. A “reference sequence” is a defined sequence used as a basis for sequence comparison. A reference sequence can be a subset of or the entirety of a specified sequence; for example, a segment of a full-length cDNA sequence, RNA sequence, DNA sequence, gene sequence or polypeptide sequence, or the complete cDNA sequence, RNA sequence, DNA sequence, gene sequence or polypeptide sequence. In some embodiments, a reference sequence is a wild-type sequence of a protein of interest or a variant thereof. In other embodiments, a reference sequence is a polynucleotide sequence encoding a wild-type protein or a variant thereof.

[0093] The term “subject” and its grammatical equivalents as used herein may refer to a human or a non-human. A subject can be a mammal. A human subject can be male or female. A human subject can be of any age. A subject can be a human embryo. A human subject can be a newborn, an infant, a child, an adolescent, or an adult. A human subject can be up to about 100 years of age. A human subject can be in need of treatment for a genetic disease or disorder.

[0094] The terms “treatment” or “treating” and their grammatical equivalents may refer to the medical management of a subject with an intent to cure, ameliorate, or ameliorate a symptom of, a disease, condition, or disorder. Treatment can include active treatment, that is, treatment directed specifically toward the improvement of a disease, condition, or disorder. Treatment can include causal treatment, that is, treatment directed toward removal of the cause of the associated disease, condition, or disorder. In addition, this treatment can include palliative treatment, that is, treatment designed for the relief of symptoms rather than the curing of the disease, condition, or disorder. Treatment can include supportive treatment, that is, treatment employed to supplement another specific therapy directed toward the improvement of the disease, condition, or disorder. In some embodiments, a condition can be pathological. In some embodiments, a treatment can not completely cure or prevent a disease, condition, or disorder. In some embodiments, a treatment ameliorates, but does not completely cure or prevent a disease, condition, or disorder. In some embodiments, a subject can be treated for 12 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, 2 years, 3 years, 4 years, 5 years, 6 years, indefinitely, or life of the subject.

[0095] The term “ameliorate” and its grammatical equivalents means to decrease, suppress, attenuate, diminish, arrest, reverse, or stabilize the development or progression of a disease.

[0096] The terms “prevent” or “preventing” means delaying, forestalling, or avoiding the onset or development of a disease, condition, or disorder for a period of time. Prevent also means reducing risk of developing a disease, disorder, or condition. Prevention includes minimizing or partially or completely inhibiting the development of a disease, condition, or disorder. In some embodiments, a composition, *e.g.* a pharmaceutical composition, prevents a disorder by delaying the onset of the disorder for 12 hours, 24 hours, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 2 weeks, 3 weeks, 4 weeks, 2 months, 3 months, 4 months, 5 months, 6 months, 1 year, 2 years, 3 years, 4 years, 5 years, 6 years, indefinitely, or life of a subject.

[0097] The term “effective amount” or “therapeutically effective amount” refers to a quantity of a composition, for example, a prime editing composition comprising a construct, that can be sufficient to result in a desired activity upon introduction into a subject as disclosed herein. An effective amount of the prime editing compositions can be provided to a target gene or cell, whether the cell is *ex vivo* or *in vivo*. An effective amount can be the amount to induce, for example, at least about a 2-fold change (increase or decrease) or more in the amount of target nucleic acid modulation observed relative to a negative control. An effective amount or dose can induce, for example, about 2-fold increase, about 3-fold increase, about 4-fold increase, about 5-fold increase, about 6-fold increase, about 7-fold increase, about 8-fold increase, about 9-fold increase, about 10-fold increase, about 25-fold increase, about 50-fold increase, about 100-fold increase, about 200-fold increase, about 500-fold increase, about 700-fold increase, about 1000-fold increase, about 5000-fold increase, or about 10,000-fold increase in target gene modulation (*e.g.*, expression of a target gene to produce a functional protein). The amount of target gene modulation can be measured by any suitable method known in the art. In some embodiments, the “effective amount” or “therapeutically effective amount” is the amount of a composition that is required to ameliorate the symptoms of a disease relative to an untreated patient. In some embodiments, an effective amount is the amount of a composition sufficient to introduce an alteration in a gene of interest in a cell (*e.g.*, a cell *in vitro* or *in vivo*).

[0098] An effective amount can be the amount to induce, when administered to a population of cells, a certain percentage of the population of cells to have a correction of a mutation. For example, in some embodiments, an effective amount can be the amount to induce, when administered to or introduced to a population of cells, installation of one or more intended nucleotide edits that correct a mutation in the target gene, in at least about 1%, 2%, 5%, about 10%, about 15%, about 20%, about 25%, about 30%, about 35%, about 40%, about 45%, about 50%, about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or about 99% of the population of cells.

[0099] The term "reverse transcriptase" or "RT" as used herein refers to a class of enzymes that synthesize a DNA molecule from an RNA template. An RT may require the primer molecule with an exposed 3' hydroxyl group. In some embodiments, the primer molecule of an RT is a DNA molecule. In some embodiments, the primer molecule of an RT is an RNA molecule. In some embodiments, an RT comprises both DNA polymerase activity and RNase H activity. The two activities can reside in two separate domains in an RT.

[0100] The term "linker" as used herein refers to a bond, a chemical group, or a molecule linking two molecules or moieties, e.g., two protein domains to form a fusion protein. In some embodiments, a linker is a peptide linker. In some embodiments, a linker is a polynucleotide or a oligonucleotide linker. For example, a RNA-binding protein recruitment sequence, such as a MS2 polynucleotide sequence, can be used to connect a Cas9 domain and a DNA polymerase domain of a prime editor, wherein one of the Cas9 domain and the DNA polymerase domain is fused to a MS2 coat protein. In some embodiments, a peptide linker can have various lengths, depending on the application of a linker or the sequences or molecules being linked by a linker.

[0101] The term "fusion protein" refers to a protein comprised of domains from more than one naturally occurring or recombinantly produced protein, where generally each domain serves a different function. A domain may comprise a particular makeup of amino acids. A domain may also comprise a structure of proteins as described herein.

[0102] Disclosed herein in some embodiments, are compositions comprising polynucleotides and constructs that comprises a nucleic acid that codes for a PEgRNA as described above, a nick guide sequence as describe above, a primer editor, a prime editing composition or any combination thereof. In certain embodiments, provided herein are prime editors for programmable prime editing of target polynucleotides, *e.g.*, target genes.

Prime Editing

[0103] The term "prime editing" refers to programmable editing of a target DNA using a prime editor complexed with a PEgRNA to incorporate an intended nucleotide edit (also referred to herein as a nucleotide change) into the target DNA through target-primed DNA synthesis. A target DNA polynucleotide, *e.g.*, a target gene of prime editing can comprise a double stranded DNA molecule having two complementary strands: a first strand that may be referred to as a "target strand" or a "non-edit strand", and a second strand that may be referred to as a "non-target strand," or an "edit strand." In some embodiments, in a prime editing guide RNA (PEgRNA), a spacer sequence is complementary or substantially complementary to a specific sequence on the target strand, which may be referred to as a "search target sequence". In some embodiments, the spacer sequence anneals with the target strand at the search target sequence. The target strand can also be referred to as the "non-Protospacer Adjacent Motif (non-PAM strand).” In some embodiments, the non-target strand can also be referred to as the “PAM strand”. In some embodiments, the PAM strand comprises a protospacer sequence and optionally a protospacer adjacent motif (PAM) sequence. In prime editing using a Cas-protein-based prime editor, a PAM sequence refers to a short DNA sequence immediately adjacent to the protospacer sequence on the PAM strand of the target gene. A PAM sequence can be specifically recognized by a programmable DNA binding protein, e.g., a Cas nickase or a Cas nuclease. In some embodiments, a specific PAM is characteristic of a specific programmable DNA binding protein, e.g., a Cas nickase or a Cas nuclease, e.g., a Cas9 nickase or a Cas9 nuclease. A protospacer sequence refers to a specific sequence in the PAM strand of the double stranded target DNA (e.g., target gene) that is complementary to the search target sequence. In a PEgRNA, a spacer sequence can have a substantially identical sequence as the protospacer sequence on the edit strand of the double stranded target DNA (e.g., target gene) except that the spacer sequence can comprise Uracil (U) and the protospacer sequence can comprise Thymine (T).

[0104] In some embodiments, the double stranded target DNA comprises a nick site on the PAM strand (or non-target strand). As used herein, a “nick site” refers to a specific position in between two nucleotides or two base pairs of the double stranded target DNA. In some embodiments, the position of a nick site is determined relative to the position of a specific PAM sequence. In some embodiments, the nick site is the particular position where a nick will occur when the double stranded target DNA is contacted with a nickase, for example, a Cas nickase, that recognizes a specific PAM sequence. In some embodiments, the nick site is upstream of a specific PAM sequence on the PAM strand of the double stranded target DNA. In some embodiments, the nick site is downstream of a specific PAM sequence on the PAM strand of the double stranded target DNA. In some embodiments, the nick site is upstream of a PAM sequence recognized by a Cas9 nickase, wherein the Cas9 nickase comprises a nuclease active RuvC domain and a nuclease inactive NHN domain. In some embodiments, the nick site is 3 nucleotides upstream of the PAM sequence, and the PAM sequence is recognized by a Streptococcus pyogenes Cas9 nickase, a *P. lavamentivorans* Cas9 nickase, a *C. diphtheriae* Cas9 nickase, a *N. cinerea* Cas9, a *S. aureus* Cas9, or a *N. lari* Cas9 nickase that comprises a nuclease active RuvC domain and a nuclease inactive NHN domain. In some embodiments, the nick site is 2 nucleotides upstream of the PAM sequence, and the PAM sequence is recognized by a *S. thermophilus* Cas9 nickase that comprises a nuclease active RuvC domain and a nuclease inactive NHN domain.

[0105] A “primer binding site” (also referred to as PBS or primer binding site sequence) is a single-stranded portion of the PEgRNA that comprises a region of complementarity to the PAM strand (i.e., the non-target strand or the edit strand). The PBS is complementary or substantially complementary to a sequence on the PAM strand of the double stranded target DNA that is immediately upstream of the nick site. In some embodiments, in the process of prime editing, the PEgRNA complexes with and directs a prime editor to bind the search target sequence on the target strand of the double stranded target DNA, and generates a nick at the nick site on the non-target strand of the double stranded target DNA. In some embodiments, the PBS is complementary to or substantially complementary to, and can anneal to, a free 3′

end on the non-target strand of the double stranded target DNA at the nick site. In some embodiments, the PBS annealed to the free 3′ end on the non-target strand can initiate target-primed DNA synthesis.

[0106] An "editing template" of a PEgRNA is a single-stranded portion of the PEgRNA that is 5′ of the PBS and comprises a region of complementarity to the PAM strand (i.e. the non-target strand or the edit strand), and comprises one or more intended nucleotide edits compared to the endogenous sequence of the double stranded target DNA. In some embodiments, the editing template and the PBS are immediately adjacent to each other. Accordingly, in some embodiments, a PEgRNA in prime editing comprises a single-stranded portion that comprises the PBS and the editing template immediately adjacent to each other. In some embodiments, the single stranded portion of the PEgRNA comprising both the PBS and the editing template is complementary or substantially complementary to an endogenous sequence on the PAM strand (i.e., the non-target strand or the edit strand) of the double stranded target DNA except for one or more non-complementary nucleotides at the intended nucleotide edit positions. As used herein, regardless of relative 5′-3′ positioning in other context, the relative positions as between the PBS and the editing template, and the relative positions as among elements of a PEgRNA, are determined by the 5′ to 3′ order of the PEgRNA as a single molecule regardless of the position of sequences in the double stranded target DNA that may have complementarity or identity to elements of the PEgRNA. In some embodiments, the editing template is complementary or substantially complementary to a sequence on the PAM strand that is immediately downstream of the nick site, except for one or more non-complementary nucleotides at the intended nucleotide edit positions. The endogenous, e.g., genomic, sequence that is complementary or substantially complementary to the editing template, except for the one or more non-complementary nucleotides at the position corresponding to the intended nucleotide edit, may be referred to as an "editing target sequence". In some embodiments, the editing template has identity or substantial identity to a sequence on the target strand that is complementary to, or having the same position in the genome as, the editing target sequence, except for one or more insertions, deletions, or substitutions at the intended nucleotide edit positions. In some embodiments, the editing template encodes a single stranded DNA, wherein the single stranded DNA has identity or substantial identity to the editing target sequence except for one or more insertions, deletions, or substitutions at the positions of the one or more intended nucleotide edits.

[0107] In some embodiments, a PEgRNA complexes with and directs a prime editor to bind to the search target sequence of the target gene. In some embodiments, the bound prime editor generates a nick on the edit strand (PAM strand) of the target gene. In some embodiments, a primer binding site (PBS) of the PEgRNA anneals with a free 3' end formed at the nick site, and the prime editor initiates DNA synthesis from the nick site, using the free 3' end as a primer. Subsequently, a single-stranded DNA encoded by the editing template of the PEgRNA is synthesized. In some embodiments, the newly synthesized single-stranded DNA comprises one or more intended nucleotide edits compared to an endogenous target gene sequence. Accordingly, in some embodiments, the editing template of a PEgRNA is complementary to a sequence in the edit strand except for one or more mismatches at the intended nucleotide edit positions in the editing template. In some embodiments, the newly synthesized single stranded DNA has identity or substantial identity to a sequence in the editing target sequence, except for one or more insertions, deletions, or substitutions at the intended nucleotide edit positions. The endogenous, e.g., genomic, sequence that is partially complementary to the editing template may be referred to as an "editing target sequence".

[0108] In some embodiments, the newly synthesized single-stranded DNA equilibrates with the editing target on the edit strand of the double stranded target DNA (e.g., the target gene) for pairing with the target strand of the targe gene. In some embodiments, the editing target sequence of the double stranded target DNA (e.g., target gene) is excised by a flap endonuclease (FEN), for example, FEN1. In some embodiments, the FEN is an endogenous FEN, for example, in a cell comprising the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the FEN is provided as part of the prime editor, either linked to other components of the prime editor or provided in *trans*. In some embodiments, the newly synthesized single stranded DNA, which comprises the intended nucleotide edit, replaces the endogenous single stranded editing target sequence on the edit strand of the double stranded target DNA (e.g., target gene). In some embodiments, the newly synthesized single stranded DNA and the endogenous DNA on the target strand form a heteroduplex DNA structure at the region corresponding to the editing target sequence of the double stranded target DNA (e.g., target gene). In some embodiments, the newly synthesized single-stranded DNA comprising the nucleotide edit is paired in the heteroduplex with the target strand of the target DNA that does not comprise the nucleotide edit, thereby creating a mismatch between the two otherwise complementary strands. In some embodiments, the mismatch is recognized by DNA repair machinery, *e.g.*, an endogenous DNA repair machinery. In some embodiments, through DNA repair, the intended nucleotide edit is incorporated into the double stranded target DNA (e.g., the target gene).

Prime Editor

[0109] The term "prime editor (PE)" refers to the polypeptide or polypeptide components involved in prime editing. In various embodiments, a prime editor includes a polypeptide domain having DNA binding activity (e.g., a DNA binding domain) and a polypeptide domain (e.g., a DNA polymerase domain) having DNA polymerase activity. In some embodiments, a prime editor comprises a polypeptide domain (e.g., a DNA binding domain) having DNA binding activity. In some embodiments, a prime editor comprises a polypeptide that comprises a DNA binding domain. In some embodiments, a prime editor comprises a DNA binding domain. In some embodiments, a prime editor comprises a polypeptide domain having DNA polymerase activity (e.g., a DNA polymerase domain). In some embodiments, a prime editor comprises a polypeptide that comprises a DNA polymerase domain. In some embodiments, a prime editor comprises a DNA polymerase domain. In some embodiments, a prime editor comprises a polypeptide that comprises a DNA binding domain and a polypeptide that comprises a DNA polymerase domain. In some embodiments, a prime editor comprises a DNA binding domain and a DNA polymerase domain. In some embodiments, the prime editor comprises a DNA binding domain and DNA polymerase domain that is linked by a linker, e.g., a peptide linker, e.g., a GS rich peptide linker. In some embodiments, the prime editor comprises a fusion polypeptide that comprises a DNA binding domain and a DNA polymerase domain linked by a linker, e.g., a peptide linker, e.g., a GS rich peptide linker.

[0110] In some embodiments, the prime editor comprises a polypeptide domain having a nuclease activity. In some embodiments, the polypeptide domain having DNA binding activity comprises a nuclease domain or nuclease activity. In some embodiments, the DNA binding domain comprises a nuclease domain or nuclease activity. In some embodiments, the polypeptide domain having the nuclease activity comprises a nickase, or a fully active nuclease. In some embodiments, the DNA binding domain comprises a nickase, or a fully active nuclease. As used herein, the term "nickase" refers to a nuclease capable of cleaving only one strand of a double-stranded DNA target. In some embodiments, the prime editor comprises a polypeptide domain that is an inactive nuclease. In some embodiments, the DNA binding domain comprises a nuclease domain that is an inactive nuclease; e.g., dCas9. In some embodiments, the DNA binding domain comprises a comprises a nucleic acid guided DNA binding domain, for example, a CRISPR-Cas protein, for example, a Cas9 nickase, a Cpf1 nickase, or another CRISPR-Cas nuclease. In some embodiments, the DNA binding domain (e.g., a nucleic acid guided DNA binding domain) is a Cas protein domain. In some embodiments, the Cas protein is a Cas9; e.g., Cas9 nuclease; e.g., dCas9, Cas9 nickase. In some embodiments, the Cas protein domain comprises a nickase or a nickase activity. In some embodiments, the DNA binding domain is a Cas9 or a variant thereof (e.g., a nickase variant). In some embodiments, the polypeptide domain having programmable DNA binding activity comprises a nucleic acid guided DNA binding domain, for example, a CRISPR-Cas protein, for example, a Cas9 nickase, a Cpf1 nickase, or another CRISPR-Cas nuclease.

[0111] In some embodiments, the polypeptide domain having DNA polymerase activity comprises a template-dependent DNA polymerase, for example, a DNA-dependent DNA polymerase or an RNA-dependent DNA polymerase. In some embodiments, the DNA binding domain comprises a template-dependent DNA polymerase for example, a DNA-dependent DNA polymerase or an RNA-dependent DNA polymerase. In some embodiments, the DNA polymerase domain comprises a reverse transcriptase domain (RT domain) or a reverse transcriptase (RT). In some embodiments, the DNA polymerase domain is a RT domain or a RT. In some embodiments, a prime editor comprises a reverse transcriptase (RT) activity. For example, the first polypeptide of the prime editor may have activity for target primed reverse transcription. In some embodiments, the polypeptide domain having DNA polymerase activity comprises a reverse transcriptase activity (e.g., activity for target primed reverse transcription).

[0112] In some embodiments, the DNA polymerase is a reverse transcriptase. In some embodiments, the prime editor comprises additional polypeptides involved in prime editing, for example, a polypeptide domain having 5' endonuclease activity, e.g., a 5' endogenous DNA flap endonucleases (e.g., FEN1), for helping to drive the prime editing process towards the edited product formation. In some embodiments, the prime editor further comprises an RNA-protein recruitment polypeptide, for example, a MS2 coat protein.

[0113] In some embodiments, a prime editor comprises a Cas polypeptide (i.e., a DNA binding domain) and a reverse transcriptase polypeptide (i.e., a DNA polymerase domain) that are derived from different species. For example, a prime editor may comprise a S. pyogenes Cas9 polypeptide and a Moloney murine leukemia virus (M-MLV) reverse transcriptase polypeptide. In some embodiments, the prime editor comprises a fusion polypeptide that comprises a comprises a Cas polypeptide (i.e., a DNA binding domain) and a reverse transcriptase polypeptide (i.e., a DNA polymerase domain) that are derived from different species. For example, a prime editor may comprise a S. pyogenes Cas9 polypeptide and a Moloney murine leukemia virus (M-MLV) reverse transcriptase (RT) polypeptide.

[0114] In some embodiments, polypeptide domains of a prime editor (e.g., a DNA binding domain and a DNA polymerase domain) are fused or linked by a peptide linker to form a fusion protein. In other embodiments, a prime editor comprises one or more polypeptide domains (e.g., a DNA binding domain and a DNA polymerase domain) provided in trans as separate proteins, which are capable of being associated to each other through non-peptide linkages or through aptamers or recruitment sequences. In some embodiments, a prime editor comprises a DNA binding domain and a DNA polymerase domain (e.g., a reverse transcriptase domain or RT) fused or linked with each other by a peptide linker (e.g., linkers disclosed set forth in SEQ ID NOs: 286-411).

[0115] In some embodiments, the prime editor comprises a DNA binding domain and a DNA polymerase domain (e.g., a reverse transcriptase domain or RT) fused or linked with each other by an RNA-protein recruitment aptamer, e.g., a MS2 aptamer, which can, in some embodiments, be linked to a PEgRNA.

[0116] In some embodiments, a prime editor further comprises one or more nuclear localization sequence (NLS). In some embodiments, one or more polypeptides of the prime editor are fused to or linked to (e.g., via a peptide linker) one or more NLSs. In some embodiments, the prime editor comprises a DNA binding domain and a DNA polymerase domain that are provided in trans, wherein the DNA binding domain and/or the DNA polymerase domain is fused or linked to one or more NLSs.

[0117] Prime editor polypeptide components can be encoded by one or more polynucleotides in whole or in part. The present disclosure contemplates polynucleotides encoding the prime editor components, for example, a polynucleotide encoding a DNA binding domain, and a polynucleotide encoding a DNA polymerase domain. The present disclosure also contemplates a single polynucleotide comprising a polynucleotide encoding a DNA binding domain, and a polynucleotide encoding a DNA polymerase domain. In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA polymerase domain. In some embodiments, the polynucleotide encoding a DNA polymerase domain is a DNA. In some embodiments, the polynucleotide encoding a DNA polymerase domain is an RNA (e.g., a mRNA). In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA binding domain. In some embodiments, the polynucleotide encoding the DNA binding domain is a DNA. In some embodiments, the polynucleotide encoding the DNA binding domain is an RNA (e.g., a mRNA). In some embodiments, the polynucleotide encoding a DNA binding domain, and the polynucleotide encoding a DNA polymerase domain are linked by a linker polynucleotide (e.g., that encodes a peptide linker) to result in a fusion protein (e.g., a prime editor) that comprises the DNA polymerase domain and DNA binding domain linked by a peptide linker. In some embodiments, the linker polynucleotide is a DNA. In some embodiments, the linker polynucleotide is an RNA (e.g., mRNA). In some embodiments, the polynucleotide sequence encoding a DNA binding domain, and the polynucleotide encoding a DNA polymerase domain are linked by a linker polynucleotide (e.g., that encodes a peptide linker) further comprises one or more polynucleotide sequences encoding one or more NLS to result in a fusion protein (e.g., a prime editor) that comprises the DNA polymerase domain and DNA binding domain linked by a peptide linker and further fused to or linked to one or more NLS.

[0118] In some embodiments, a single polynucleotide (e.g., a single mRNA) construct, or vector encodes the prime editor fusion protein. In some embodiments, multiple polynucleotides, constructs, or vectors each encode a polypeptide domain or portion of a domain of a prime editor, or a portion of a prime editor fusion protein. For example, a prime editor fusion protein can comprise an N-terminal portion fused to an intein-N and a C-terminal portion fused to an intein-C, each of which is individually encoded by an AAV vector. In some embodiments, components of a prime editor disclosed herein (e.g., a polypeptide comprising a DNA binding domain and/or a polypeptide comprising a DNA polymerase domain) can be brought together post- translationally via a split-intein.

[0119] In some embodiments, a prime editor polypeptide may comprise an amino acid sequence, wherein the initial methionine (at position 1) is optionally not present. In some embodiments, a prime editor polypeptide sequence may comprise a N-terminal methionine residue. In some embodiments, a prime editor polypeptide sequence may lack a N- terminus methionine. In some embodiments, the N-terminal methionine encoded by the translation initiation codon, e.g., ATG, may be removed from the prime editor polypeptide after translation. In some embodiments, the N-terminal methionine encoded by the translation initiation codon, e.g., ATG, may remain present in the prime editor polypeptide sequence. In some embodiments, the amino acid sequence of a prime editor polypeptide can be N-terminally modified by one or more processing enzymes, e.g., by Methionine aminopeptidases (MAP).

[0120] In some embodiments, a prime editor comprises a DNA polymerase domain and a DNA binding domain, wherein the amino acid sequences of the DNA polymerase domain and/or the DNA binding domain comprise a N terminus methionine. In some embodiments, a prime editor comprises a DNA polymerase domain that comprises an amino acid sequence that lacks a N-terminus methionine relative to a reference DNA polymerase amino acid sequence. In some embodiments, a prime editor comprises a DNA binding domain that comprises an amino acid sequence that lacks a N-terminus methionine relative to a reference DNA binding domain amino acid sequence.

[0121] In some embodiments, a prime editor and/or a component thereof (e.g., a DNA binding domain or a polypeptide comprising a DNA binding domain and/or a DNA polymerase domain or a polypeptide comprising a DNA polymerase domain) can be engineered. In some embodiments, the polypeptide components of a prime editor do not naturally occur in the same organism or cellular environment. In some embodiments, the polypeptide components of a prime editor can be of different origins or from different organisms. In some embodiments, a prime editor comprises a DNA binding domain and a DNA polymerase domain that are derived from different species.

[0122] In some embodiments, a prime editor comprises a RT or an RT domain (e.g., a M-MLV RT) that is rationally engineered. Such an engineered RT or RT domain can comprise, for example, sequences or amino acid changes different from a naturally occurring RT or RT domain. In some embodiments, the engineered RT or RT domain comprises improved RT activity relative to a corresponding naturally occurring RT or RT domain. In some embodiments, the engineered RT or RT domain comprises improved prime editing efficiency relative to a corresponding naturally occurring RT or RT domain, when used in a prime editor.

[0123] In some embodiments, a prime editor polypeptide comprises a DNA binding domain (e.g., a Cas9) comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 14 or to any one of amino acid sequences set forth in SEQ ID NOs: 2, 6, 7, or 596-613.

[0124] In some embodiments, a prime editing composition comprises a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain is truncated at C-Terminus at a position after amino acid L478 as set forth in SEQ ID NO:1, 5, or 623. In some embodiments, a prime editing composition comprises a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain is truncated at C-Terminus at a position truncated at a position between L478 and G504 as set forth in SEQ ID NO:1, 5, or 623.

[0125] In some embodiments, a prime editor polypeptide comprises a DNA polymerase domain comprising a MMLV-RT or a mutant, fragment or variant thereof. In some embodiments, a prime editor comprises a wild type MMLV-RT. In some embodiments, a prime editor comprises a MMLV-RT variant comprising one or more amino acid substitutions, insertions, and/or deletions, e.g., a MMLV-RT variant comprising one or more amino acid substitutions, insertions, and/or deletions compared to the reference MMLV-RT sequence set forth in SEQ ID NO: 1. In some embodiments, the MMLVRT variant comprises one or more D200N,T306K,W313F,T330P,L603W amino acid substitutions as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the MMLVRT variant comprises D200N, T306K, W313F, T330P, and L603W amino acid substitutions as compared to reference MMLVRT sequence SEQ ID No 1 (the variant also referred to as a MMLVRT$_{5M}$ variant). In some embodiments, the MMLV RT variant comprises one or more of D524N, L435K, Y133R, Y271R amino acid substitution as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the MMLV RT variant has one or more amino acid deletion compared to the reference MMLVRT sequence SEQ ID No 1. For example, in some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1. By truncated at the C terminus, it is meant that amino acids C terminal to the truncation position are deleted from the MMLV RT sequence as compared to reference sequence, i.e. the MMLV RT variant that is truncated at the C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1 contains only amino acids at positions 1-504 as set forth in SEQ ID No: 1 (such truncation may be referred to herein as a 504X, or G504X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1 (a L478X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus at any amino acid position between positions 478 and 505 as set forth in SEQ ID NO:1. In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 365 and 366 as set forth in SEQ ID NO: 1 (a P365X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 278 and 279 as set forth in SEQ ID NO: 1 (a R278X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 328 and 329 as set forth in SEQ ID NO: 1 (a T328X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 378 and 379 as set forth in SEQ ID NO: 1 (a K478X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 428 and 429 as set forth in SEQ ID NO: 1 (a M428X truncation). In some embodiments, a prime editor polypeptide comprises a DNA polymerase domain (e.g., a MMLV-RT) comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 67 or to any one of amino acid sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623. In some embodiments, a prime editor polypeptide comprises a MMLV-RT domain comprising an amino acid sequence SEQ ID NOs: 5. In some embodiments, a prime editor polypeptide comprises a C-terminal truncated MMLV-RT domain having the amino acid sequence of SEQ ID NO: 36.

[0126] In some embodiments, a prime editor polypeptide comprises one or more peptide linkers that connect a DNA binding domain and a DNA polymerase domain. In some embodiments, the prime editor comprises, from N terminus to C terminus, a DNA binding domain, a peptide linker, and a DNA polymerase domain. In some embodiments, the prime editor comprises, from C terminus to N terminus, a DNA binding domain, a peptide linker, and a DNA polymerase domain. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 286-411. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to SEQ ID NO: 302. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to SEQ ID NO: 302. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that comprises an amino acid sequence of SEQ ID NO: 302.

[0127] In some embodiments, a prime editor polypeptide comprises one or more NLSs. In some embodiments, a DNA binding domain of a prime editor comprises one or more NLSs. In some embodiments, a DNA polymerase domain of a prime editor comprises one or more NLSs. In some embodiments, a DNA binding domain of a prime editor comprises two or more NLSs. In some embodiments, a DNA polymerase domain of a prime editor comprises two or more NLSs. In some embodiments, a prime editor comprises a fusion protein comprising one or more or two or more NLSs in between a DNA binding domain and a DNA polymerase domain. The NLS sequence can be any NLS known in the art. In some embodiments, a prime editor comprises a NLS comprising an amino acid sequence that is at least at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 2 or to any one of amino acid sequences set forth in SEQ ID NOs: 8-24, or 621. In some embodiments, a prime editor comprises a fusion protein comprising a DNA binding domain and a DNA polymerase domain. In some embodiments, the prime editor comprises a fusion protein comprising from N terminus to C terminus a DNA binding domain and a DNA polymerase domain. In some embodiments, the fusion protein comprises a NLS at the N terminus, wherein the NLS comprises the sequence of SEQ ID NO 8, 9, or 10. In some embodiments, the fusion protein comprises a NLS at the N terminus, wherein the NLS comprises a sequence selected from the group consisting of SEQ ID NOs 11-24. In some embodiments, the fusion protein comprises a NLS at the N terminus, wherein the NLS comprises the sequence of SEQ ID NO 11, 12, 13, or 14. In some embodiments, a prime editor comprises (a) a DNA binding domain and (b) a DNA polymerase domain comprising a MMLV-RT or a mutant, fragment or variant thereof, wherein the DNA binding domain and the DNA polymerase domain are connect by a peptide linker to form a fusion protein. In some embodiments, the prime editor fusion protein comprises the DNA binding domain and the DNA polymerase domain from N terminus to C terminus. In some embodiments, the prime editor fusion protein comprises the DNA binding domain and the DNA polymerase domain from C terminus to N terminus. In some embodiments, the DNA binding domain comprises an amino acid sequence that is at least at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 14 or to any one of amino acid sequences set forth in SEQ ID NOs: 2, 6, 7, or 596-613. In some embodiments, the DNA polymerase domain comprises a MMLVRT5M variant. In some embodiments, the DNA polymerase comprises a MMLV RT variant having one or more of D524N, L435K, Y133R, Y271R amino acid substitution as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the DNA polymerase comprises a MMLV RT variant having one or more of D200N, T306K, W313F, T330P, and L603W amino acid substitution as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the DNA polymerase comprises a MMLV RT G504X truncation variant, a MMLV RT L478 truncation variant, a MMLV RT K478X truncation variant, a MMLV RT M428X truncation variant, a MMLV RT T328X truncation variant, a MMLV RT R278X truncation variant, In some embodiments, the DNA polymerase domain comprises an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 67 or to any one of amino acid sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623. In some embodiments, the peptide linker connecting the DNA binding domain and the DNA polymerase domain comprises an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411. In some embodiments, the peptide linker comprises a sequence having at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 289-311. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to SEQ ID NO: 302. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to SEQ ID NO: 302. In some embodiments, a prime editor comprises a peptide linker comprising an amino acid sequence that comprises an amino acid sequence of SEQ ID NO: 302. In some embodiments, the prime editor further comprises one or more NLS comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 2 or to any one of amino acid sequences set forth in SEQ ID NOs: 8-24, or 621 wherein the NLS is fused or linked (e.g., via a linker comprising an amino acid sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411) to the C-terminus or N terminus of the DNA binding domain or the DNA polymerase domain.

[0128] In some embodiments, a prime editor polypeptide comprises a DNA binding domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 14 or to any one of amino acid sequences set forth in SEQ ID NOs: 2, 6, 7, or 596-613, further comprising a DNA polymerase domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 67 or to any one of amino acid sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623 and optionally wherein the DNA binding domain and the DNA polymerase domain are fused or linked by a peptide linker having an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411 and optionally further comprises one or more NLS comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 2 or to any one of amino acid sequences set forth in SEQ ID NOs: 8-23, or 621 wherein the NLS is fused or linked (e.g., via a linker comprising an amino acid sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 3 or to any one of amino acid sequences set forth in SEQ ID NOs: 286-411) to the C-terminal or N terminal of the DNA binding domain or the DNA polymerase domain.

[0129] In some embodiments, a prime editor may comprise a DNA binding domain having an amino acid sequence that is selected from any of the amino acid sequence selected from 2, 6, 7, or 596-613, a DNA polymerase domain having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623, and optionally a linker having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 286-411. In some embodiments, a prime editor further comprises one or more nuclear localization sequence (NLS) having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 8-23, or 621 or described herein. In some embodiments, the NLS is fused to the N-terminus of a DNA polymerase domain described herein. In some embodiments, the NLS is fused to the C-terminus of the DNA polymerase domain. In some embodiments, the NLS is fused to the N- terminus or the C-terminus of a DNA binding domain. In some embodiments, a linker sequence is disposed between the NLS and a domain of the prime editor, e.g., a linker comprising an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 286-411.

[0130] In some embodiments, a prime editor polypeptide comprises a DNA binding domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequences as set forth in SEQ ID NOs: 7, further comprising a DNA polymerase domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or

100% identical an amino acid sequence as set forth in SEQ ID NO: 5, optionally wherein the DNA binding domain and the DNA polymerase domain are fused or linked by a peptide linker having an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequence as set forth in SEQ ID NOs: 289 and optionally further comprises one or more NLS comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 2 or to any one of amino acid sequences set forth in SEQ ID NOs: 9, 10, or 11 wherein the NLS is fused or linked (e.g., via a linker comprising an amino acid sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequences recited as set forth in SEQ ID NO: 288) to the C-terminal or N terminal of the DNA binding domain or the DNA polymerase domain.

[0131] In some embodiments, a prime editor polypeptide comprises a DNA binding domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequences as set forth in SEQ ID NOs: 7, further comprising a DNA polymerase domain comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical an amino acid sequence as set forth in SEQ ID NO: 36, optionally wherein the DNA binding domain and the DNA polymerase domain are fused or linked by a peptide linker having an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequence as set forth in SEQ ID NOs: 289 and optionally further comprises one or more NLS comprising an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 2 or to any one of amino acid sequences set forth in SEQ ID NOs: 9, 10, or 11 wherein the NLS is fused or linked (e.g., via a linker comprising an amino acid sequence at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to an amino acid sequences recited as set forth in SEQ ID NO: 288) to the C-terminal or N terminal of the DNA binding domain or the DNA polymerase domain.

[0132] In some embodiments, a prime editor may comprise a DNA binding domain having an amino acid sequence as set forth in SEQ ID NO: 7, a DNA polymerase domain having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 5 or 36 and optionally a linker having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs:302 or 309. In some embodiments, a prime editor further comprises one or more nuclear localization sequence (NLS) having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 9, 10 or 11 as described herein. In some embodiments, a prime editor may comprise a DNA binding domain having an amino acid sequence as set forth in SEQ ID NO: 7, a DNA polymerase domain having an amino acid sequence as set forth in SEQ ID NOs: 5, optionally a linker having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs:288, 289, or 302 and optionally further comprises one or more nuclear localization sequence (NLS) having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 9, 10 or 11 as described herein. In some embodiments, a prime editor may comprise a DNA binding domain having an amino acid sequence as set forth in SEQ ID NO: 7, a DNA polymerase domain having an amino acid sequence as set forth in SEQ ID NOs: 36, optionally a linker having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs:288, 289, or 302 and optionally further comprises one or more nuclear localization sequence (NLS) having an amino acid sequence that is selected from any of the amino acid sequence selected from SEQ ID NOs: 9, 10 or 11 as described herein.

[0133] In some embodiments, a prime editor may comprise an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in any of the Tables 14-65 or to any one of amino acid sequences set forth in SEQ ID NOs: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, 625, 647. In some embodiments, a prime editor may comprise an amino acid sequence that is selected from any of the amino acid sequence selected from any one of the amino acid sequences recited in any of the Tables 15-65 or to any one of amino acid sequences set forth in SEQ ID NOs: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, 625, 647.

[0134] In some embodiments, the prime editor comprises an amino acid sequence that has no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 differences e.g., mutations e.g., amino acid deletions, amino acid insertions, and/or amino acid substitutions compared to any of the amino acid sequences set forth in SEQ ID NOs: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, 625, or 647. In some embodiments, the prime editor comprises an amino acid sequence that has no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 differences e.g., mutations e.g., amino acid deletions, amino acid insertions, and/or amino acid substitutions compared to any of the amino acid sequences listed in any one of the Tables 15-65. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, 625, or 647 (Tables 15-65). In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 25, 34, 35, 77, 78, 85, 86, 620, 622, 624, 625, or 647. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 25, 624, or 625. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 34, 35, 647. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 77, 78, or 620. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences set forth in SEQ ID NOs: 85, 86, or 622. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences listed in any of the tables 15-65. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences listed in any of the tables 15-17. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences listed in Table 15. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences listed in Table 16. In some embodiments, the prime editor comprises an amino acid sequence identical to any one of the sequences listed in Table 17. In some embodiments, the prime editor comprises an amino acid sequence that lacks an N-terminus methionine compared to a corresponding prime editor sequence selected from any one of the sequences set forth in SEQ ID NO: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, or 625 (Tables 15-65).

[0135] In some embodiments, a prime editor comprises a fusion protein comprising the structure: N-Cas9 nickase-Peptide linker-RT-C. In some embodiments, a prime editor comprises a fusion protein comprising the structure: N-Cas9 nickase-Peptide linker-MMLV RT variant-C. In some embodiments, the Cas9 nickase comprises a mutation in the HNH domain and comprises an active RuvC domain. In some embodiments, the Cas9 nickase comprises a H840A mutation in the HHN domain. In some embodiments, the MMLV RT variant is MMLVRT$_{5M}$. In some embodiments, the MMLV RT variant is truncated between positions corresponding to positions 504 and 505 as compared to MMLVRT$_{5M}$. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 286-411. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID Nos 302. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID 309. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 302. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 309. In some embodiments, the prime editor comprises a fusion protein comprising at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 78, 105, 117, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, and 227. In some embodiments, the prime editor comprises a fusion protein comprising a sequence selected from the group consisting of SEQ ID Nos 78, 105, 117, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, and 227. In some embodiments, the prime editor comprises a fusion protein comprising at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 86, 111, 122, 128, 134, 140, 146, 152, 158, 164, 170, 176, 182, 188, 194, 200, 206, 212, 218, 224, and 230. In some embodiments, the prime editor comprises a fusion protein comprising a sequence selected from the group consisting of SEQ ID Nos 86, 111, 122, 128, 134, 140, 146, 152, 158, 164, 170, 176, 182, 188, 194, 200, 206, 212, 218, 224, and 230. In some embodiments, the prime editor comprises a fusion protein that comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 78. In some embodiments, the prime editor comprises a fusion protein comprising the sequence of SEQ ID NO: 78. In some embodiments, the prime editor comprises a fusion protein that comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 86. In some embodiments, the prime editor comprises a fusion protein comprising the sequence of SEQ ID NO: 86.

[0136] In some embodiments, a prime editor comprises a fusion protein comprising the structure: N-terminal NLS-Cas9 nickase-Peptide linker-RT-C-terminal NLS. In some embodiments, a prime editor comprises a fusion protein comprising the structure: Cas9 nickase-peptide linker-MMLV RT variant. In some embodiments, the Cas9 nickase comprises a mutation in the HNH domain and comprises an active RuvC domain. In some embodiments, the Cas9 nickase comprises a H840A mutation in the HHN domain. In some embodiments, the MMLV RT variant is MMLVRT$_{5M}$. In some embodiments, the MMLV RT variant is truncated between positions corresponding to positions 504 and 505 as compared to MMLVRT$_{5M}$. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 286-411. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID Nos 302. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID 309. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 302. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 309. In some embodiments, the N-terminal NLS or the C-terminal comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID Nos 11-24 and 621. In some embodiments, the N-terminal NLS comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID Nos 8-10 and 621. In some embodiments, the N-terminal NLS comprises a sequence selected from SEQ ID Nos 8-10 and 621. In some embodiments, the C-terminal NLS comprises the sequence of SEQ ID NO: 8. In some embodiments, the C-terminal NLS comprises the sequence of SEQ ID NO: 9. In some embodiments, the C-terminal NLS comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID Nos 11-24. In some embodiments, the C-terminal NLS comprises a sequence selected from SEQ ID Nos 11-24. In some embodiments, the C-terminal NLS comprises the sequence of SEQ ID NO: 11. In some embodiments, the C-terminal NLS comprises the sequence of SEQ ID NO: 24. In some embodiments, the prime editor comprises a fusion protein comprising at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 77, 93, 104, 620, and 116. In some embodiments, the prime editor comprises a fusion protein comprising a sequence selected from the group consisting of SEQ ID Nos 77, 93, 104, 620, and 116. In some embodiments, the prime editor comprises a fusion protein comprising at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 85, 96, 622, and 110. In some embodiments, the prime editor comprises a fusion protein comprising a sequence selected from the group consisting of SEQ ID Nos 85, 96, 622, and 110. In some embodiments, the prime editor comprises a fusion protein that comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 77. In some embodiments, the prime editor comprises a fusion protein comprising the sequence of SEQ ID NO: 77 or 620. In some embodiments, the prime editor comprises a fusion protein that comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 85 or 622. In some embodiments, the prime editor comprises a fusion protein comprising the sequence of SEQ ID NO: 85 or 622.

Prime Editor Nucleotide Polymerase Domain

[0137] In some embodiments, a prime editor comprises a polypeptide domain (e.g., a DNA polymerase domain) comprising a DNA polymerase activity. In some embodiments, the prime editor comprises a polypeptide that comprises a DNA polymerase domain. In some embodiments, a prime editing composition comprises a polynucleotide that encodes a polymerase domain, e.g., a DNA polymerase domain. In some embodiments, a prime editor comprises a nucleotide polymerase domain, *e.g.,* a DNA polymerase domain. In some embodiments, the DNA polymerase domain can be a wild-type DNA polymerase domain, a full-length DNA polymerase protein domain, or can be a functional mutant, a functional variant, or a functional fragment thereof. In some embodiments, the DNA polymerase domain is a template dependent DNA polymerase domain. For example, the DNA polymerase can rely on a template polynucleotide strand, *e.g.,* the editing template sequence, for new strand DNA synthesis. In some embodiments, the prime editor comprises a DNA polymerase domain that is a DNA-dependent DNA polymerase. For example, a prime editor having a DNA-dependent DNA polymerase can synthesize a new single stranded DNA using a PEgRNA editing template that comprises a DNA sequence as a template. In such cases, the PEgRNA is a chimeric or hybrid PEgRNA, and comprising an extension arm comprising a DNA strand. In some embodiments, the chimeric or hybrid PEgRNA can comprise an RNA portion (including the spacer and the gRNA core) and a DNA portion (the extension arm comprising the editing template that includes a strand of DNA).

[0138] In some embodiments, the prime editor comprises a DNA polymerase domain that is a RNA-dependent DNA polymerase. In some embodiments, the DNA polymerase domain can be a wild type polymerase, for example, from eukaryotic, prokaryotic, archaeal, or viral organisms. In some embodiments, the DNA polymerase domain is a modified DNA polymerase, for example, a wild-type DNA polymerase that is modified by genetic engineering, mutagenesis, or directed evolution-based processes.

[0139] In some embodiments, the DNA polymerase is a bacteriophage polymerase, for example, a T4, T7, or phi29 DNA polymerase. In some embodiments, the DNA polymerase is an archaeal polymerase, for example, pol I type archaeal polymerase or a pol II type archaeal polymerase. In some embodiments, the DNA polymerase comprises a thermostable archaeal DNA polymerase. In some embodiments, the DNA polymerase comprises a eubacterial DNA polymerase, for example, Pol I, Pol II, or Pol III polymerase. In some embodiments, the DNA polymerase is a Pol I family DNA polymerase. In some embodiments, the DNA polymerase comprises is a E.coli Pol I DNA polymerase. In some embodiments, the DNA polymerase is a Pol II family DNA polymerase. In some embodiments, the DNA polymerase is a Pyrococcus furiosus (Pfu) Pol II DNA polymerase. In some embodiments, the DNA Polymerase is a Pol IV family DNA polymerase. In some embodiments, the DNA polymerase is a E.coli Pol IV DNA polymerase.

[0140] In some embodiments, the DNA polymerase is an eukaryotic DNA polymerase. In some embodiments, the DNA polymerase is a Pol-beta DNA polymerase, a Pol-lambda DNA polymerase, a Pol-sigma DNA polymerase, or a Pol-mu DNA polymerase. In some embodiments, the DNA polymerase is a Pol-alpha DNA polymerase. In some embodiments, the DNA polymerase is a POLA1 DNA polymerase. In some embodiments, the DNA polymerase is a POLA2 DNA polymerase. In some embodiments, the DNA polymerase is a Pol-delta DNA polymerase. In some embodiments, the DNA polymerase is a POLD1 DNA polymerase. In some embodiments, the DNA polymerase is a POLD2 DNA polymerase. In some embodiments, the DNA polymerase is a human POLD1 DNA polymerase. In some embodiments, the DNA polymerase is a human POLD2 DNA polymerase. In some embodiments, the DNA polymerase is a POLD3 DNA polymerase. In some embodiments, the DNA polymerase is a POLD4 DNA polymerase. In some embodiments, the DNA polymerase is a Pol-epsilon DNA polymerase. In some embodiments, the DNA polymerase is a POLE1 DNA polymerase. In some embodiments, the DNA polymerase is a POLE2 DNA polymerase. In some embodiments, the DNA polymerase is a POLE3 DNA polymerase. In some embodiments, the DNA polymerase is a Pol-eta (POLH) DNA polymerase. In some embodiments, the DNA polymerase is a Pol-iota (POLI) DNA polymerase. In some embodiments, the DNA polymerase is a Pol-kappa (POLK) DNA polymerase. In some embodiments, the DNA polymerase is a Rev1 DNA polymerase. In some embodiments, the DNA polymerase is a human Rev1 DNA polymerase. In some embodiments, the DNA polymerase is a viral DNA-dependent DNA polymerase. In some embodiments, the DNA polymerase is a B family DNA polymerases. In some embodiments, the DNA polymerase is a herpes simplex virus (HSV) UL30 DNA polymerase. In some embodiments, the DNA polymerase is a cytomegalovirus (CMV) UL54 DNA polymerase.

[0141] In some embodiments, the DNA polymerase is an archaeal polymerase. In some embodiments, the DNA polymerase is a Family B/pol I type DNA polymerase. For example, in some embodiments, the DNA polymerase is a homolog of Pfu from Pyrococcus furiosus. In some embodiments, the DNA polymerase is a pol II type DNA polymerase. For example, in some embodiments, the DNA polymerase is a homolog of P. furiosus DP1/DP2 2-subunit polymerase. In some embodiments, the DNA polymerase lacks 5′ to 3′ nuclease activity. Suitable DNA polymerases (pol I or pol II) can be derived from archaea with optimal growth temperatures that are similar to the desired assay temperatures.

[0142] In some embodiments, the DNA polymerase is a thermostable archaeal DNA polymerase. In some embodiments, the thermostable DNA polymerase is isolated or derived from Pyrococcus species (furiosus, species GB-D, woesii, abysii, horikoshii), Thermococcus species (kodakaraensis KOD1, litoralis, species 9 degrees North-7, species JDF-3, gorgonarius), Pyrodictium occultum, and Archaeoglobus fulgidus.

[0143] Polymerases may also be from eubacterial species. In some embodiments, the DNA polymerase is a Pol I family DNA polymerase. In some embodiments, the DNA polymerase is an E.coli Pol I DNA polymerase. In some embodiments, the DNA polymerase is a Pol II family DNA polymerase. In some embodiments, the DNA polymerase is a Pyrococcus furiosus (Pfu) Pol II DNA polymerase. In some embodiments, the DNA Polymerase is a Pol III family DNA polymerase. In some embodiments, the DNA Polymerase is a Pol IV family DNA polymerase. In some embodiments, the DNA polymerase is an E.coli Pol IV DNA polymerase. In some embodiments, the Pol I DNA polymerase is a DNA polymerase functional variant that lacks or has reduced 5′ to 3′ exonuclease activity. Suitable thermostable pol I DNA polymerases can be isolated from a variety of thermophilic eubacteria, including Thermus species and Thermotoga maritima such as Thermus aquaticus (Taq), Thermus thermophilus (Tth) and Thermotoga maritima (Tma UlTma).

[0144] In some embodiments, a prime editor comprises an RNA-dependent DNA polymerase domain, for example, a reverse transcriptase (RT). In some embodiments, the DNA polymerase domain is an RNA-dependent DNA polymerase domain, for example, a reverse transcriptase (RT). In some embodiments, the DNA polymerase domain is a reverse transcriptase (RT) domain, for example, a reverse transcriptase (RT). In some embodiments, the reverse transcriptase (RT), or a RT domain is a M-MLV RT (e.g., a wild-type M-MLV RT, a reference M-MLV RT, a functional mutant, a functional variant, or a functional fragment thereof). An RT or an RT domain can be a wild-type RT domain, a full-length RT domain, or may be a functional mutant, a functional variant, or a functional fragment thereof. An RT or an RT domain of a prime editor can comprise a wild-type RT a full length RT, a functional mutant, a functional variant, or a functional fragment thereof or can be engineered or evolved to contain specific amino acid substitutions, truncations, or variants. An engineered RT can comprise sequences or amino acid changes different from a naturally occurring RT or a corresponding reference RT. In some embodiments, the engineered RT can have improved reverse transcription activity over a naturally occurring RT or RT domain. In some embodiments, the engineered RT can have improved features over a naturally occurring RT, for example, improved thermostability, reverse transcription efficiency, or target fidelity. In some embodiments, a prime editor comprising the engineered RT has improved prime editing efficiency over a prime editor having a reference naturally occurring RT.

[0145] In some embodiments, the reverse transcriptase domain or RT can be between 200 and 800 amino acids in length, between 300 and 700 amino acids in length, or at least 400 and 600 amino acids in length. In some embodiments, the reverse transcriptase domain or RT can be at least 200 amino acids in length, at least 300 amino acids in length, at least 400 amino acids in length, at least 500 amino acids in length, or at least 600 amino acids in length. In some embodiments, the reverse transcriptase domain or RT is 250 amino acids in length. In some embodiments, the reverse transcriptase domain or RT is 350 amino acids in length. In some embodiments, the reverse transcriptase domain or RT is 450 amino acids in length. In some embodiments, the reverse transcriptase domain or RT is 550 amino acids in length. In some embodiments, the reverse transcriptase domain or RT is 650 amino acids in length.

[0146] In some embodiments, a prime editor comprises a eukaryotic RT, for example, a yeast, drosophila, rodent, or primate RT. In some embodiments, the prime editor comprises a Group II intron RT, for example, a. *Geobacillus stearothermophilus* Group II Intron (GsI-IIC) RT or a Eubacterium rectale group II intron (Eu.re.I2) RT. In some embodiments, the prime editor comprises a retron RT.

[0147] In some embodiments, a prime editor comprises a virus RT, for example, a retrovirus RT. Non-limiting examples of virus RT include Moloney murine leukemia virus (M-MLV or MLVRT); human T-cell leukemia virus type 1 (HTLV-1) RT; bovine leukemia virus (BLV) RT; Rous Sarcoma Virus (RSV) RT; human immunodeficiency virus (HIV) RT, M-MFV RT, Avian Sarcoma-Leukosis Virus (ASLV) RT, Rous Sarcoma Virus (RSV) RT, Avian Myeloblastosis Virus (AMV) RT, Avian Erythroblastosis Virus (AEV) Helper Virus MCAV RT, Avian Myelocytomatosis Virus MC29 Helper Virus MCAV RT, Avian Reticuloendotheliosis Virus (REV-T) Helper Virus REV-A RT, Avian Sarcoma Virus UR2 Helper Virus (UR2AV) RT, Avian Sarcoma Virus Y73 Helper Virus YAV RT, Rous Associated Virus (RAV) RT, and Myeloblastosis Associated Virus (MAV) RT, all of which may be suitably used in the methods and composition described herein.

[0148] In some embodiments, the prime editor comprises a wild-type M-MLV RT, a reference M-MLV RT, a functional mutant, a functional variant, or a functional fragment thereof. In some embodiments, the RT domain or a RT is a M-MLV RT (e.g., wild-type M-MLV RT, a reference M-MLV RT, a functional mutant, a functional variant, or a functional fragment thereof). In some embodiments, a reference M-MLV RT is a wild-type M-MLV RT. An exemplary sequence of a wild-type M-MLV RT is provided in SEQ ID NO:623. An exemplary sequence of a reference M-MLV RT is provided in SEQ ID NO: 1. Exemplary MMLV-RT amino acid and nucleotide sequences are disclosed in Table 67. In some embodiments, the MMLVRT variant comprises D200N, T306K, W313F, T330P, and L603W amino acid substitutions as compared to reference MMLVRT sequence SEQ ID No 1. The variant, having the sequence of SEQ ID NO: 5, is referred to here in as “MMLVRT$_{5M}$”or or “MMLVRT5M”.

[0149] In some embodiments, a prime editor comprises an RT that comprises an engineered RNase domain compared to a corresponding reference RT (e.g., a reference M-MLV RT or a wild-type M-MLV RT). In some embodiments, the RT of the prime editor comprises one or more amino acid substitutions, insertions, or deletions compared to a reference RT. In some embodiments, the RT of the prime editor is truncated compared to a corresponding reference RT (e.g., a reference M-MLV RT or a wild-type M-MLV RT). A polypeptide is “truncated” when, compared to a reference polypeptide sequence, the polypeptide lacks an end portion, for example, a N-terminal portion or a C-terminal portion. A polypeptide is truncated after amino acid position n means that the polypeptide, compared to a reference polypeptide sequence, lacks amino acids that are C-terminal to amino acid n or corresponding amino acids thereof, but retains amino acid n. In other words, “truncated after amino acid at position n” or “truncated at C terminus between positions n and n+1” refers to a truncation of a polypeptide between positions n and n+1, wherein amino acids that are C-terminal to amino acid n are deleted compared to a reference polypeptide sequence. In some embodiments, a polypeptide truncated after amino acid n, when compared to a reference polypeptide sequence, comprises amino acid n and all amino acids N terminal to amino acid n and lacks amino acids C terminal to amino acid n, or corresponding amino acids thereof.

[0150] In some embodiments, a polypeptide truncated before amino acid n, or a polypeptide truncated at N terminus between positions n-1 and n, when compared to a reference polypeptide sequence, comprises amino acid n and all amino acids C terminal to amino acid n and lacks amino acids N terminal to amino acid n, or corresponding amino acids thereof. In some embodiments, a truncated polypeptide is truncated at the N terminus, at the C terminus, or both the N terminus and the C terminus. A C terminal truncated polypeptide may also be truncated at its N terminus. An N terminal truncated polypeptide may also be truncated at its C terminus. In some embodiments, the RT of the prime editor consists of 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15% or 10% of amino acids of a corresponding reference RT. In some embodiments, the prime editor comprises a truncated RT compared to a corresponding reference RT, wherein the truncation is at the N-terminus of the RT. In some embodiments, the prime editor comprises a truncated RT compared to a corresponding reference RT, wherein the truncation is at the C-terminus of RT. In some embodiments, the prime editor comprises a truncated RT compared to a corresponding reference RT, wherein the truncation is within the middle of corresponding reference RT. In some embodiments, the prime editor comprises a truncated RT compared to a corresponding referenceRT, wherein the RT domain is truncated at both the N-terminus and the C-terminus. In some embodiments, the prime editor comprises a truncated RT compared to a corresponding reference RT, wherein the RT is truncated at the N-terminus, the C-terminus, and/or the middle of the RT referenced by the corresponding RT. In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550 or more amino acids are truncated at the N-terminus of the RT in a prime editor compared to a corresponding reference RT. In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550 or more amino acids are truncated at the C-terminus of the RT in a prime editor compared a corresponding reference RT. In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 1. In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 5.

[0151] In some embodiments, a prime editor comprises an RT that is a Moloney murine leukemia virus (M-MLV) reverse transcriptase (M-MLV RT). In some embodiments, the M-MLV RT of the prime editor comprises one or more amino acid substitutions, insertions, or deletions compared to a wild-type M-MLV RT, a reference M-MLV RT, or $\mathrm{MMLVRT_{5M}}$. In some embodiments, a prime editor comprises a truncated M-MLV RT compared to a wild-type M-MLV RT or a reference M-MLV RT or $\mathrm{MMLVRT_{5M}}$. In some embodiments, the M-MLV RT of the prime editor consists of 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15% or 10% of amino acids of a wild-type M-

MLV RT or a reference M-MLV RT or MMLVRT$_{5M}$. In some embodiments, the M-MLV RT of the prime editor is truncated at the N-terminus compared to a wild-type M-MLV RT or a reference M-MLV RT, or MMLVRT$_{5M}$. In some embodiments, the M-MLV RT of the prime editor is truncated at the C-terminus compared to a wild-type M-MLV RT or a reference M-MLV RT, or MMLVRT$_{5M}$. In some embodiments, the M-MLV RT of the prime editor is truncated compared to a wild-type M-MLV RT or a reference M-MLV RT, wherein the truncation is within the middle of the RT referenced by a wild-type M-MLV RT or a reference M-MLV RT, or MMLVRT$_{5M}$. In some embodiments, the M-MLV RT of the prime editor comprises a truncated M-MLV RT compared to a wild-type M-MLV RT or a reference M-MLV RT,, or MMLVRT$_{5M}$ wherein RT is truncated at both the N-terminus and the C-terminus. In some embodiments, the M-MLV RT of the prime editor comprises a truncated M-MLV RT compared to a wild-type M-MLV RT or a reference M-MLV RT, or or MMLVRT$_{5M}$, wherein the RT is truncated at the N-terminus, the C-terminus, and/or the middle of the RT as reference by a wild-type M-MLVRT or a reference M-MLV RT., or MMLVRT$_{5M}$

[0152] In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, or more amino acids are truncated at the N-terminus of the M-MLV RT in a prime editor compared to a wild-type M-MLV RT or a reference M-MLV RT or MMLVRT$_{5M}$. In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550 or more amino acids are truncated at the C-terminus of the M-MLV RT in a prime editor compared a wild-type M-MLV RT or a reference M-MLV RT or MMLVRT$_{5M}$.

[0153] In some embodiments, a prime editor comprises a reverse transcriptase (RT) that comprises a RNase domain. For example, in some embodiments, the RT of the prime editor is a virus RT domain that comprises a RNase domain. In some embodiments, the RT of the prime editor is a virus RT domain that comprises a RNase H domain. In some embodiments, the RT of the prime editor comprises a RNase H domain having 5' and/or 3' ribonuclease activity. In some embodiments, the RT of the prime editor comprises a RNase H domain having 3' and/or 5' nuclease activity toward the RNA strand when contacted with a DNA-RNA hybrid double strand.

[0154] In some embodiments, a prime editor comprises an RT that comprises an engineered RNase domain compared to a corresponding reference RT. In some embodiments, a prime editor comprises a RT that comprises an engineered RNase H domain compared to a corresponding reference RT. In some embodiments, the RT of the prime editor comprises one or more amino acid substitutions, insertions, or deletions in the RNase H domain compared to a corresponding. In some embodiments, the one or more amino acid substitutions, insertions, or deletions in the RNase H domain reduces or abolishes RNase activity of the RNase H domain. In some embodiments, the RT of the prime editor comprises a RNase H domain that has decreased or abolished RNase activity. In some embodiments, the RT of the prime editor comprises an inactivated RNase H domain. In some embodiments, the RT of the prime editor comprises one or more amino acid substitutions in a RNase H domain that decrease or abolish activity of the RNase H domain as compared to a corresponding reference RT. In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT. In some embodiments, the truncation in the RNase H domain decreases or abolishes RNase activity of the RNase H domain. In some embodiments, the RT of the prime editor comprises a RNase H domain that consists of 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15% or 10% of amino acids of a corresponding wild-type RNase H domain (e.g., a wild-type RNase H domain from a reference M-MLV RT or a wild-type M-MLV RT or MMLVRT$_{5M}$). In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 1. In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 5.

[0155] In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT , wherein the truncation is at the N-terminus of the RNase H domain. In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT , wherein the truncation is at the C-terminus of the RNase H domain. In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT , wherein the truncation is within the middle of the RNase H domain referenced by the RNase H domain of the corresponding reference RT . In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT , wherein the truncated RNase H domain is truncated at both the N-terminus and the C-terminus of the RNase H domain. In some embodiments, the RT of the prime editor comprises a truncated RNase H domain compared to a corresponding reference RT , wherein the truncated RNase H domain is truncated at the N-terminus, the C-terminus, and/or the middle of the RNase H domain referenced by the RNase H domain of the corresponding reference RT . In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550 or more amino acids are truncated at the N-terminus of the RNase H domain of the RT in a prime editor compared to the RNase H domain of a corresponding reference RT . In some embodiments, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550 or more amino acids are truncated at the C-terminus of the RNase H domain of the RT in a prime editor compared to the RNase H domain of a corresponding reference RT . In some embodiments, the RT of the prime editor lacks a RNase H domain. In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 1. In some embodiments, a reference RT sequence has the sequence of SEQ ID NO: 5.

[0156] In some embodiments, a prime editor comprises an RT that is a Moloney murine leukemia virus (M-MLV) reverse transcriptase (M-MLV RT) that comprises an RNase H domain. In some embodiments, the M-MLV RT of the prime editor comprises one or more amino acid substitutions, insertions, or deletions in the RNase H domain compared to the RNase H domain of a wild-type M-MLV RT. In some embodiments, the one or more amino acid substitutions, insertions, or deletions in the RNase H domain reduces or abolishes RNase activity of the RNase H domain. In some embodiments, the M-MLV RT of the prime editor comprises a RNase H domain that has decreased or abolished RNase activity compared to a RNase H domain in a wild-type M-MLV RT. In some embodiments, the M-MLV RT of the prime editor comprises an inactivated RNase H domain.

[0157] In some embodiments, a prime editor comprises a M-MMLV RT comprising one or more of amino acid substitutions P51$, S67, E69$, L139$, T197$, D200$, H204$, F209$, E302$, T306$, F309$, W313$, T330$, L345$, L435$, N454$, D524$, E562$, D583$, H594$, L603$, E607$, or D653$ as compared to a reference M-MMLV RT as set forth in SEQ ID NO:1, where $ is any amino acid other than the wild-type amino acid.. In some embodiments, the prime editor comprises a M-MMLV RT comprising one or more of amino acid substitutions P51L, S67K, E69K, L139P, T197A, D200N, H204R, F209N, E302K, E302R, T306K, F309N, W313F, T330P, L345G, L435G, N454K, D524G, E562Q, D583N, H594Q, L603W, E607K, and D653N as compared to a reference M-MMLV RT as set forth in SEQ ID NO: 1. In some embodiments, the prime editor comprises a M-MLV RT comprising one or more amino acid substitutions D200N, T330P, L603W, T306K, and W313F as compared to a reference M-MMLV as set forth in SEQ ID NO:1. In some embodiments, the prime editor comprises a M-MLV RT comprising amino acid substitutions D200N, T330P, L603W, T306K, and W313F as compared to a reference M-MMLV RT as set forth in SEQ ID NO:1.

[0158] In some embodiments, a prime editor comprising a reverse transcriptase harboring the D200N, T330P, L603W, T306K, and W313F as compared to the reference M-MMLV RT set forth in SEQ ID NO: 1, maybe referred to as a "PE2" prime editor, and the corresponding prime editing system a PE2 prime editing system. In some embodiments, a prime editor comprises a M-MMLV RT comprising one or more of amino acid substitutions D200N, T306K, W313F, T330P, L603W, or any combination thereof as compared to the reference M-MMLV RT as set forth in SEQ ID NO: 1, or SEQ ID NO: 623, where X is any amino acid other than the wild-type amino acid. In some embodiments, a prime editor comprises a M-MMLV RT comprising one or more of amino acid substitutions Y134X, Y272X, L435X, D524X, or any combination thereof as compared to the reference M-MMLV RT as set forth in SEQ ID NO: 1, or SEQ ID NO: 623, where X is any amino acid other than the wild-type amino acid. In some embodiments, a prime editor comprises a M-MMLV RT comprising one or more of amino acid substitutions Y134R, Y272R, L435K, D524N, or any combination thereof as compared to the reference M-MMLV RT as set forth in SEQ ID NO: 1, or SEQ ID NO: 623, where X is any amino acid other than the wild-type amino acid

[0159] In some embodiments, the MMLVRT variant comprises one or more of D200N,T306K,W313F,T330P, and L603W amino acid substitutions as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the MMLVRT variant comprises D200N, T306K, W313F, T330P, and L603W amino acid substitutions as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the MMLV RT variant comprises one or more of D524N, L435K, Y133R, Y271R amino acid substitution as compared to reference MMLVRT sequence SEQ ID No 1. In some embodiments, the MMLV RT variant has one or more amino acid deletion compared to the reference MMLVRT sequence SEQ ID No 1. For example, in some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1 (such truncation may be referred to herein as a 504X, or G504X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1 (a L478X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus at any amino acid position between positions 478 and 505 as set forth in SEQ ID NO:1. In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 365 and 366 as set forth in SEQ ID NO: 1 (a P365X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 278 and 279 as set forth in SEQ ID NO: 1 (a R278X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 328 and 329 as set forth in SEQ ID NO: 1 (a T328X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 378 and 379 as set forth in SEQ ID NO: 1 (a K478X truncation). In some embodiments, the MMLV RT variant is truncated at the C terminus between positions corresponding to amino acids 428 and 429 as set forth in SEQ ID NO: 1 (a M428X truncation). In some embodiments, the truncated M-MLV RT variants further comprise a D200$, T306$, W313$, and/or T330$ amino acid substitution compared to a corresponding reference M-MLV RT as set forth in SEQ ID NO: 1, wherein $ is any amino acid other than the original amino acid. In some embodiments, the truncated M-MLV RT variants further comprise a D200N, T306K, W313F, and/or T330P amino acid substitution compared to a corresponding reference M-MLV RT as set forth in SEQ ID NO: 1. In some embodiments, a prime editor polypeptide comprises a DNA polymerase domain (e.g., a MMLV-RT) comprising an amino acid sequence that is at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of the amino acid sequences recited in Table 67 or to any one of amino acid sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623. In some embodiments, a prime editor polypeptide comprises a MMLV-RT domain comprising an amino acid sequence SEQ ID NOs: 5. In some embodiments, a prime editor polypeptide comprises a C-terminal truncated MMLV-RT domain having the amino acid sequence of SEQ ID NO: 36.

[0160] In some embodiments, a M-MLV RT comprises an amino acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of the sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 1. In some embodiments, the M-

MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 623. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 623. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 4. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 5. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 36. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 45. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 54. In some embodiments, the M-MLV RT comprises an amino acid sequence set forth in SEQ ID NO: 63. In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA polymerase domain that comprises an amino acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of the sequences set forth in SEQ ID NOs: 1, 4, 5, 36, 45, 54, 63, or 623.

[0161] In some embodiments, an RT variant may be a functional fragment of a corresponding RT (e.g., a M-MLV RT) that has 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 21, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, or up to 100, or up to 200, or up to 300, or up to 400, or up to 500 or more amino acid changes compared to a corresponding RT, e.g., (e.g., a M-MLV RT). In some embodiments, the RT variant comprises a fragment of a corresponding RT, e.g., a (e.g., a M-MLV RT), such that the fragment is about 70% identical, about 80% identical, about 90% identical, about 95% identical, about 96% identical, about 97% identical, about 98% identical, about 99% identical, about 99.5% identical, or about 99.9% identical to the corresponding fragment of the corresponding RT. In some embodiments, the fragment is 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% identical, 96%, 97%, 98%, 99%, or 99.5% of the amino acid length of a corresponding RT (e.g., a M-MLV RT).

[0162] In some embodiments, the RT functional fragment is at least 100 amino acids in length. In some embodiments, the fragment is at least 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, or up to 600 or more amino acids in length.

[0163] In some embodiments, a prime editor comprises a eukaryotic RT, for example, a yeast, drosophila, rodent, or primate RT. In some embodiments, the prime editor comprises a Group II intron RT, for example, a. *Geobacillus stearothermophilus* Group II Intron (GsI-IIC) RT or a Eubacterium rectale group II intron (Eu.re.I2) RT. In some embodiments, the prime editor comprises a retron RT.

[0164] In some embodiments, a M-MLV RT of a prime editor comprises a Y133$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y. In some embodiments, the M-MLV RT of the prime editor comprises a Y133R amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0165] In some embodiments, a M-MLV RT of a prime editor comprises a Y271$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y.

[0166] In some embodiments, the M-MLV RT of the prime editor comprises a Y271R amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0167] In some embodiments, a M-MLV RT of a prime editor comprises a D524$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for D. In some embodiments, the M-MLV RT of the prime editor comprises a D524N amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0168] In some embodiments, a M-MLV RT of a prime editor comprises a L435$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for L. In some embodiments, the M-MLV RT of the prime editor comprises a L435K amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0169] In some embodiments, a M-MLV RT of a prime editor comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, the M-MLV RT of the prime editor comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0170] In some embodiments, a M-MLV RT of a prime editor comprises a Y133$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y.

[0171] In some embodiments, the M-MLV RT of the prime editor comprises a Y133R amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0172] In some embodiments, a M-MLV RT of a prime editor comprises a Y271$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y.

[0173] In some embodiments, the M-MLV RT of the prime editor comprises a Y271R amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0174] In some embodiments, a prime editor comprises a truncated M-MLVRT, wherein the M-MLVRT is truncated at C terminus between positions corresponding to amino acids 478 and 479, 478 and 479, 479 and 480, 480 and 481, 481 and 482, 482 and 483, 483 and 484, 484 and 485, 485 and 486, 486 and 487, 487 and 488, 488 and 489, 489 and 490, 490 and 491, 491 and 492, 492 and 493, 493 and 494, 494 and

495, 495 and 496, 496 and 497, 497 and 498, 498 and 499, 499 and 500, 500 and 501, 501 and 502, 502 and 503, 503 and 504, or 504 and 505 as set forth in SEQ ID NO: 1. In some embodiments, a prime editor comprises a truncated M-MLVRT, wherein the M-MLVRT is truncated after any amino acid that is C-terminal to amino acid 504 as set for the in SEQ ID NO: 1. In some embodiments, a prime editor comprises a truncated M-MLVRT, wherein the M-MLVRT is truncated after any amino acid that is C-terminal to amino acid 478 as set for the in SEQ ID NO: 1. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 505-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1 SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 504 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (G504 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 505-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 504 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0175] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions C terminal to amino acid 365 of the M-MLV RT are deleted as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 365 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (P365 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C terminal to amino acid 365 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 365 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 365 and 366 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus after an amino acid between L478 and G504 compared to SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus after amino acid L478 compared to SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 428 and 429 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 378 and 379 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 366 and 367 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 328 and 329 as set forth in SEQ ID NO: 1, 5, or 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 278 and 279 as set forth in SEQ ID NO: 1, 5, or 623.

[0176] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 479-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT of the prime editor comprises a truncated RNase H domain, wherein amino acids C terminal to position 478 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, or SEQ ID NO: 623 (L478 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 479-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 478 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0177] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 429-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 428 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (M428 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 429-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 428 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0178] In some embodiments a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 379-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 378 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (K378 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 379-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 378 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0179] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 367-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 365 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (P365 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 367-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1 SEQ ID NO: 5, or SEQ IDNO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 365 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0180] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 328-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 328 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (T328 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 328-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 328 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0181] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 279-679 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids C terminal to position 278 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 (R278 truncation). In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 279-679 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1 SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids C- terminal to position 278 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0182] In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids at positions 1-22 of the M-MLV RT are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, a prime editor comprises a truncated M-MLV RT, wherein amino acids N terminal to position 24 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids 1-22 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. In some embodiments, the M-MLV RT (e.g., a truncated M-MLV RT) comprises a deletion of amino acids N- terminal to position 24 relative to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0183] In some embodiments, a prime editor comprises an RT domain having one or more amino acid substitutions and/or one or more amino acid deletions compared a corresponding reference RT or a wild-type RT. In some embodiments, a prime editor comprises a M-MLV RT that has one or more amino acid substitutions and one or more amino acid deletions compared to a wild-type M-MLV RT or a reference RT (e.g., SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623). In some embodiments, the M-MLV RT comprises an amino acid sequence that comprises one or more amino acid substitutions and/or one or more amino acid deletions compared to a reference M-MLV RT set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623. Any one of the amino acid truncations, deletions, and substitutions described herein or known in the art can be combined in a prime editor RT, *e.g.*, a M-MLV RT. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0184] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 479-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 479-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0185] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 429-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 429-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0186] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 379-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 379-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0187] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0188] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 328-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 328-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0189] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 279-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 279-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0190] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$, Y271$, L435$, and/or D524$ amino acid substitution, and wherein amino acids at positions 1-22 are truncated as compared to a reference M-MLV RT as set forth SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 1-22 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0191] In some embodiments, a prime editor comprises a M-MLV RT that comprises a L435$ amino acid substitution, and wherein amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for L. In some embodiments, a prime editor comprises a M-MLV RT that comprises a L435K amino acid substitution, and wherein amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0192] In some embodiments, a prime editor comprises a M-MLV RT that comprises a L435$ amino acid substitution, and wherein amino acids at positions 1-22 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for L. In some embodiments, a prime editor comprises a M-MLV RT that comprises a L435K amino acid substitution, and wherein amino acids at positions 1-22 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0193] In some embodiments, a prime editor comprises a M-MLV RT, wherein the M-MLV RT comprises a L435$ amino acid substitution, and wherein amino acids at positions 1-22 and amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for L. In some embodiments, a prime editor comprises a M-MLV RT, wherein the M-MLV RT comprises a L435K amino acid substitution, and wherein amino acids at positions 1-22 and amino acids at positions 505-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0194] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$ amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0195] In some embodiments, a prime editor comprises a M-MLV RT comprises a Y271$ amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y271R amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0196] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133$ and a Y271$ amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for Y. In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R and a Y271R amino acid substitution, and wherein amino acids at positions 367-679 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0197] In some embodiments, a prime editor comprises a M-MLV RT that comprises a Y133R, Y271R, L435K, and/or D524N amino acid substitution, and wherein amino acids at positions 1-22 are truncated as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid except for the original amino acid.

[0198] In some embodiments, a M-MLV RT comprises a deletion of amino acids C-terminal to position P365, a Y133$ amino acid substitution, and/or a Y271$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, wherein $ is any amino acid other than the original. In some embodiments, a M-MLV RT comprises a deletion of amino acids 366-679, a Y133$ amino acid substitution, and/or a Y271$ amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original. In some embodiments, a M-MLV RT comprises a deletion of amino acids C-terminal to position P365, a Y133R amino acid substitution, and/or a Y271R amino acid substitution as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original. In some embodiments, a M-MLV RT comprises a deletion of amino acids C-terminal to position G504, and/or a L435$ amino acid substitution compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original. In some embodiments, a M-MLV RT comprises a deletion of amino acids residues 505-679, and/or a L435$ amino acid substitution compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original. In some embodiments, the M-MLV RT comprises a deletion of amino acids C-terminal to position G504, a deletion of amino acid residues 1-22, and/or a L435$ amino acid substitution compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original. In some embodiments, a M-MLV RT comprises a deletion of amino acids residues 505-679, a deletion of N-terminus amino acid residues 1-22, and/or a L435$ amino acid substitution compared to a reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623 wherein $ is any amino acid other than the original.

[0199] In some embodiments, a DNA polymerase domain, e.g., a reverse transcriptase domain, for example a M-MLV RT can comprise one or more mutations (e.g., one or more amino acid substitution, amino acid deletion, and/or amino acid insertion). Mutant reverse transcriptase can, for example, be obtained by mutating the gene or genes encoding the reverse transcriptase of interest by site-directed or random mutagenesis. In some embodiments, the mutation increases the efficiency of the DNA polymerase domain, e.g., a reverse transcriptase domain, e.g., by increasing editing efficiency, by increasing reverse transcriptase activity, and/or by increasing stability (e.g., thermostability). In some embodiments, a prime editor comprising the DNA polymerase domain comprising one or more mutations disclosed herein, can exhibit at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 100%, at least 150%, at least 200%, at least 300%, at least 400%, at least

500%, at least 600%, at least 700%, at least 800%, at least 900%, or at least 1000% increase in editing efficiency compared to a prime editor comprising a corresponding non-mutated DNA polymerase. In some embodiments, a DNA polymerase domain that is a M-MLV RT comprises one or more mutations selected from the group consisting of a P51$, a S67$, an E69$, an L139$, a T197$, a D200$, a H204$, a F209$, an E302$, a T306$, a F309$, a W313$, a T330$, an L435$, a P448$, a D449$, an N454$, a D524$, an E562$, a D583$, an H594$, an L603$, an E607$, a G615$, an H634$, a G637$, an H638$, a D653$, or an L671$ mutation relative to the reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623, where $ is any amino acid other than the wild-type amino acid. In some embodiments, a DNA polymerase domain, for example, a M-MLV RT can comprise one or more amino acid substitution selected from the group consisting of a P51L, a S67K, an E69K, an L139P, a T197A, a D200N, a H204R, a F209N, an E302K, a T306K, a F309N, a W313F, a T330P, an L435G, a P448A, a D449G, an N454K, a D524G, an E562Q, a D583N, an H594Q, an L603W, an E607K, a G615, an H634Y, a G637R, an H638G, a D653N, or an L671P relative to the reference M-MLV RT as set forth in SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 623.

[0200] In some embodiments, the engineered RT may have improved stability, reverse transcription activity over a naturally occurring RT or RT domain. In some embodiments, the engineered RT may have improved features over a naturally occurring RT, for example, improved thermostability, reverse transcription efficiency, or target fidelity. In some embodiments, a prime editor comprising the engineered RT has improved prime editing efficiency over a prime editor having a reference naturally occurring RT.

[0201] A prime editor comprising any of the engineered RTs described herein can have altered functional features compared to a reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1). In some embodiments, a prime editor comprising an engineered RT described herein has improved stability compared to a reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1). In some embodiments, a prime editor comprising an engineered RT described herein has improved thermostability compared to a reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1). In some embodiments, a prime editor comprising an engineered RT described herein has improved solubility or reduced aggregation compared to a reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1). In some embodiments, the prime editor comprising the engineered RT has improved prime editing efficiency compared to a reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1). In some embodiments, the prime editor comprising the engineered RT has increased prime editing efficiency by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 110%, at least 120%, at least 130%, at least 140%, at least 150%, at least 160%, at least 170%, at least 180%, at least 190%, at least 200%, at least 210%, at least 220%, at least 230%, at least 240%, at least 250%, at least 260%, at least 270%, at least 280%, at least 290%, at least 300% or more compared to the reference prime editor having the corresponding reference RT (e.g., or a reference RT as set forth in SEQ ID NO: 1). In some embodiments, the prime editor comprising the engineered RT has increased prime editing efficiency by at least 1.1 fold, 1.2 fold, 1.3 fold, 1.4 fold, 1.5 fold, 1.6 fold, 1.7 fold, 1.8 fold, 1.9 fold, 2 fold, 2.1 fold, 2.2 fold, 2.3 fold, 2.4 fold, 2.5 fold, 2.6 fold, 2.7 fold, 2.8 fold, 2.9 fold, 3 fold, 3.1 fold, 3.2 fold, 3.3 fold, 3.4 fold, 3.5 fold, 3.6 fold, 3.7 fold, 3.8 fold, 3.9 fold, 4 fold, 4.1 fold, 4.2 fold, 4.3 fold, 4.4 fold, 4.5 fold, 4.6 fold, 4.7 fold, 4.8 fold, 4.9 fold, 5 fold or more compared to the reference prime editor having the corresponding reference RT (e.g., a reference RT such as set forth in SEQ ID NO: 1).

Programmable DNA binding domain

[0202] In some embodiments, a prime editor comprises a polypeptide domain having DNA binding activity (e.g., a DNA binding domain). In some embodiments, a prime editor comprises a polypeptide domain having DNA binding activity (e.g., a DNA binding domain). In some embodiments, a prime editor comprises a DNA binding domain. In some embodiments, the DNA binding domain comprises an amino acid sequence that is at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical, or 100% identical to any one of amino acid sequences set forth in SEQ ID NOs: 2, 6, 7, 596-613 (Table 14). In some embodiments, the DNA-binding domain comprises an amino acid sequence that has no more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 differences e.g., mutations e.g., deletions or substitutions compared to any one of the amino acid sequences set forth in SEQ ID NOs: 2, 6, 7, 596-613. In some embodiments, the DNA binding domain comprises an amino acid sequence that lacks a N-terminus methionine compared to a corresponding DNA binding domain (e.g., a DNA binding domain set forth in any one of SEQ ID NOs: 2, 6, 7, 596-613. (Table 14). In some embodiments, the amino acid sequence of a DNA binding domain can be N-terminally modified by one or more processing enzymes, e.g., by Methionine aminopeptidases (MAP).

[0203] In some embodiments, the DNA binding domain comprises a nuclease activity, for example, an RNA-guided DNA endonuclease activity of a Cas polypeptide. In some embodiments, the DNA binding domain comprises a nuclease domain or nuclease activity. In some embodiments, the DNA binding domain comprises a nickase, or a fully active nuclease. As used herein, the term “nickase” refers to a nuclease capable of cleaving only one strand of a double-stranded DNA target. In some embodiments, the DNA binding domain is an inactive nuclease.

[0204] In some embodiments, the DNA-binding domain of a prime editor is a programmable DNA binding domain. A programmable DNA binding domain refers to a protein domain that is designed to bind a specific nucleic acid sequence, *e.g.*, a target DNA or a target RNA. In some embodiments, the DNA-binding domain is a polynucleotide programmable DNA-binding domain that can associate with a guide polynucleotide (*e.g.*, a PEgRNA) that guides the DNA-binding domain to a specific DNA sequence, *e.g.,* a search target sequence in a double stranded target DNA (e.g., the target gene). In some embodiments, the DNA-binding domain comprises a Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) Associated (Cas) protein. A Cas protein may comprise any Cas protein described herein or a functional fragment or functional variant thereof. In some embodiments, a DNA-binding domain may also comprise a zinc-finger protein domain. In other cases, a DNA-binding domain comprises a transcription activator-like effector domain (TALE). In some embodiments, the DNA-binding domain comprises a DNA nuclease. For example, the DNA-binding domain of a prime editor may comprise an RNA-guided DNA endonuclease, *e.g.,* a Cas protein. In some embodiments, the DNA-binding domain comprises a zinc finger nuclease (ZFN) or a transcription activator like effector domain nuclease (TALEN), where one or more zinc finger motifs or TALE motifs are associated with one or more nucleases, *e.g.*, a Fok I nuclease domain.

[0205] In some embodiments, the DNA-binding domain comprise a nuclease activity. In some embodiments, the DNA-binding domain of a prime editor comprises an endonuclease domain having single strand DNA cleavage activity. For example, the endonuclease domain may comprise a FokI nuclease domain. In some embodiments, the DNA-binding domain of a prime editor comprises a nuclease having full nuclease activity. In some embodiments, the DNA-binding domain of a prime editor comprises a nuclease having modified or reduced nuclease activity as compared to a wild-type endonuclease domain. For example, the endonuclease domain may comprise one or more amino acid substitutions as compared to a wild-type endonuclease domain. In some embodiments, the DNA-binding domain of a prime editor has nickase activity. In some embodiments, the DNA-binding domain of a prime editor comprises a Cas protein domain that is a nickase. In some embodiments, compared to a wild-type Cas protein, the Cas nickase comprises one or more amino acid substitutions in a nuclease domain that reduces or abolishes its double strand nuclease activity but retains DNA binding activity. In some embodiments, the Cas nickase comprises an amino acid substitution in a HNH domain. In some embodiments, the Cas nickase comprises an amino acid substitution in a RuvC domain.

[0206] In some embodiments, the DNA-binding domain comprises a CRISPR associated protein (Cas protein) domain. A Cas protein may be a Class 1 or a Class 2 Cas protein. A Cas protein can be a type I, type II, type III, type IV, type V Cas protein, or a type VI Cas protein. Non-limiting examples of Cas proteins include Cas9, Cas12a (Cpf1), Cas12e (CasX), Cas12d (CasY), Cas12b1 (C2c1), Cas12b2, Cas12c (C2c3), C2c4, C2c8, C2c5, C2c10, C2c9, Cas14a, Cas14b, Cas14c, Cas14d, Cas14e, Cas14f, Cas14g, Cas14h, Cas14u, Cns2, Cas Φ, and homologs, functional fragments, or modified versions thereof. A Cas protein can be a chimeric Cas protein that is fused to other proteins or polypeptides. A Cas protein can be a chimera of various Cas proteins, for example, comprising domains of Cas proteins from different organisms.

[0207] A Cas protein, *e.g.*, Cas9, can be from any suitable organism. In some aspects, the organism is *Streptococcus pyogenes* (*S. pyogenes*). In some aspects, the organism is *Staphylococcus aureus* (*S. aureus*). In some aspects, the organism is *Streptococcus thermophilus* (*S. thermophilus*). In some embodiments, the organism is *Staphylococcus lugdunensis*.

[0208] A Cas protein, *e.g.*, Cas9, can be a wild-type or a modified form of a Cas protein. A Cas protein, *e.g.*, Cas9, can be a nuclease active variant, nuclease inactive variant, a nickase, or a functional variant or functional fragment of a wild-type Cas protein. In some embodiments, a Cas protein, *e.g.*, Cas9, can comprise an amino acid change such as a deletion, insertion, substitution, fusion, chimera, or any combination thereof relative to a wild-type version of the Cas protein. In some embodiments, a Cas protein can be a polypeptide with at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity or sequence similarity to a wild type exemplary Cas protein.

[0209] A Cas protein, *e.g.*, Cas9, may comprise one or more domains. Non-limiting examples of Cas domains include, guide nucleic acid recognition and/or binding domain, nuclease domains (*e.g.*, DNase or RNase domains, RuvC, HNH), DNA binding domain, RNA binding domain, helicase domains, protein-protein interaction domains, and dimerization domains. In various embodiments, a Cas protein comprises a guide nucleic acid recognition and/or binding domain can interact with a guide nucleic acid, and one or more nuclease domains that comprise catalytic activity for nucleic acid cleavage.

[0210] In some embodiments, a Cas protein, *e.g.*, Cas9, comprises one or more nuclease domains. A Cas protein can comprise an amino acid sequence having at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a nuclease domain (*e.g.*, RuvC domain, HNH domain) of a wild-type Cas protein. In some embodiments, a Cas protein comprises a single nuclease domain. For example, a Cpf1 may comprise a RuvC domain but lacks HNH domain. In some embodiments, a Cas protein comprises two nuclease domains, *e.g.*, a Cas9 protein can comprise an HNH nuclease domain and a RuvC nuclease domain.

[0211] In some embodiments, a prime editor comprises a Cas protein, *e.g.*, Cas9, wherein all nuclease domains of the Cas protein are active. In some embodiments, a prime editor comprises a Cas protein having one or more inactive nuclease domains. One or a plurality of the nuclease domains (*e.g.*, RuvC, HNH) of a Cas protein can be deleted or mutated so that they are no longer functional or comprise reduced nuclease activity. In some embodiments, a Cas protein, *e.g.*, Cas9, comprising mutations in a nuclease domain has reduced (*e.g.* nickase) or abolished nuclease activity while maintaining its ability to target a nucleic acid locus at a search target sequence when complexed with a guide nucleic acid, *e.g.* a PEgRNA.

[0212] In some embodiments, a prime editor comprises a Cas nickase that can bind to the double stranded target DNA in a sequence-specific manner and generate a single-strand break at a protospacer within double-stranded DNA in the double stranded target DNA, but not a double-strand break. For example, the Cas nickase can cleave the edit strand or the non-edit strand of the double stranded target DNA but may not cleave both. In some embodiments, a prime editor comprises a Cas nickase comprising two nuclease domains (*e.g.*, Cas9), with one of the two nuclease domains modified to lack catalytic activity or deleted. In some embodiments, the Cas nickase of a prime editor comprises a nuclease inactive RuvC domain and a nuclease active HNH domain. In some embodiments, the Cas nickase of a prime editor comprises a nuclease inactive HNH domain and a nuclease active RuvC domain. In some embodiments, a prime editor comprises a Cas9 nickase having an amino acid substitution in the RuvC domain. In some embodiments, the Cas9 nickase comprises a D10$ amino acid substitution compared to a wild-type S. pyogenes Cas9, wherein $ is any amino acid other than D. In some embodiments, a prime editor comprises a Cas9 nickase having an amino acid substitution in the HNH domain. In some embodiments, the Cas9 nickase comprises a H840$ amino acid substitution compared to a wild-type S. pyogenes Cas9, wherein $ is any amino acid other than H.

[0213] In some embodiments, a prime editor comprises a Cas protein that can bind to the double stranded target DNA in a sequence-specific manner but lacks or has abolished nuclease activity and may not cleave either strand of a double stranded DNA in a double stranded target DNA. Abolished activity or lacking activity can refer to an enzymatic activity less than 1%, less than 2%, less than 3%, less than 4%, less than 5%, less than 6%, less than 7%, less than 8%, less than 9%, or less than 10% activity compared to a wild-type exemplary activity (*e.g.*, wild-type Cas9 nuclease activity). In some embodiments, a Cas protein of a prime editor completely lacks nuclease activity. A nuclease, *e.g.*, Cas9, that lacks nuclease activity may be referred to as nuclease inactive or "nuclease dead" (abbreviated by "d"). A nuclease dead Cas protein (*e.g.*, dCas, dCas9) can bind to a target polynucleotide but may not cleave the target polynucleotide. In some aspects, a dead Cas protein is a dead Cas9 protein. In some embodiments, a prime editor comprises a nuclease dead Cas protein wherein all of the nuclease domains (*e.g.*, both RuvC and HNH nuclease domains in a Cas9 protein; RuvC nuclease domain in a Cpf1 protein) are mutated to lack catalytic activity or are deleted.

[0214] A Cas protein can be modified. A Cas protein, *e.g.*, Cas9, can be modified to increase or decrease nucleic acid binding affinity, nucleic acid binding specificity, and/or enzymatic activity. Cas proteins can also be modified to change any other activity or property of the protein, such as stability. For example, one or more nuclease domains of the Cas protein can be modified, deleted, or inactivated, or a Cas protein can be truncated to remove domains that are not essential for the function of the protein or to optimize (*e.g.*, enhance or reduce) the activity of the Cas protein.

[0215] A Cas protein can be a fusion protein. For example, a Cas protein can be fused to a cleavage domain, an epigenetic modification domain, a transcriptional regulation domain, or a polymerase domain. A Cas protein can also be fused to a heterologous polypeptide providing increased or decreased stability. The fused domain or heterologous polypeptide can be located at the N-terminus, the C-terminus, or internally within the Cas protein.

[0216] A Cas protein may be provided in any form. For example, a Cas protein may be provided in the form of a protein, such as a Cas protein alone or complexed with a guide nucleic acid. A Cas protein may be provided in the form of a nucleic acid encoding the Cas protein, such as an RNA (e.g., messenger RNA (mRNA)) or DNA. The nucleic acid encoding the Cas protein may be codon optimized for efficient translation into protein in a particular cell or organism.

[0217] Nucleic acids encoding Cas proteins may be stably integrated in the genome of the cell. Nucleic acids encoding Cas proteins may be operably linked to a promoter active in the cell. Nucleic acids encoding Cas proteins may be operably linked to a promoter in an expression construct. Expression constructs may include any nucleic acid constructs capable of directing expression of a gene or other nucleic acid sequence of interest (e.g., a Cas gene) and which may transfer such a nucleic acid sequence of interest to a target cell.

[0218] In some embodiments, a Cas protein may comprise a modified form of a wild type Cas protein. In some embodiments, the modified form of the wild type Cas protein may comprise one or more mutations (e.g., amino acid deletion, insertion, and/or substitution) that reduces the nucleic acid-cleaving activity of the Cas protein. For example, the modified form of the Cas protein may have less than 90%, less than 80%, less than 70%, less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, or less than 1% of the nucleic acid-cleaving activity compared to the corresponding protein (e.g., Cas9 from S. pyogenes). In some embodiments, the modified form of Cas protein may have no substantial nucleic acid-cleaving activity. When a Cas protein is a modified form that has no substantial nucleic acid-cleaving activity, it may be referred to as enzymatically inactive and/or "dead" (abbreviated by "d"). A dead Cas protein (e.g., dCas, dCas9) may bind to a target polynucleotide but may not cleave the target polynucleotide. In some embodiments, a dead Cas protein is a dead Cas9 protein.

[0219] Enzymatically inactive can refer to a polypeptide that can bind to a nucleic acid sequence in a polynucleotide in a sequence-specific manner but may not cleave a target polynucleotide. An enzymatically inactive site-directed polypeptide may comprise an enzymatically inactive domain (e.g., nuclease domain). Enzymatically inactive can refer to no activity. Enzymatically inactive may refer to substantially no activity. Enzymatically inactive can refer to essentially no activity. Enzymatically inactive can refer to an activity less than 1%, less than 2%, less than 3%, less than 4%, less than 5%, less than 6%, less than 7%, less than 8%, less than 9%, or less than 10% activity compared to a corresponding wild-type exemplary activity (e.g., nucleic acid cleaving activity, wild-type Cas9 activity).

[0220] In some embodiments, one or a plurality of the nuclease domains (e.g., RuvC, HNH) of a Cas protein may be deleted or mutated so that they are no longer functional or comprise reduced nuclease activity. For example, in a Cas protein comprising at least two nuclease domains (e.g., Cas9), if one of the nuclease domains is deleted or mutated, the resulting Cas protein, known as a nickase, may generate a single-strand break at a CRISPR RNA (crRNA) recognition sequence within a double- stranded DNA but not a double-strand break. Such a nickase can cleave the complementary strand or the non-complementary strand but may not cleave both. If all of the nuclease domains of a Cas protein (e.g., both RuvC and HNH nuclease domains in a Cas9 protein; RuvC nuclease domain in a Cpf1 protein) are deleted or mutated, the resulting Cas protein may have a reduced or no ability to cleave both strands of a double-stranded target DNA. An example of a mutation that may convert a Cas9 protein into a nickase is a D10A amino acid substituion (aspartate to alanine at position 10 of Cas9 as set forth in SEQ ID NO: 2) mutation in the RuvC domain of Cas9 from S. pyogenes. A mutation corresponding to the H840A amino acid substitution (histidine to alanine at amino acid position 840 as set forth in SEQ ID NO: 2) in the HNH domain of Cas9 from S. pyogenes may convert the Cas9 into a nickase. An example of a mutation that may convert a Cas9 protein into a dead Cas9 is a D10A (aspartate to alanine at position 10 of Cas9) mutation in the RuvC domain and H840A (histidine to alanine at amino acid position 840) in the HNH domain of Cas9 from S. pyogenes.

[0221] In some embodiments, a dead Cas protein may comprise one or more mutations relative to a wild-type version of the protein. The mutation can result in less than 90%, less than 80%, less than 70%, less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, or less than 1% of the nucleic acid-cleaving activity in one or more of the plurality of nucleic acid-cleaving domains of the wild-type Cas protein. The mutation may result in one or more of the plurality of nucleic acid-cleaving domains retaining the ability to cleave the complementary strand of the target nucleic acid but reducing its ability to cleave the non-complementary strand of the target nucleic acid. The mutation may result in one or more of the plurality of nucleic acid-cleaving domains retaining the ability to cleave the non-complementary strand of the target nucleic acid but reducing its ability to cleave the complementary strand of the target nucleic acid. The mutation may result in one or more of the plurality of nucleic acid-cleaving domains lacking the ability to cleave the complementary strand and the non-complementary strand of the target nucleic acid. The residues to be mutated in a nuclease domain may correspond to one or more catalytic residues of the nuclease. For example, residues in the wild type exemplary S. pyogenes Cas9 polypeptide such as Asp10, His840, Asn854 and Asn856 may be mutated to inactivate one or more of the plurality of nucleic acid-cleaving domains (e.g., nuclease domains). The residues to be mutated in a nuclease domain of a Cas protein may correspond to residues Asp10, His840, Asn854 and Asn856 in the wild type S. pyogenes Cas9 polypeptide, for example, as determined by sequence and/or structural alignment.

[0222] As non-limiting examples, one or more of amino acid residues D10, G12, G17, E762, H840, N854, N863, H982, H983, A984, D986, and/or A987 in a SpCas9 as set forth in SEQ ID NO: 2, or corresponding amino acid residues in another Cas9 protein may be mutated. For example, a Cas9 protein variant may comprise one or more of D10A, G12A, G17A, E762A, H840A, N854A, N863A, H982A, H983A, A984A, and/or D986A amino acid substitutions as set forth in SEQ ID NO: 2 or corresponding mutations. In some embodiments, mutations other than alanine substitutions can be suitable.

[0223] In some embodiments, the DNA-binding domain comprises a Cas protein domain that is a nickase. In some embodiments, the Cas nickase comprises one or more amino acid substitutions in a nuclease domain compared to a corresponding Cas protein. In some embodiments, the one or more amino acid substitutions in a nuclease domain reduces or abolishes its double strand nuclease activity but retains DNA binding activity. In some embodiments, the Cas nickase comprises an amino acid substitution in a HNH domain compared to a corresponding Cas protein. In some embodiments, the Cas nickase comprises an amino acid substitution in a RuvC domain compared to a corresponding Cas protein. In some embodiments, the Cas nickase is a Cas9 nickase. In some embodiments, the Cas9 nickase comprises one or more mutation in the HNH domain compared to a corresponding Cas9 protein. In some embodiments, one or more mutation in the HNH domain that reduces or abolishes nuclease activity of the HNH domain. Sequences of exemplary Cas9 nickase variants are provided in SEQ ID NOs: 7, 597, 598, 600, 601, 603, 606, 607, 609, 610, 612, or 613. In some embodiments, a Cas protein domain is a nuclease active variant, nuclease inactive variant, a nickase, or a functional variant or functional fragment of a wild type Cas protein.

[0224] In some embodiments, the Cas protein domain can be between 800 and 1500 amino acids in length, between 1400 and 900 amino acids in length, or at least 1000 and 1300 amino acids in length. In some embodiments, the Cas9 protein domain may be at least 800 amino acids in length, at least 900 amino acids in length, at least 1000 amino acids in length, at least 1100 amino acids in length, or at least 1200 amino acids in length. In some embodiments, the Cas9 protein domain is 1057 amino acids in length. In some embodiments, the Cas protein domain is 1069 amino acids in length. In some embodiments, the Cas protein domain is 1369 amino acids in length.

[0225] In some embodiments, the Cas protein domain recognizes the PAM sequence "NGA," wherein N is any nucleotide. In some embodiments, the Cas protein domain recognizes the PAM sequence "NGN," wherein N is any nucleotide. In some embodiments, the Cas protein domain recognizes the PAM sequence "NRN," wherein N is any nucleotide. In some embodiments, the Cas protein domain recognizes the PAM sequence "NNGRRT," wherein N is any nucleotide. In some embodiments, the Cas protein domain recognizes the PAM sequence "NNGG," wherein N is any nucleotide.

[0226] In some embodiments, a prime editor provided herein comprises a Cas protein domain that contains modifications that allow altered PAM recognition. In prime editing using a Cas-protein-based prime editor, a "protospacer adjacent motif (PAM)", PAM sequence, or PAM-like motif, may be used to refer to a short DNA sequence immediately adjacent to the protospacer sequence on the PAM strand of the target gene. In some embodiments, the PAM is recognized by the Cas nuclease in the prime editor during prime editing. In certain embodiments, the PAM is required for target binding of the Cas protein domain. The specific PAM sequence required for Cas protein domain recognition may depend on the specific type of the Cas protein. A PAM can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides in length. In some embodiments, a PAM is between 2-6 nucleotides in length. In some embodiments, the PAM can be a 5′ PAM (i.e., located upstream of the 5′ end of the protospacer). In other embodiments, the PAM can be a 3′ PAM (i.e., located downstream of the 5′ end of the protospacer). In some embodiments, the Cas protein of a prime editor recognizes a canonical PAM, for example, a SpCas9 recognizes 5′-NGG-3′ PAM.

[0227] In some embodiments, a Cas protein domain comprises one or more nuclease domains. In some embodiments, a Cas protein domain may comprise an amino acid sequence having at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a nuclease domain of a wild-type Cas protein. In some embodiments, a Cas protein domain may comprise an amino acid sequence having at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a nuclease domain of a reference Cas protein (e.g., a Cas protein selected from any one of SEQ ID NOs: 2, 6, 7, 596-613. In some embodiments, a Cas protein domain comprises a single nuclease domain.

[0228] In some embodiments, a prime editor comprises a Cas protein domain that can bind to the target gene in a sequence-specific manner but lacks or has abolished nuclease activity and may not cleave either strand of a double stranded DNA in a target gene. Abolished activity or lacking activity can refer to an enzymatic activity less than 1%, less than 2%, less than 3%, less than 4%, less than 5%, less than 6%, less than 7%, less than 8%, less than 9%, or less than 10% activity compared to a wild-type exemplary activity (e.g., wild-type Cas9 nuclease activity).

[0229] Exemplary Cas protein domains are shown in Table 14. In some embodiments, a DNA binding domain (e.g., the Cas protein domain or a Cas protein) is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613. In some embodiments, a DNA binding domain (e.g., a Cas protein domain or a Cas protein) comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613 (e.g., Table 14). In some embodiments, a Cas protein or a Cas protein domain comprises an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613 (e.g., Table 14). In some embodiments, a Cas protein or a Cas protein domain comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613 (e.g., Table 14). In some embodiments, a Cas protein or a Cas protein domain comprises an amino acid sequence that lacks a N-terminus methionine compared to a corresponding Cas protein or Cas protein domain (e.g., any one of Cas protein or Cas protein domain set forth in SEQ ID NO: 2, 6, 7, 596-613). In some embodiments, a prime editing composition comprises a polynucleotide that encodes a DNA binding domain (e.g., a Cas protein or a Cas protein domain) that comprises an amino acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to an amino acid sequence of any one of SEQ ID NOs: 2, 6, 7, 596-613. In some embodiments, a prime editing composition comprises a polynucleotide that encodes a DNA binding domain (e.g., a Cas protein or a Cas protein domain) that comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613. In some embodiments, a polynucleotide that encodes a DNA binding domain (e.g., a Cas protein or a Cas protein domain) is a DNA polynucleotide. In some embodiments, a polynucleotide that encodes a DNA binding domain (e.g., a Cas protein or a Cas protein domain) is a RNA polynucleotide. In some embodiments, a polynucleotide (e.g., a DNA polynucleotide) that encodes a DNA binding domain e.g., a Cas protein or a Cas protein domain comprises a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of SEQ ID NO: 627, or SEQ ID NO: 629. In some embodiments, a polynucleotide (e.g., a DNA polynucleotide) that encodes a DNA binding domain e.g., a Cas protein or a Cas protein domain, comprises a nucleic acid sequence that is selected from the group consisting of SEQ ID NO: 627, and SEQ ID NO: 629.

[0230] In some embodiments, a polynucleotide (e.g., an RNA polynucleotide) that encodes a DNA binding domain e.g., a Cas protein or a Cas protein domain, comprises a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of SEQ ID NO: 628, or SEQ ID NO: 630. In some embodiments, a polynucleotide (e.g., a RNA polynucleotide) that encodes a DNA binding domain e.g., a Cas protein or a Cas protein domain, comprises a nucleic acid sequence that is selected from the group consisting of SEQ ID NO: 628, or SEQ ID NO: 630.

[0231] In some embodiments, the Cas protein of a prime editor is a Class 2 Cas protein. In some embodiments, the Cas protein is a type II Cas protein. In some embodiments, the Cas protein is a Cas9 protein, a modified version of a Cas9 protein, a Cas9 protein homolog, mutant, variant, or a functional fragment thereof. As used herein, a Cas9, Cas9 protein, Cas9 polypeptide or a Cas9 nuclease refers to an RNA guided nuclease comprising one or more Cas9 nuclease domains and a Cas9 gRNA binding domain having the ability to bind a guide polynucleotide, *e.g.*, a PEgRNA. A Cas9 protein may refer to a wild-type Cas9 protein from any organism or a homolog, ortholog, or paralog from any organisms; any functional mutants or functional variants thereof; or any functional fragments or domains thereof. In some embodiments, a prime editor comprises a full-length Cas9 protein. In some embodiments, the Cas9 protein can generally comprises at least about 50%, 60%, 70%, 80%, 90%, 100% sequence identity to a wild-type reference Cas9 protein (*e.g.*, Cas9 from *S. pyogenes*). In some embodiments, the Cas9 comprises an amino acid change such as a deletion, insertion, substitution, fusion, chimera, or any combination thereof as compared to a wild-type reference Cas9 protein. Exemplary Cas9 sequences are provided in Table 14.

[0232] In some embodiments, a Cas9 protein may comprise a Cas9 protein from *Streptococcus pyogenes* (Sp), *Staphylococcus aureus* (Sa), *Streptococcus canis* (Sc), *Streptococcus thermophilus* (St), *Staphylococcus lugdunensis* (Slu), *Neisseria meningitidis* (Nm), *Campylobacter jejuni* (Cj), *Francisella novicida* (Fn), or *Treponema denticola* (Td), or any Cas9 homolog or ortholog from an organism known in the art. In some embodiments, a Cas9 polypeptide is a SpCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in NCBI Accession No. WP_038431314 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a SaCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in Uniprot Accession No. J7RUA5 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a ScCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in Uniprot Accession No. A0A3P5YA78 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a StCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in NCBI Accession No. WP_007896501.1 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a SluCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in any of NCBI Accession No. WP_230580236.1 or WP_250638315.1 or WP_242234150.1, WP_241435384.1, WP_002460848.1, KAK58371.1, or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a NmCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in any of NCBI Accession No. WP_002238326.1 or WP_061704949.1 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a CjCas9 polypeptide, e.g., comprising an amino acid sequence as set forth in any of NCBI Accession No. WP_100612036.1, WP_116882154.1, WP_116560509.1, WP_116484194.1, WP_116479303.1, WP_115794652.1, WP_100624872.1, or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a FnCas9 polypeptide, e.g., comprising the amino acid sequence as set forth in Uniprot Accession No. A0Q5Y3 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a TdCas9 polypeptide, e.g., comprising the amino acid sequence as set forth in NCBI Accession No. WP_147625065.1 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a chimera comprising domains from two or more of the organisms described herein or those known in the art. In some embodiments, a Cas9 polypeptide is a Cas9 polypeptide from

Streptococcus macacae, e.g., comprising the amino acid sequence as set forth in NCBI Accession No. WP_003079701.1 or a fragment or variant thereof. In some embodiments, a Cas9 polypeptide is a Cas9 polypeptide generated by replacing a PAM interaction domain of a SpCas9 with that of a *Streptococcus macacae* Cas9 (Spy-mac Cas9).

[0233] An exemplary *Streptococcus pyogenes* Cas9 (SpCas9) amino acid sequence is provided in SEQ ID NO: 2.

[0234] In some embodiments, a prime editor comprises a Cas9 protein from *Staphylococcus lugdunensis* (Slu Cas9). An exemplary amino acid sequence of a Slu Cas9 is provided in SEQ ID NO: 606.

[0235] In some embodiments, a Cas9 protein comprises a variant Cas9 protein containing one or more amino acid substitutions. In some embodiments, a wildtype Cas9 protein comprises a RuvC domain and an HNH domain. In some embodiments, a prime editor comprises a nuclease active Cas9 protein that may cleave both strands of a double stranded target DNA sequence. In some embodiments, the nuclease active Cas9 protein comprises a functional RuvC domain and a functional HNH domain. In some embodiments, a prime editor comprises a Cas9 nickase that can bind to a guide polynucleotide and recognize a target DNA but can cleave only one strand of a double stranded target DNA. In some embodiments, the Cas9 nickase comprises only one functional RuvC domain or one functional HNH domain. In some embodiments, a prime editor comprises a Cas9 that has a non-functional HNH domain and a functional RuvC domain. In some embodiments, the prime editor can cleave the edit strand (*i.e.*, the PAM strand), but not the non-edit strand of a double stranded target DNA sequence. In some embodiments, a prime editor comprises a Cas9 having a non-functional RuvC domain that can cleave the target strand (*i.e.*, the non-PAM strand), but not the edit strand of a double stranded target DNA sequence. In some embodiments, a prime editor comprises a Cas9 that has neither a functional RuvC domain nor a functional HNH domain, which may not cleave any strand of a double stranded target DNA sequence.

[0236] In some embodiments, a prime editor comprises a Cas9 having a mutation in the RuvC domain that reduces or abolishes the nuclease activity of the RuvC domain. In some embodiments, the Cas9 comprises a mutation at amino acid D10 as compared to a wild type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 comprises a D10A mutation as compared to a wild type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 polypeptide comprises a mutation at amino acid D10, G12, and/or G17 as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 polypeptide comprises a D10A mutation, a G12A mutation, and/or a G17A mutation as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof.

[0237] In some embodiments, a prime editor comprises a Cas9 polypeptide having a mutation in the HNH domain that reduces or abolishes the nuclease activity of the HNH domain. In some embodiments, the Cas9 polypeptide comprises a mutation at amino acid H840 as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 polypeptide comprises a H840A mutation as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 polypeptide comprises a mutation at amino acid E762, D839, H840, N854, N856, N863, H982, H983, A984, D986, and/or a A987 as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof. In some embodiments, the Cas9 polypeptide comprises a E762A, D839A, H840A, N854A, N856A, N863A, H982A, H983A, A984A, and/or a D986A mutation as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or a corresponding mutation thereof.

[0238] In some embodiments, a prime editor comprises a Cas9 having one or more amino acid substitutions in both the HNH domain and the RuvC domain that reduce or abolish the nuclease activity of both the HNH domain and the RuvC domain. In some embodiments, the prime editor comprises a nuclease inactive Cas9, or a nuclease dead Cas9 (dCas9). In some embodiments, the dCas9 comprises a H840$ substitution and a D10X mutation compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2 or corresponding mutations thereof, wherein $ is any amino acid other than H for the H840$ substitution and any amino acid other than D for the D10$ substitution. In some embodiments, the dead Cas9 comprises a H840A and a D10A mutation as compared to a wild-type SpCas9 as set forth in SEQ ID NO: 2, or corresponding mutations thereof.

[0239] In some embodiments, the N-terminal methionine is removed from a Cas9 nickase, or from any Cas9 variant, ortholog, or equivalent disclosed or contemplated herein. For example, methionine-minus Cas9 nickases include the following sequences SEQ ID NO. 7, 598, 601, 604, 607, 610, 613, or a variant thereof having an amino acid sequence that has at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% sequence identity thereto.

[0240] Besides dead Cas9 and Cas9 nickase variants, the Cas9 proteins used herein may also include other Cas9 variants having at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to any reference Cas9 protein, including any wild type Cas9, or mutant Cas9 (e.g., a dead Cas9 or Cas9 nickase), or fragment Cas9, or circular permutant Cas9, or other variant of Cas9 disclosed herein or known in the art. In some embodiments, a Cas9 variant may have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 21, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50 or more amino acid changes compared to a reference Cas9, e.g., a wild type Cas9. In some embodiments, the Cas9 variant comprises a fragment of a reference Cas9 (e.g., a gRNA binding domain or a DNA-cleavage domain), such that the fragment is at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to the corresponding fragment of the reference Cas9, e.g., a wild type Cas9. In some embodiments, the fragment is at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% identical, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.5% of the amino acid length of a corresponding wild type Cas9. In some embodiments, a reference Cas9 comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 6, 7, 596-613.In some embodiments, a prime editor comprises a Cas protein, *e.g.*, Cas9, containing modifications that allow altered PAM recognition. In prime editing using a Cas-protein-based prime editor, a "*protospacer* adjacent motif (PAM)", PAM sequence, or PAM-like motif, may be used to refer to a short DNA sequence immediately following the protospacer sequence on the PAM strand of the double stranded target DNA (e.g., target gene). In some embodiments, the PAM is recognized by the Cas nuclease in the prime editor during prime editing. In certain embodiments, the PAM is required for target binding of the Cas protein. The specific PAM sequence required for Cas protein recognition may depend on the specific type of the Cas protein. A PAM can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more nucleotides in length. In some embodiments, a PAM is between 2-6 nucleotides in length. In some embodiments, the PAM can be a 5' PAM (*i.e.*, located upstream of the 5' end of the protospacer). In other embodiments, the PAM can be a 3' PAM (*i.e.*, located downstream of the 5' end of the protospacer). In some embodiments, the Cas protein of a prime editor recognizes a canonical PAM, for example, a SpCas9 recognizes 5'-NGG-3' PAM. In some embodiments, the Cas protein of a prime editor has altered or non-canonical PAM specificities. Exemplary PAM sequences and corresponding Cas variants are described in **Table 1a** below. It should be appreciated that for each of the variants provided, the Cas protein comprises one or more of the amino acid substitutions as indicated compared to a wild-type Cas protein sequence, for example, the Cas9 as set forth in SEQ ID NO: 2. The PAM motifs as shown in **Table 1a** below are in the order of 5' to 3'.

Table 1a: Cas protein variants and corresponding PAM sequences. W: A or T; V: A or C or G; R: A or G

Variant	PAM
spCas9 (wild type)	NGG, NGA, NAG, NGNGA
spCas9- VRVRFRR R1335V/L1111R/D1135V/G1218R/E1219F/A1322R/T1337R	NG
spCas9-VQR (D1135V/R1335Q/T1337R)	NGA
spCas9-EQR (D1135E/R1335Q/T1337R)	NGA
spCas9-VRER (D1135V/G1218R/R1335E/T1337R)	NGCG
spCas9-VRQR (D1135V, G1218R, R1335Q, T1337R)	NGA
Cas9-NG (L1111R, D1135V, G1218R, E1219F, A1322R, T1337R, R1335V)	NGN
SpG Cas9 (D1135L, S1136W, G1218K, E1219Q, R1335Q, T1337R)	NGN
SyRY Cas9 (A61R, L1111R, N1317R, A1322R, and R1333P)	NRN
xCas9 (E480K, E543D, E1219V, K294R, Q1256K, A262T, S409I, M694I)	NGN

SluCa9	NNGG
saCas9	NNGRRT (SEQ ID NO: 614), NNGRRN (SEQ ID NO: 615)
saCas9-KKH (E782K, N968K, R1015H)	NNNRRT (SEQ ID NO: 616)
spCas9-MQKSER (D1135M, S1136Q, G1218K, E1219S, R1335E, T1337R)	NGCG/NGCN
spCas9-LRKIQK (D1135L, S1136R, G1218K, E1219I, R1335Q, T1337K)	NGTN
spCas9-LRVSQK (D1135L, S1136R, G1218V, E1219S, R1335Q, T1337K)	NGTN
spCas9-LRVSQL(D1135L, S1136R, G1218V, E1219S, R1335Q, T1337L)	NGTN
Cpf1	TTTV
Spy-Mac	NAA
NmCas9	NNNNGATT (SEQ ID NO: 617)
StCas9	NNAGAAW (SEQ ID NO: 618)
TdCas9	NAAAAC (SEQ ID NO: 619)

[0241] In some embodiments, a prime editor comprises a Cas9 polypeptide comprising one or mutations selected from the group consisting of: A61R, L111R, D1135V, R221K, A262T, R324L, N394K, S409I, S409I, E427G, E480K, M495V, N497A, Y515N, K526E, F539S, E543D, R654L, R661A, R661L, R691A, N692A, M694A, M694I, Q695A, H698A, R753G, M763I, K848A, K890N, Q926A, K1003A, R1060A, L1111R, R1114G, D1135E, D1135L, D1135N, S1136W, V1139A, D1180G, G1218K, G1218R, G1218S, E1219Q, E1219V, E1219V, Q1221H, P1249S, E1253K, N1317R, A1320V, P1321S, A1322R, I1322V, D1332G, R1332N, A1332R, R1333K, R1333P, R1335L, R1335Q, R1335V, T1337N, T1337R, S1338T, H1349R, and any combinations thereof as compared to a wildtype SpCas9 polypeptide as set forth in SEQ ID NO: 2.

[0242] In some embodiments, a prime editor comprises a SaCas9 polypeptide. In some embodiments, the SaCas9 polypeptide comprises one or more of mutations E782K, N968K, and R1015H as compared to a wild-type SaCas9 (e.g., SEQ ID NO: 596). In some embodiments, a prime editor comprises a FnCas9 polypeptide, for example, a wild-type FnCas9 polypeptide or a FnCas9 polypeptide comprising one or more of mutations E1369R, E1449H, or R1556A as compared to the wild-type FnCas9. In some embodiments, a prime editor comprises a ScCas9, for example, a wild-type ScCas9 or a ScCas9 polypeptide comprises one or more of mutations I367K, G368D, I369K, H371L, T375S, T376G, and

T1227K as compared to the wild-type ScCas9. In some embodiments, a prime editor comprises a St1 Cas9 polypeptide, a St3 Cas9 polypeptide, or a Slu Cas9 polypeptide.

[0243] In some embodiments, a prime editor comprises a Cas polypeptide that comprises a circular permutant Cas variant. For example, a Cas9 polypeptide of a prime editor may be engineered such that the N-terminus and the C-terminus of a Cas9 protein (*e.g.*, a wild-type Cas9 protein, or a Cas9 nickase) are topically rearranged to retain the ability to bind DNA when complexed with a guide RNA (gRNA). An exemplary circular permutant configuration may be N-terminus-[original C-terminus]-[original N-terminus]-C-terminus. Any of the Cas9 proteins described herein, including any variant, ortholog, or naturally occurring Cas9 or equivalent thereof, may be reconfigured as a circular permutant variant.

[0244] In some embodiments, prime editors described herein may also comprise Cas proteins other than Cas9. For example, in some embodiments, a prime editor as described herein may comprise a Cas12a (Cpf1) polypeptide or functional variants thereof. In some embodiments, the Cas12a polypeptide comprises a mutation that reduces or abolishes the endonuclease domain of the Cas12a polypeptide. In some embodiments, the Cas12a polypeptide is a Cas12a nickase. In some embodiments, the Cas protein comprises an amino acid sequence that comprises at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a naturally occurring Cas12a polypeptide.

[0245] In some embodiments, a prime editor comprises a Cas protein that is a Cas12b (C2c1) or a Cas12c (C2c3) polypeptide. In some embodiments, the Cas protein comprises an amino acid sequence that comprises at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a naturally occurring Cas12b (C2c1) or Cas12c (C2c3) protein. In some embodiments, the Cas protein is a Cas12b nickase or a Cas12c nickase. In some embodiments, the Cas protein is a Cas12e, a Cas12d, a Cas13, Cas14a, Cas14b, Cas14c, Cas14d, Cas14e, Cas14f, Cas14g, Cas14h, Cas14u, or a Cas Φ polypeptide. In some embodiments, the Cas protein comprises an amino acid sequence that comprises at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a naturally-occurring Cas12e, Cas12d, Cas13, Cas14a, Cas14b, Cas14c, Cas14d, Cas14e, Cas14f, Cas14g, Cas14h, Cas14u, or Cas Φprotein. In some embodiments, the Cas protein is a Cas12e, Cas12d, Cas13, or Cas Φ nickase.

Flap Endonuclease

[0246] In some embodiments, a prime editor further comprises additional polypeptide components, for example, a flap endonuclease (FEN, *e.g.* FEN1). In some embodiments, the flap endonuclease excises the 5' single stranded DNA of the edit strand of the double stranded target DNA (e.g., the target gene) and assists incorporation of the intended nucleotide edit into the double stranded target DNA (e.g., the target gene). In some embodiments, the FEN is linked or fused to another component. In some embodiments, the FEN is provided in trans, for example, as a separate polypeptide or polynucleotide encoding the FEN.

[0247] In some embodiments, a prime editor or prime editing composition comprises a flap nuclease. In some embodiments, the flap nuclease is a FEN1, or any FEN1 functional variant, functional mutant, or functional fragment thereof. In some embodiments, the flap nuclease has amino acid sequence that is at least about 70% identical, at least about 80% identical, at least about 90% identical, at least about 95% identical, at least about 96% identical, at least about 97% identical, at least about 98% identical, at least about 99% identical, at least about 99.5% identical, or at least about 99.9% identical to any of the flap nucleases described herein or known in the art.

Nuclear Localization Sequences

[0248] In some embodiments, a prime editor further comprises one or more nuclear localization sequence (NLS). In some embodiments, the NLS helps promote translocation of a protein into the cell nucleus. In some embodiments, a prime editor comprises a fusion protein, *e.g.*, a fusion protein comprising a DNA binding domain and a DNA polymerase, that comprises one or more NLSs. In some embodiments, one or more polypeptides of the prime editor are fused to or linked to one or more NLSs. In some embodiments, the prime editor comprises a DNA binding domain and a DNA polymerase domain that are provided in trans, wherein the DNA binding domain and/or the DNA polymerase domain is fused or linked to one or more NLSs.

[0249] In certain embodiments, a prime editor or prime editing complex comprises at least one NLS. In some embodiments, a prime editor or prime editing complex comprises at least two NLSs. In embodiments with at least two NLSs, the NLSs can be the same NLS, or they can be different NLSs.

[0250] In some instances, a prime editor may further comprise at least one nuclear localization sequence (NLS). In some cases, a prime editor may further comprise 1 NLS. In some cases, a prime editor may further comprise 2 NLSs.

[0251] In addition, the NLSs can be expressed as part of a prime editor complex. In some embodiments, a NLS can be positioned almost anywhere in a protein's amino acid sequence, and generally comprises a short sequence of three or more or four or more amino acids. The location of the NLS fusion can be at the N-terminus, the C-terminus, or positioned anywhere within a sequence of a prime editor or a component thereof (*e.g.*, inserted between the DNA-binding domain and the DNA polymerase domain of a prime editor fusion protein, between the DNA binding domain and a linker sequence, between a DNA polymerase and a linker sequence, between two linker sequences of a prime editor fusion protein or a component thereof, in either N-terminus to C-terminus or C-terminus to N-terminus order). In some embodiments, a prime editor is fusion protein that comprises an NLS at the N terminus. In some embodiments, a prime editor is fusion protein that comprises an NLS at the C terminus. In some embodiments, a prime editor is fusion protein that comprises at least one NLS at both the N terminus and the C terminus. In some embodiments, the prime editor is a fusion protein that comprises two NLSs at the N terminus and/or the C terminus.

[0252] Any NLSs that are known in the art are also contemplated herein. The NLSs may be any naturally occurring NLS, or any non-naturally occurring NLS (*e.g.*, an NLS with one or more mutations relative to a wild-type NLS). In some embodiments, the one or more NLSs of a prime editor comprise bipartite NLSs. In some embodiments, a nuclear localization signal (NLS) is predominantly basic. In some embodiments, the one or more NLSs of a prime editor are rich in lysine and arginine residues. In some embodiments, the one or more NLSs of a prime editor comprise proline residues. In some embodiments, a nuclear localization signal (NLS) comprises the sequence MDSLLMNRRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO:16), KRTADGSEFESPKKKRKV (SEQ ID NO: 8), KRTADGSEFEPKKKRKV (SEQ ID NO: 11)

[0253] In some embodiments, a NLS is a monopartite NLS. For example, in some embodiments, a NLS is a SV40 large T antigen NLS; PKKKRKV (SEQ ID NO: 12). In some embodiments, a NLS is a bipartite NLS. In some embodiments, a bipartite NLS comprises two basic domains separated by a spacer sequence comprising a variable number of amino acids. In some embodiments, a NLS is a bipartite NLS. In some embodiments, a bipartite NLS consists of two basic domains separated by a spacer sequence comprising a variable number of amino acids. In some embodiments, a NLS comprises an amino acid sequence that is at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOs: 8-24 and 621. In some embodiments, a NLS comprises an amino acid sequence selected from the group consisting of 8-24 and 621. In some embodiments, a prime editing composition comprises a polynucleotide that encodes a NLS that comprises an amino acid sequence that is at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the amino acid sequence of any one of SEQ ID NOs: 8-24 and 621. In some embodiments, a prime editing composition comprises a polynucleotide that encodes a NLS that comprises an amino acid sequence selected from the group consisting of 8-24 and 621. In some embodiments, a polynucleotide (e.g., a DNA polynucleotide or a RNA polynucleotide) encoding a NLS comprises a nucleic acid sequence that is at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the nucleic acid sequence of any one of SEQ ID NOs: 637, 638, 631 or 632. In some embodiments, the polynucleotide sequence (e.g., a DNA polynucleotide) encoding a NLS comprises a nucleic acid sequence that is at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the nucleic acid sequence of any one of SEQ ID NOs: 637, or 631. In some embodiments, the polynucleotide sequence (e.g., a RNA polynucleotide) encoding a NLS comprises a nucleic acid sequence that is at least about 50%, 60%, 70%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the nucleic acid sequence of any one of SEQ ID NOs: 638, or 632.

[0254] Any NLSs that are known in the art are also contemplated herein. The NLSs may be any naturally occurring NLS, or any non-naturally occurring NLS (*e.g.*, an NLS with one or more mutations relative to a wild-type NLS). In some embodiments, the one or more NLSs of a prime editor comprise bipartite NLSs. In some embodiments, the one or more NLSs of a prime editor are rich in lysine and arginine residues. In some embodiments, the one or more NLSs of a prime editor comprise proline residues. Non-limiting examples of NLS sequences are provided in **Table 2** below.

[0255] Table 2: Exemplary nuclear localization sequences

Description	Sequence	SEQ ID NO:
SV40 BPNLS	KRTADGSEFESPKKKRKV	8
SV40 BPNLS with N term Methionine	MKRTADGSEFESPKKKRKV	9
c-Myc BPNLS-NLS	PAAKRVKLDGGKRTADGSEFESPKKKRKV	10
c-myc BPNLS with N term Methionine	MPAAKRVKLDGGKRTADGSEFESPKKKRKV	621
SV40 BPNLS1	KRTADGSEFEPKKKRKV	11
SV40 NLS	PKKKRKV	12
BPNLS-NLS	KRTADSQHSTPPKTKRKVEFESPKKKRKV	13
BPNLS-NLS1	KRTADSQHSTPPKTKRKVEFEPKKKRKV	14
NLS	MKRTADGSEFESPKKKRKV	15
NLS	MDSLLMNRRKFLYQFKNVRWAKGRRETYLC	16
NLS of Nucleoplasmin	AVKRPAATKKAGQAKKKKLD	17
NLS of EGL-13	MSRRRKANPTKLSENAKKLAKEVEN	18
NLS of C-Myc	PAAKRVKLD	19
NLS of Tus-protein	KLKIKRPVK	20
NLS of polyoma large T-AG	VSRKRPRP	21
NLS of Hepatitis D virus antigen	EGAPPAKRAR	22
NLS of murine p53	PPQPKKKPLDGE	23
Exemplary linker-NLS	SGGSKRTADGSEFEPKKKRKV	24

Linkers

[0256] Polypeptides comprising components of a prime editor, *e.g.*, the DNA binding domain and the DNA polymerase domain, may be fused via linkers, *e.g.*, peptide or non-peptide linkers or may be provided *in trans* relevant to each other. For example, a reverse transcriptase may be expressed, delivered, or otherwise provided as an individual component rather than as a part of a fusion protein with the DNA binding domain. In such cases, components of the prime editor may be associated through non-peptide linkages or co-localization functions. In some embodiments, a prime editor further comprises additional components capable of interacting with, associating with, or capable of recruiting other components of the prime editor or the prime editing system. For example, a prime editor may comprise an RNA-protein recruitment polypeptide that can associate with an RNA-protein recruitment RNA aptamer. In some embodiments, an RNA-protein recruitment polypeptide can recruit, or be recruited by, a specific RNA sequence.

[0257] Non-limiting examples of RNA-protein recruitment polypeptide and RNA aptamer pairs include a MS2 coat protein and a MS2 RNA hairpin, a PCP polypeptide and a PP7 RNA hairpin, a Com polypeptide and a Com RNA hairpin, a Ku protein and a telomerase Ku binding RNA motif, and a Sm7 protein and a telomerase Sm7 binding RNA motif. In some embodiments, the prime editor comprises a DNA binding domain fused or linked to an RNA-protein recruitment polypeptide. In some embodiments, the prime editor comprises a DNA polymerase domain fused or linked to an RNA-protein recruitment polypeptide. In some embodiments, the DNA binding domain and the DNA polymerase domain fused to the RNA-protein recruitment polypeptide, or the DNA binding domain fused to the RNA-protein recruitment polypeptide and the DNA polymerase domain are co-localized by the corresponding RNA-protein recruitment RNA aptamer of the RNA-protein recruitment polypeptide. In some embodiments, the corresponding RNA-protein recruitment RNA aptamer fused or linked to a portion of the PEgRNA or ngRNA. For example, an MS2 coat protein fused or linked to the DNA polymerase and a MS2 hairpin installed on the PEgRNA for co-localization of the DNA polymerase and the RNA-guided DNA binding domain (*e.g.*, a Cas9 nickase).

[0258] In certain embodiments, components of a prime editor are directly fused to each other. In certain embodiments, components of a prime editor are associated to each other via a linker.

[0259] As used herein, a linker can be any chemical group or a molecule linking two molecules or moieties, *e.g.*, a DNA binding domain and a DNA polymerase domain of a prime editor. In some embodiments, a linker is an organic molecule, group, polymer, or chemical moiety. In some embodiments, the linker comprises a non-peptide moiety. The linker may be as simple as a covalent bond, or it may be a polymeric linker many atoms in length, for example, a polynucleotide sequence. In some embodiments, the linker is a covalent bond (*e.g.*, a carbon-carbon bond, disulfide bond, carbon-heteroatom bond, etc.). In certain embodiments, the linker is a carbon-nitrogen bond of an amide linkage. In some embodiments, the linker is a polymeric linker many atoms in length, for example, a polypeptide sequence.

[0260] In some embodiments, a linker joins two domains of a prime editor, for example, a DNA binding domain and a DNA polymerase domain. In some embodiments, linkers join each of, or at least two of, two or more domains of a prime editor, for example, a DNA binding domain, a DNA polymerase domain, a RNA-binding protein domain (*e.g.*, a MS2 coat protein that binds to MS2 recruitment aptamer RNA sequence), and/or a flap nuclease domain. In some embodiments, linkers join each of, or at least two of, two or more domains of a prime editor, for example, a DNA binding domain, a DNA polymerase domain, an RNA-binding protein domain (*e.g.*, a MS2 coat protein that binds to MS2 recruitment aptamer RNA sequence), a flap nuclease domain, and/or one or more nuclear localization sequences.

[0261] In some embodiments, the linker is an amino acid or is a peptide comprising a plurality of amino acids. In certain embodiments, two or more components of a prime editor are linked to each other by a peptide linker. In some embodiments, a peptide linker is 5-100 amino acids in length, for example, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 30-35, 35-40, 40-45, 45-50, 50-60, 60-70, 70-80, 80-90, 90-100, 100-120, 120-130, 130-140, 140-150, or 150-200 amino acids in length. In some embodiments, the peptide linker is 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 35, 45, 50, 55, 60, 60, 65, 70, 70, 75, 80, 85, 90, 90, 95, 100, 101, 102, 103, 104, 105, 110, 120, 130, 140,150, 160, 175, 180, 190, or 200 amino acids in length. In some embodiments, the peptide linker is 5-100 amino acids in length. In some embodiments, the peptide linker is 10-80 amino acids in length. In some embodiments, the peptide linker is 15-70 amino acids in length. In some embodiments, the peptide linker is 16 amino acids in length, 24 amino acids in length, 64 amino acids in length, or 96 amino acids in length. In some embodiments, the peptide linker is at least 50 amino acids in length. In some embodiments, the peptide linker is at least 40 amino acids in length. In some embodiments, the peptide linker is at least 30 amino acids in length. In some embodiments, the peptide linker is 46 amino acids in length. In some embodiments, the peptide linker is 92 amino acids in length.

[0262] For example, the DNA binding domain and the DNA polymerase domain of a prime editor may be joined by a peptide or protein linker. In some embodiments, a prime editor comprises a fusion protein comprising one or more peptide linkers that join a DNA binding domain, *e.g.*, a Cas9 nickase domain, and a DNA polymerase domain, *e.g.*, a M-MLV reverse transcriptase domain.

[0263] In some other embodiments, the peptide linker comprises the amino acid motif GGGS, GGSS, GGS (SEQ ID NO: 287), GGGGS, SGGS (SEQ ID NO: 288), EAAAK, or any combination thereof. In some embodiments, the peptide linker comprises amino acid sequence (GGGGS)n (SEQ ID NO: 376), (G)n (SEQ ID NO: 377), (EAAAK)n (SEQ ID NO: 378), (GGS)n (SEQ ID NO: 379), (SGGS)n (SEQ ID NO: 380), (GGSS)n (SEQ ID NO: 381), (XP)n (SEQ ID NO: 382), or any combination thereof, wherein n is independently an integer between 1 and 30, and wherein X is any amino acid. In some embodiments, the peptide linker comprises the amino acid sequence (GGS)n (SEQ ID NO: 379), wherein n is 1, 3, or 7. In some embodiments, the peptide linker comprises the amino acid sequence SGSETPGTSESATPES (SEQ ID NO: 295), which may be referred to as an XTEN motif. In some embodiments, the peptide linker comprises 2, 3, 4, 5, or 6 contiguous XTEN motifs. In some embodiments, the peptide linker comprises the amino acid sequence SGGSSGGSSGSETPGTSESATPESSGGSSGGS (SEQ ID NO: 296). In some embodiments, the peptide linker comprises the amino acid sequence SGGSGGSGGS (SEQ ID NO: 383). In some embodiments, the peptide linker comprises the amino acid sequence SGGS (SEQ ID NO: 288). In other embodiments, the peptide linker comprises the amino acid sequence SGGSSGGSSGSETPGTSESATPESAGSYPYDVPDYAGSAAPAAKKKKLDGSGSGGSSGGS (SEQ ID NO: 384).

[0264] In some embodiments, the peptide linker comprises at least 2 GGSS motifs. In some embodiments, the peptide linker comprises at least 3 GGSS motifs. In some embodiments, the peptide linker comprises at least 4 GGSS motifs. In some embodiments, the peptide linker comprises at least 5 GGSS motifs. In some embodiments, the peptide linker comprises at least 6 GGSS motifs. In some embodiments, the peptide linker comprises at least 7 GGSS motifs. In some embodiments, the peptide linker comprises at least 8 GGSS motifs. In some embodiments, the peptide linker comprises at least 9 GGSS motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGSS motifs. In some embodiments, the peptide linker comprises at least 2 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 3 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 4 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 5 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 6 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 7 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 8 contiguous GGSS motifs. In some embodiments, the peptide linker comprises at least 9 contiguous GGSS motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous GGSS motifs. In some embodiments, the peptide linker further comprises at least one GGS motif. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGSS motifs. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous GGSS motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGSS motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous GGSS motifs.

[0265] In some embodiments, the peptide linker comprises at least 2 SGGS motifs. In some embodiments, the peptide linker comprises at least 3 SGGS motifs. In some embodiments, the peptide linker comprises at least 4 SGGS motifs. In some embodiments, the peptide linker comprises at least 5 SGGS motifs. In some embodiments, the peptide linker comprises at least 6 SGGS motifs. In some embodiments, the peptide linker comprises at least 7 SGGS motifs. In some embodiments, the peptide linker comprises at least 8 SGGS motifs. In some embodiments, the peptide linker comprises at least 9 SGGS motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 SGGS motifs. In some embodiments, the peptide linker comprises at least 2 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 3 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 4 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 5 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 6 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 7 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 8 contiguous SGGS motifs. In some embodiments, the peptide linker comprises at least 9 contiguous SGGS motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous SGGS motifs. In some embodiments, the peptide linker further comprises at least one GGS motif. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 SGGS motifs. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous SGGS motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 SGGS motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous SGGS motifs.

[0266] In some embodiments, the peptide linker comprises at least 3 EAAAK motifs. In some embodiments, the peptide linker comprises at least 4 EAAAK motifs. In some embodiments, the peptide linker comprises at least 5 EAAAK motifs. In some embodiments, the peptide linker comprises at least 6 EAAAK motifs. In some embodiments, the peptide linker comprises at least 7 EAAAK motifs. In some embodiments, the peptide linker comprises at least 8 EAAAK motifs. In some embodiments, the peptide linker comprises at least 9 EAAAK motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 EAAAK motifs. In some embodiments, the peptide linker comprises at least 3 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 4 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 5 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 6 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 7 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 8 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises at least 9 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous EAAAK motifs. In some embodiments, the peptide linker further comprises at least one GGS motif. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 EAAAK motifs. In some embodiments, the peptide linker comprises at least one GGS motif and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous EAAAK motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 EAAAK motifs. In some embodiments, the peptide linker comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GGS motifs and 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous EAAAK motifs.

[0267] In some embodiments, the peptide linker comprises the amino acid sequence of (GGSS)m-(GGS)n, wherein m and n are each any integer between 0 and 50. In some embodiments, m and n are the same. In some embodiments, m and n are different. In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:385). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:386). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:387). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:388). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:389). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:390). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:391). In some embodiments, the peptide linker comprises the amino acid sequence of ((SEQ ID NO:392). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:393). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:394). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:395). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:396). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:397). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:398). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:399). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:400). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:401). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:402). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:403). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:404). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:405). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:406). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:407). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:408). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:409). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:410). In some embodiments, the peptide linker comprises the amino acid sequence of (SEQ ID NO:411). In some embodiments, the peptide linker comprises the amino acid sequence of any one of SEQ ID NOs: 286-411.

[0268] Exemplary peptide linker sequences are provided in **Table 3** below:

[0269] Table 3. Exemplary peptide linker sequences.

New SEQ ID	Linker sequence
286	GS
287	GGS
288	SGGS
289	SGGSSGGSSGSETPGTSESATPESSGGSSGGSS
290	SGGSSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSSGGS
291	SGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGS
292	SGGSSGGSSGSETPGTSESATPESSGGS
293	SGGSSGSETPGTSESATPESSGGS
294	SGGSSGSETPGTSESATPES
295	SGSETPGTSESATPES
296	SGGSSGGSSGSETPGTSESATPESSGGSSGGS
297	SGGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
298	SGGSPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
299	SGGSPAPAPAPAPAPAPAPAPSGGS
300	SGGSPAPAPAPAPAPSGGS
301	SGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
302	SGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
303	SGGSSGGSSGGSSGGSSGGSSGGS
304	SGGSSGGSSGGSSGGSSGGS
305	SGGSSGGSSGGSSGGS
306	SGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
307	SGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
308	AEAAAKEAAAKEAAAKEAAAKA
309	SGGSEAAAKEAAAKEAAAKEAAAKSGGS

New SEQ ID	Linker sequence
310	SGGSEAAAKEAAAKEAAAKSGGS
311	SGGSEAAAKEAAAKSGGS
312	GGGSSGGSSGSETPGTSESATPESSGGSSGGSS
313	GGGSSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSSGGS
314	GGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGS
315	GGGSSGGSSGSETPGTSESATPESSGGS
316	GGGSSGSETPGTSESATPESSGGS
317	GGGSSGSETPGTSESATPES
318	GGSETPGTSESATPES
319	GGGSSGGSSGSETPGTSESATPESSGGSSGGS
320	GGGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
321	GGGSPAPAPAPAPAPAPAPAPAPAPAPSGGS
322	GGGSPAPAPAPAPAPAPAPAPSGGS
323	GGGSPAPAPAPAPAPSGGS
324	GGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
325	GGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
326	GGGSSGGSSGGSSGGSSGGSSGGS
327	GGGSSGGSSGGSSGGSSGGS
328	GGGSSGGSSGGSSGGS
329	GGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
330	GGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
331	GEAAAKEAAAKEAAAKEAAAKA
332	GGGSEAAAKEAAAKEAAAKEAAAKSGGS
333	GGGSEAAAKEAAAKEAAAKSGGS
334	GGGSEAAAKEAAAKSGGS
335	SGGSEAAAKEAAAKSGGSSGGSSGSETPGTSESATPESSGGSSGGSS
336	SGGSEAAAKEAAAKSGGSSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSSGGS
337	SGGSEAAAKEAAAKSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGS
338	SGGSEAAAKEAAAKSGGSSGGSSGSETPGTSESATPESSGGS
339	SGGSEAAAKEAAAKSGGSSGSETPGTSESATPESSGGS
340	SGGSEAAAKEAAAKSGGSSGSETPGTSESATPES
341	SGGSEAAAKEAAAKSGSETPGTSESATPES
342	SGGSEAAAKEAAAKSGGSSGGSSGSETPGTSESATPESSGGSSGGS
343	SGGSEAAAKEAAAKSGGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
344	SGGSEAAAKEAAAKSGGSPAPAPAPAPAPAPAPAPAPAPAPAPSGGS

New SEQ ID	Linker sequence
345	SGGSEAAAKEAAAKSGGSPAPAPAPAPAPAPAPAPSGGS
346	SGGSEAAAKEAAAKSGGSPAPAPAPAPAPSGGS
347	SGGSEAAAKEAAAKSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
348	SGGSEAAAKEAAAKSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
349	SGGSEAAAKEAAAKSGGSSGGSSGGSSGGSSGGSSGGS
350	SGGSEAAAKEAAAKSGGSSGGSSGGSSGGSSGGS
351	SGGSEAAAKEAAAKSGGSSGGSSGGSSGGS
352	SGGSEAAAKEAAAKSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
353	SGGSEAAAKEAAAKSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGS
354	SGGSEAAAKEAAAKAEAAAKEAAAKEAAAKEAAAKA
355	SGGSEAAAKEAAAKSGGSEAAAKEAAAKEAAAKEAAAKSGGS
356	SGGSEAAAKEAAAKSGGSEAAAKEAAAKEAAAKSGGS
357	SGGSEAAAKEAAAKSGGSEAAAKEAAAKSGGS
358	SGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
359	SGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
360	SGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
361	SGGSGGSGSETPGTSESATPESSGGSGGS
362	SGGSGGSGSETPGTSESATPESSGSETPGTSESATPESSGGSGGS
363	SGGSGSETPGTSESATPESSGSETPGTSESATPESSGGS
364	SGGSGGSGSETPGTSESATPESSGGS
365	SGGSGSETPGTSESATPESSGGS
366	SGGSGSETPGTSESATPES
367	SGGSGGSGGSGGSGGSGGSGGSGGSGGSGGS
368	SGGSGGSGGSGGSGGSGGSGGSGGS
369	SGGSGGSGGSGGSGGSGGS
370	SGGSGGSGGSGGSGGS
371	SGGSGGSGGSGGS
372	GGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
373	GGSPAPAPAPAPAPAPAPAPAPAPAPAPSGGS
374	GGSPAPAPAPAPAPAPAPAPSGGS
375	GGSPAPAPAPAPAPSGGS
376	(GGGGS)n
377	(G)n
378	(EAAAK)n
379	(GGS)n

New SEQ ID	Linker sequence
380	(SGGS)n
381	(GGSS)n
382	(XP)n
383	SGGSGGSGGS
384	SGGSSGGSSGSETPGTSESATPESAGSYPYDVPDYAGSAAPAAKKKKLDGSGSGGSSGGS
385	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
386	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
387	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
388	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
389	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
390	GGSSGGSSGGSSGGSSGGSSGGSSGGSSGGS
391	GGSSGGSSGGSSGGSSGGSSGGSSGGS
392	GGSSGGSSGGSSGGSSGGSSGGS
393	GGSSGGSSGGSSGGSSGGS
394	GGSSGGSSGGSSGGS
395	GGSSGGSSGGS
396	GGSSGGS
397	GGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGS
398	GGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGS
399	GGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGS
400	GGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGS
401	GGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKGGS
402	GGSEAAAKEAAAKEAAAKEAAAKEAAAKGGS
403	GGSEAAAKEAAAKEAAAKEAAAKGGS
404	GGSEAAAKEAAAKEAAAKGGS
405	GGSEAAAKEAAAKGGS
406	GGSEAAAKGGS
407	GGSSSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESGGSS
408	GGSSSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESGGSS
409	GGSSSGSETPGTSESATPESSGSETPGTSESATPESSGSETPGTSESATPESGGSS
410	GGSSSGSETPGTSESATPESSGSETPGTSESATPESGGSS
411	GGSSSGSETPGTSESATPESGGSS

[0270] In some embodiments, two or more polypeptide components of a prime editor are linked to each other by a non-peptide linker. In some embodiments, the linker comprises a non-peptide moiety. In some embodiments, the linker is a carbon-nitrogen bond of an amide linkage. In certain embodiments, the linker is a cyclic or acyclic, substituted or unsubstituted, branched or unbranched aliphatic or heteroaliphatic linker. In certain embodiments, the linker is polymeric (*e.g.*, polyethylene, polyethylene glycol, polyamide, polyester, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminoalkanoic acid. In certain embodiments, the linker comprises an aminoalkanoic acid (*e.g.*, glycine, ethanoic acid, alanine, beta-alanine, 3- aminopropanoic acid, 4-aminobutanoic acid, 5-pentanoic acid, etc.). In certain embodiments, the linker comprises a monomer, dimer, or polymer of aminohexanoic acid (Ahx). In certain embodiments, the linker is based on a carbocyclic moiety (*e.g.*, cyclopentane, cyclohexane). In other embodiments, the linker comprises a polyethylene glycol moiety (PEG). In certain embodiments, the linker comprises an aryl or heteroaryl moiety. In certain embodiments, the linker is based on a phenyl ring. The linker may include functionalized moieties to facilitate attachment of a nucleophile (*e.g.*, thiol, amino) from the peptide to the linker. Any electrophile may be used as part of the linker. Exemplary electrophiles include, but are not limited to, activated esters, activated amides, Michael acceptors, alkyl halides, aryl halides, acyl halides, and isothiocyanates.

[0271] Components of a prime editor may be connected to each other in any order. In some embodiments, the DNA binding domain and the DNA polymerase domain of a prime editor may be fused to form a fusion protein, or may be joined by a peptide or protein linker, in any order from the N terminus to the C terminus. In some embodiments, a prime editor comprises a DNA binding domain fused or linked to the C-terminal end of a DNA polymerase domain. In some embodiments, a prime editor comprises a DNA binding domain fused or linked to the N-terminal end of a DNA polymerase domain. In some embodiments, the prime editor comprises a fusion protein comprising the structure NH2-[DNA binding domain]-[DNA polymerase]-COOH; or NH2-[polymerase]-[DNA binding domain]-COOH, wherein each instance of "]-[" indicates the presence of an optional linker sequence. In some embodiments, a prime editor comprises a fusion protein and a DNA polymerase domain provided in trans, wherein the fusion protein comprises the structure NH2-[DNA binding domain]-[RNA-protein recruitment polypeptide]-COOH. In some embodiments, a prime editor comprises a fusion protein and a DNA binding domain provided in trans, wherein the fusion protein comprises the structure NH2-[DNA polymerase domain]-[RNA-protein recruitment polypeptide]-COOH.

[0272] In addition, the NLSs may be expressed as part of a prime editor composition, fusion protein, or complex. The location of the NLS fusion can be at the N-terminus, the C-terminus, or positioned anywhere within a sequence of a prime editor or a component thereof (e.g., inserted between the DNA binding domain and the DNA polymerase domain of a prime editor fusion protein, between the DNA binding domain and a linker sequence, between a DNA polymerase and a linker sequence, between two linker sequences of a prime editor fusion protein or a component thereof, in either N-terminus to C-terminus or C-terminus to N-terminus order). In some embodiments, a prime editor is a fusion protein that comprises an NLS at the N terminus. In some embodiments, a prime editor is a fusion protein that comprises an NLS at the C terminus. In some embodiments, a prime editor is a fusion protein that comprises at least one NLS at both the N terminus and the C terminus. In some embodiments, the prime editor is a fusion protein that comprises two NLSs at the N terminus and/or the C terminus.

[0273] In some embodiments, a prime editing comprises a fusion protein that comprises one or more peptide linkers and one or more NLSs. In some embodiments, a prime editor fusion protein comprises one or more a bipartite NLSs. In some embodiments, a prime editor fusion protein comprises one or more bipartite NLSs and one or more peptide linkers. In some embodiments, a prime editor fusion protein comprises two bipartite NLSs and one or more peptide linkers. In some embodiments, the one or more bipartite NLSs are cmyc bipartite NLSs. In some embodiments, the two bipartite NLSs are each at the N-terminus and the C-terminus of the prime editor fusion protein, respectively. In some embodiments, a prime editor fusion protein comprises a bipartite NLSs and a XTEN linker. In some embodiments, a prime editor fusion protein comprises two bipartite NLSs and a XTEN linker. In some embodiments, a prime editor fusion protein comprises a bipartite NLSs and a peptide linker comprising a (GGSS) motif. In some embodiments, a prime editor fusion protein comprises two bipartite NLSs and a peptide linker comprising a (GGSS) motif. In some embodiments, a prime editor fusion protein comprises a bipartite NLSs and a peptide linker comprising 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, or more (GGSS) motifs. In some embodiments, a prime editor fusion protein comprises two bipartite NLSs and a peptide linker comprising 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, or more (GGSS) motifs. In some embodiments, a prime editor fusion protein comprises a bipartite NLSs and a peptide linker comprising 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, or more (EAAAK) motifs. In some embodiments, a prime editor fusion protein comprises two bipartite NLSs and a peptide linker comprising 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, or more (EAAAK) motifs.

[0274] In some embodiments, a prime editor comprises a fusion protein comprising a DNA binding domain (*e.g.*, Cas9(H840A)) and a reverse transcriptase (*e.g.*, a variant MMLV RT) having the of the following structure, from N-terminus to C-terminus: [NLS]- [Cas9(H840A)]-[peptide linker]-[MMLV_RT(D200N)(T330P)(L603W)(T306K)(W313F)], wherein amino acid substitutions are indicated in parentheses.

[0275] In some embodiments, a prime editor comprises a fusion protein comprising the structure, from N-terminus to C-terminus:

[NLS1]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase];

[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS1];

[NLS1]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS2];

[NLS1]-[NLS2]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS];

[NLS1]-[NLS2]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS3]-[NLS4];

[NLS1]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS2]-[NLS3];

[NLS1]-[NLS2]-[NLS3]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS4];

[NLS1]-[NLS2]-[NLS3]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS4]-[NLS5];

[NLS1]-[NLS2]-[NLS3]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS4]-[NLS5]-[NLS6];

[NLS1]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS2]-[NLS3]-[NLS4];

[NLS1]-[NLS2]-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS3]-[NLS4]-[NLS5];

[NLS1]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain];

[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS1];

[NLS1]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS2];

[NLS1]-[NLS2]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS];

[NLS1]-[NLS2]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS3]-[NLS4];

[NLS1]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS2]-[NLS3];

[NLS1]-[NLS2]-[NLS3]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS4];

[NLS1]-[NLS2]-[NLS3]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS4]-[NLS5];

[NLS1]-[NLS2]-[NLS3]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS4]-[NLS5]-[NLS6];

[NLS1]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS2]-[NLS3]-[NLS4]; or

[NLS1]-[NLS2]-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS3]-[NLS4]-[NLS5].

[0276] In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus:

[NLS]n-[DNA binding domain]-[peptide linker]-[Reverse transcriptase]-[NLS]m, or [NLS]n-[Reverse transcriptase]-[peptide linker]-[DNA binding domain]-[NLS]m, wherein n and m are any integer between 0 and 50, wherein [NLS]n refers to n NLS motif sequences, and wherein [NLS]m refers to m NLS motif sequences. The n NLS motif sequences may or may not be the same. In some embodiments, m and n are the same. In some embodiments, n and m are different.

[0277] The DNA polymerase can be any of the DNA polymerase described herein or known in the art. In some embodiments, the DNA polymerase is a Cas9 nickase (nCas9). In some embodiments, the DNA polymerase is a nCas9 comprising a nuclease inactivating amino acid substitution in a HNH domain. In some embodiments, the DNA polymerase is a nCas9 comprising a H840A amino acid substitution as compared to a wild type SpCas9.

[0278] The Reverse transcriptase can be any of the reverse transcriptase described herein or known in the art. In some embodiments, the reverse transcriptase is a M-MLV RT. In some embodiments, the reverse transcriptase is a M-MLV RT functional variant with any one of the amino acid substitutions or truncations as described herein. In some embodiments, .

[0279] In some embodiments, any one of NLS1, NLS2, NLS3, NLS4, NLS5, NLS6 is independently a NLS known in the art or described herein. In some embodiments, any one of NLS1, NLS2, NLS3, NLS4, NLS5, NLS6 is a bipartite NLS. In some embodiments, any one of NLS1, NLS2, NLS3, NLS4, NLS5, NLS6 is a c-Myc NLS comprising the amino acid sequence PAAKRVKLD (SEQ ID NO: 19). In some embodiments, any one of NLS1, NLS2, NLS3, NLS4, NLS5, NLS6 is a monopartite NLS. In some embodiments, any one of NLS1, NLS2, NLS3, NLS4, NLS5, NLS6 is a SV40NLS.

[0280] In some embodiments, two or more of the NLSs1-6 are the same. In some embodiments, the NLSs 1-6 are different from each other.

[0281] In any of the prime editor structures, the peptide linker may be any peptide linker described herein or known in the art. In some embodiments, the peptide linker comprises the amino acid sequence, from N terminus to C-terminus: (GGSS)m-(GGS)n, wherein m and n are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the amino acid sequence, from N terminus to C-terminus: (GGS)n-(GGSS)m, wherein m and n are each any integer between 0 and 50. In some embodiments, m and n are the same. In some embodiments, m and n are different. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)2-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)3-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)4-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)5-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)6-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)7-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)8-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)9-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)10-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)11-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)12-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)13-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)14-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)15-(GGS). In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)2. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)3. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)4. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)5. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)6. In some embodiments, the peptide linker comprises the amino acid sequence (GGSS)-(GGS)7. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)8. In some embodiments, the peptide linker comprises the amino acid sequence (GGSS)-(GGS)9. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)10. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)11. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)12. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)13. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)14. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)-(GGS)15.

[0282] In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)2-(GGS)2. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)3-(GGS)3. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)4-(GGS)4. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)5-(GGS)5. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)6-(GGS)6. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)7-(GGS)7. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)8-(GGS)8. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)9-(GGS)9. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)10-(GGS)10. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)11-(GGS)11. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)12-(GGS)12. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)13-(GGS)13. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)14-(GGS)14. In some embodiments, the peptide linker comprises the amino acid sequence from N terminus to C-terminus: (GGSS)15-(GGS)15.

[0283] In some embodiments, the peptide linker comprises a (GGSS) motif. In some embodiments, the peptide linker comprises an XTEN motif comprising the sequence SGSETPGTSESATPES (SEQ ID NO: 295). In some embodiments, the peptide linker comprises two or more (GGSS) motifs. In some embodiments, the peptide linker comprises an XTEN motif and a (GGSS) motif. In some embodiments, the peptide linker comprises one or more XTEN motifs and two or more (GGSS) motifs. In some embodiments, the peptide linker comprises two more XTEN motifs and two or more (GGSS) motifs. In some embodiments, the one or more or two or more XTEN motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more XTEN motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more (GGSS) motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more (GGSS) motifs are at the N terminus of the peptide linker. In some embodiments, the peptide linker comprises one or more

XTEN motifs flanked by a (GGSS) motif at each end. In some embodiments, the peptide linker comprises one or more XTEN motifs flanked by two or more (GGSS) motifs at each end.

[0284] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)n-(XTEN)m-(GGSS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)2-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)2-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)2-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)1-(XTEN)3-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)3-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)3-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)4-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)4-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)5-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)5-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)6-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)6-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)6-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)6-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)7-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)7-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)7-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)7-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)8-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)8-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)8-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)8-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)9-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)9-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)9-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)9-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)10-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)10-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN)10-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)10-(GGSS)10.

[0285] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)2-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)3-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)4-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)5-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)6-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)7-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)8-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)9-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (GGSS)10-(XTEN)5.

[0286] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2 -(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2 -(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(GGSS)10-. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(GGSS)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(GGSS)10.

[0287] In some embodiments, the peptide linker comprises the sequence (GGSS)n, wherein n is any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence (GGSS)2. In some embodiments, the peptide linker comprises the sequence (GGSS)3. In some embodiments, the peptide linker comprises the sequence (GGSS)4. In some embodiments, the peptide linker comprises the sequence (GGSS)5. In some embodiments, the peptide linker comprises the sequence (GGSS)6. In some embodiments, the peptide linker comprises the sequence (GGSS)7. In some embodiments, the peptide linker comprises the sequence (GGSS)8. In some embodiments, the peptide linker comprises the sequence (GGSS)9. In some embodiments, the peptide linker comprises the sequence (GGSS)10. In some embodiments, the peptide linker comprises the sequence (GGSS)11. In some embodiments, the peptide linker comprises the sequence (GGSS)12. In some embodiments, the peptide linker comprises the sequence (GGSS)13. In some embodiments, the peptide linker comprises the sequence (GGSS)14. In some embodiments, the peptide linker comprises the sequence (GGSS)15. In some embodiments, the peptide linker comprises the sequence (GGSS)16. In some embodiments, the peptide linker comprises the sequence (GGSS)17. In some embodiments, the peptide linker comprises the sequence (GGSS)18. In some embodiments, the peptide linker comprises the sequence (GGSS)19. In some embodiments, the peptide linker comprises the sequence (GGSS)20.

[0288] In some embodiments, the peptide linker comprises a GGSS motif, an XTEN motif, and a GGS motif. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)n-(XTEN)m-(GGS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, n, m, and w are the same integer. In some embodiments, n, m, and w are each different from each other. In some embodiments, the peptide linker comrpsies the sequence, from N-terminus to C-terminus: (GGSS)n-(XTEN)m-(GGSS)x-(GGS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, n, m, x, and w are the same integer. In some embodiments, n, m, x, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)2-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGS)3. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGS)3. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGS)3. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)4-(GGS)4. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGS)4. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGS)4. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)5-(GGS)5. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGS)5. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGS)5.

[0289] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)2-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGSS)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)2-(XTEN)2-(GGSS)2-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)3-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)-(GGS)3. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGSS)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)3-(XTEN)3-(GGSS)3-(GGS)3. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)4-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)-(GGS)4. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGSS)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)4-(XTEN)4-(GGSS)4-(GGS)4. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)5-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)-(XTEN)-(GGSS)-(GGS)5. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGSS)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGSS)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)5-(XTEN)5-(GGSS)5-(GGS)5.

[0290] In some embodiments, the peptide linker comprises a (EAAAK) motif. In some embodiments, the peptide linker comprises two or more (EAAAK) motifs. In some embodiments, the peptide linker comprises an XTEN motif and a (EAAAK) motif. In some embodiments, the peptide linker comprises one or more XTEN motifs and two or more (EAAAK) motifs. In some embodiments, the peptide linker comprises two more XTEN motifs and two or more (EAAAK) motifs. In some embodiments, the one or more or two or more XTEN motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more XTEN motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more (EAAAK) motifs are at the N terminus of the peptide linker. In some embodiments, the one or more or two or more (EAAAK) motifs are at the N terminus of the peptide linker. In some embodiments, the peptide linker comprises one or more XTEN motifs flanked by a (EAAAK) motif at each end. In some embodiments, the peptide linker comprises one or more XTEN motifs flanked by two or more (EAAAK) motifs at each end.

[0291] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (EAAAK)n-(XTEN)m-(EAAAK)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)2-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)2-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-

(XTEN)-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)2-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)2-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)2-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)1-(XTEN)3-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)3-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)3-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)3-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)3-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)3-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)3-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)3-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)4-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)4-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)4-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)4-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)5-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)5-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)5-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)5-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)6-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)6-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)6-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)6-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)7-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)7-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)7-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)7-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)8-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)8-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)8-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)8-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)9-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)9-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)9-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)9-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)10-(EAAAK).

In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)10-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN)10-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)10-(EAAAK)10.

[0292] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)2-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)3-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)4-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)5-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)6-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)7-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)8-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)9-(XTEN)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (EAAAK)10-(XTEN)5.

[0293] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK). In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)2. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)3. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)4. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)5. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2 -(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-

(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)6. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)7. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)8. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2 -(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)9. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)-(EAAAK)10-. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)2-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)3-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)4-(EAAAK)10. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: (XTEN)5-(EAAAK)10.

[0294] In some embodiments, the peptide linker comprises the sequence (EAAAK)n, wherein n is any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence (EAAAK)2. In some embodiments, the peptide linker comprises the sequence (EAAAK)3. In some embodiments, the peptide linker comprises the sequence (EAAAK)4. In some embodiments, the peptide linker comprises the sequence (EAAAK)5. In some embodiments, the peptide linker comprises the sequence (EAAAK)6. In some embodiments, the peptide linker comprises the sequence (EAAAK)7. In some embodiments, the peptide linker comprises the sequence (EAAAK)8. In some embodiments, the peptide linker comprises the sequence (EAAAK)9. In some embodiments, the peptide linker comprises the sequence (EAAAK)10. In some embodiments, the peptide linker comprises the sequence (EAAAK)11. In some embodiments, the peptide linker comprises the sequence (EAAAK)12. In some embodiments, the peptide linker comprises the sequence (EAAAK)13. In some embodiments, the peptide linker comprises the sequence (EAAAK)14. In some embodiments, the peptide linker comprises the sequence (EAAAK)15. In some embodiments, the peptide linker comprises the sequence (EAAAK)16. In some embodiments, the peptide linker comprises the sequence (EAAAK)17. In some embodiments, the peptide linker comprises the sequence (EAAAK)18. In some embodiments, the peptide linker comprises the sequence (EAAAK)19. In some embodiments, the peptide linker comprises the sequence (EAAAK)20.

[0295] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)n-A, wherein n is any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)2-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)3-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)4-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)5-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)6-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)7-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)8-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)9-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)10-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)11-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)12-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)13-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)14-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)15-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)16-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)17-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)18-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)19-A. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: A-(EAAAK)20-A.

[0296] In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)n-SGGS, wherein n is any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)2-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)3-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)4-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)5-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)6-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to

C-terminus: SGGS-(EAAAK)7-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)8-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)9-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)10-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)11-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)12-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)13-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)14-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)15-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)16-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)17-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)18-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)19-SGGS. In some embodiments, the peptide linker comprises the sequence from N-terminus to C-terminus: SGGS-(EAAAK)20-SGGS.

[0297] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)n-(EAAAK)m-(GGS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)6-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)7-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)8-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)9-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)10-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)11-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)12-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)13-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)14-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(EAAAK)15-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)2-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)3-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)4-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)5-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)6-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)7-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)8-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)9-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)10-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)11-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)12-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)13-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)14-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(EAAAK)15-(GGS)2.In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)n-(XTEN)m-(EAAAK)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGSS)n-(EAAAK)m-(XTEN)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (EAAAK)n-(XTEN)m-(GGSS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (EAAAK)n-(GGSS)m-(XTEN)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (XTEN)n-(GGSS)m-(EAAAK)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (XTEN)n-(EAAAK)m-(GGSS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other.

[0298] In some embodiments, the peptide linker comprises the sequence (PAPA)n, wherein n is any integer between 0 and 50. In some embodiments, the peptide linker comprises the sequence (PAPA)2. In some embodiments, the peptide linker comprises the sequence (PAPA)3. In some embodiments, the peptide linker comprises the sequence (PAPA)4. In some embodiments, the peptide linker comprises the sequence (PAPA)5. In some embodiments, the peptide linker comprises the sequence (PAPA)6. In some embodiments, the peptide linker comprises the sequence (PAPA)7. In some embodiments, the peptide linker comprises the sequence (PAPA)8. In some embodiments, the peptide linker comprises the sequence (PAPA)9. In some embodiments, the peptide linker comprises the sequence (PAPA)10. In some embodiments, the peptide linker comprises the sequence (PAPA)11. In some embodiments, the peptide linker comprises the sequence (PAPA)12. In some embodiments, the peptide linker comprises the sequence (PAPA)13. In some embodiments, the peptide linker comprises the sequence (PAPA)14. In some embodiments, the peptide linker comprises the sequence (PAPA)15. In some embodiments, the peptide linker comprises the sequence (PAPA)16. In some embodiments, the peptide linker comprises the sequence (PAPA)17. In some embodiments, the peptide linker comprises the sequence (PAPA)18. In some embodiments, the peptide linker comprises the sequence (PAPA)19. In some embodiments, the peptide linker comprises the sequence (PAPA)20.

[0299] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)n-(PAPA)m-(GGS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)2-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)3-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)4-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)5-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)6-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)7-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)8-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)9-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)10-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)11-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)12-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)13-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)14-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)15-(GGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)2-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)3-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)4-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)5-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)6-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)7-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)8-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)9-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)10-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)11-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)12-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)13-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)14-(GGS)2. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)2-(PAPA)15-(GGS)2.

[0300] In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)n-(PAPA)m-(PSGGS)w, wherein n, m, w are each any integer between 0 and 50. In some embodiments, m, n, and w are the same, or two of m, n, and w are the same. In some embodiments, m, n, and w are each different from each other. In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)2-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)3-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)4-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)5-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)6-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)7-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)8-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)9-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)10-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)11-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)12-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)13-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)14-(PSGGS). In some embodiments, the peptide linker comprises the sequence, from N-terminus to C-terminus: (GGS)-(PAPA)15-(PSGGS).

[0301] In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 286-411. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence selected from the group consisting of SEQ ID Nos 289-311. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID Nos 302. In some embodiments, the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID 309. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 302. In some embodiments, the peptide linker comprises the sequence of SEQ ID No 309.

Nuclear localization signals

[0302] In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus. In some embodiments, a prime editor fusion protein comprises a first NLS at the N terminus and a second NLS at the C terminus. In some embodiments the first and second NLS are identical. In some embodiments the first and second NLS are not identical. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises a first NLS at the N terminus of the DNA polymerase domain and a second NLS at the C terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises a first NLS at the C terminus of the DNA polymerase domain and a second NLS at the N terminus of the DNA binding domain. In some embodiments, the first and the second NLS are identical. In some embodiments the first and the second NLS are not identical. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises two or more NLS. In some embodiments, a prime editor fusion protein comprises two or more NLS at the N terminus and/or C terminus. In some embodiments, a prime editor fusion protein comprises an NLS between DNA binding domain and DNA polymerase domain.

[0303] In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus, wherein the NLS comprises the sequence MKRTADGSEFESPKKKRKV (SEQ ID NO: 9). In some embodiments, the prime editor fusion protein comprises an NLS at the N terminus, wherein the NLS comprises the sequence (KRTADGSEFESPKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus, wherein the NLS comprises the sequence MPAAKRVKLDGGKRTADGSEFESPKKKRKV (SEQ ID NO:15). In some embodiments, the prime editor fusion protein comprises an NLS at the N terminus, wherein the NLS comprises the sequence (PAAKRVKLDGGKRTADGSEFESPKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

[0304] In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence KRTADGSEFESPKKKRKV (SEQ ID NO: 8). In some embodiments, the prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence (KRTADGSEFESPKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

[0305] In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence PKKKRKV (SEQ ID NO: 12). In some embodiments, the prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence (PKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

[0306] In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence KRTADSQHSTPPKTKRKV-EFES-PKKKRKV. In some embodiments, the prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence (KRTADSQHSTPPKTKRKV-EFES-PKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

[0307] In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence KRTADSQHSTPPKTKRKV-EFE-PKKKRKV. In some embodiments, the prime editor fusion protein comprises an NLS at the C terminus, wherein the NLS comprises the sequence (KRTADSQHSTPPKTKRKV-EFE-PKKKRKV)n, wherein n is any integer between 0 and 50, between 1 and 50, between 2 and 40, between 2 and 25, between 2 and 10, or between 2 and 5.

[0308] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence KRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence KRTADGSEFESPKKKRKV.

[0309] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence KRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence PKKKRKV.

[0310] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence KRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence KRTADSQHSTPPKTKRKV-EFES-PKKKRKV.

[0311] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence KRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence KRTADSQHSTPPKTKRKV-EFE-PKKKRKV.

[0312] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence PAAKRVKLDGGKRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence PAAKRVKLDGGKRTADGSEFESPKKKRKV.

[0313] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence PAAKRVKLDGGKRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence PKKKRKV.

[0314] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence PAAKRVKLDGGKRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence KRTADSQHSTPPKTKRKV-EFES-PKKKRKV.

[0315] In some embodiments, a prime editor fusion protein comprises one or more NLSs at the N terminus and one or more NLSs at the C terminus, wherein the NLSs at the N terminus comprises the sequence PAAKRVKLDGGKRTADGSEFESPKKKRKV, and wherein the NLSs at the C terminus comprises the sequence KRTADSQHSTPPKTKRKV-EFE-PKKKRKV.

[0316] In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: BPNLS-DNA binding domain-(GGSS)2-XTEN-(GGSS2)-Reverse transcriptase-BPNLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: SV40BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE-SV40BPNLS1. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: SV40BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE(G504X)-SV40BPNLS1.

[0317] In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: BPNLS-DNA binding domain-(GGSS)2-XTEN-(GGSS2)-Reverse transcriptase-BPNLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: SV40BPNLS-DNA binding domain-SGGS-(EAAAK)4-SGGS-REVERSE TRANSCRIPTASE-SV40BPNLS1. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: SV40BPNLS-DNA binding domain-SGGS-(EAAAK)4-SGGS-REVERSE TRANSCRIPTASE(G504X)-SV40BPNLS1.

[0318] In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: c-MycNLS-BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE-BPNLS-NLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: C-mycNLS-BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE-BPNLS-SV40NLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: BPNLS-DNA binding domain-(EAAAK)8-REVERSE TRANSCRIPTASE-BPNLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: BPNLS-DNA binding domain-(GGSS)2-XTEN-(GGSS)2-REVERSE TRANSCRIPTASE-NLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: BPNLS-DNA binding domain-(GGSS)2-XTEN-(GGSS)2-REVERSE TRANSCRIPTASE-SV40NLS.In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: C-mycNLS-BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE(G504X)-BPNLS-NLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: C-mycNLS -BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE-BPNLS-SV40NLS. In some embodiments, a prime editor fusion protein comprises the structure, from N-terminus to C-terminus: C-mycNLS -BPNLS-DNA binding domain-(SGGS)8-REVERSE TRANSCRIPTASE(G504X)-BPNLS-NLS.

[0319] In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus. In some embodiments, a prime editor fusion protein comprises a first NLS at the N terminus and a second NLS at the C terminus. In some embodiments the first and second NLS are identical. In some embodiments the first and second NLS are not identical. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises a first NLS at the N terminus of the DNA polymerase domain and a second NLS at the C terminus of the DNA binding domain. In some embodiments, a prime editor fusion protein comprises an NLS at the N terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises a first NLS at the C terminus of the DNA polymerase domain and a second NLS at the N terminus of the DNA binding domain. In some embodiments, the first and the second NLS are identical. In some embodiments the first and the second NLS are not identical. In some embodiments, a prime editor fusion protein comprises an NLS at the C terminus of the DNA polymerase domain. In some embodiments, a prime editor fusion protein comprises two or more NLS. In some embodiments, a prime editor fusion protein comprises two or more NLS at the N terminus and/or C terminus. In some embodiments, a prime editor fusion protein comprises an NLS between DNA binding domain and DNA polymerase domain. In some embodiments, NLS or the two or more NLSs comprise a bipartite NLS (BPNLS). In some embodiments, the BPNLS is a bipartite SV40 NLS or a bipartite Xenopus nucleoplasmin NLS. In some embodiments, the BPNLS comprises an amino acid sequence selected from the group consisting of SEQ ID Nos 8-23.

[0320] In some embodiments, a prime editor fusion protein, a polypeptide component of a prime editor, or a polynucleotide encoding the prime editor fusion protein or polypeptide component, may be split into an N-terminal half and a C-terminal half or polypeptides that encode the N-terminal half and the C terminal half, and provided to a target DNA in a cell separately. For example, in certain embodiments, a prime editor fusion protein may be split into a N-terminal and a C-terminal half for separate delivery in AAV vectors, and subsequently translated and colocalized in a target cell to reform the complete polypeptide or prime editor protein. In such cases, separate halves of a protein or a fusion protein may each comprise a split-intein to facilitate colocalization and reformation of the complete protein or fusion protein by the mechanism of intein facilitated trans splicing. In some embodiments, a prime editor comprises a N-terminal half fused to an intein-N, and a C-terminal half fused to an intein-C, or polynucleotides or vectors (*e.g.* AAV vectors) encoding each thereof. When delivered and/or expressed in a target cell, the intein-N and the intein-C can be excised via protein trans-splicing, resulting in a complete prime editor fusion protein in the target cell.

[0321] In some embodiments, a prime editor is a fusion protein that comprises the amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to the amino acid sequence of any one of SEQ ID NOs: 77, 78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116,117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 167, 170, 173, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, and 230. In some embodiments, a prime editor comprises a fusion protein that comprises the amino acid sequence of SEQ ID NO: 34, 35, 77, 78, 85, 86, 620, 622, 624, 625, or 647. In some embodiments, a prime editor comprises a fusion protein that comprises a DNA binding domain comprising the amino acid sequence of any one of SEQ ID Nos 2, 6, 7, or 596-613. In some embodiments, a prime editor comprises a fusion protein that comprises a reverse transcriptase comprising the amino acid sequence of any one of SEQ ID Nos: 1, 4, 5, 36, 45, 54, 63, or 623. In some embodiments, a prime editor is a fusion protein that comprises the amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% identity to the amino acid sequence of SEQ ID No: 77. In some embodiments, a prime editor is a fusion protein that comprises the amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% identity to the amino acid sequence of SEQ ID No: 78. In some embodiments, a prime editor is a fusion protein that comprises the amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% identity to the amino acid sequence of SEQ ID No: 85. In some embodiments, a prime editor is a fusion protein that comprises the amino acid sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% identity to the amino acid sequence of SEQ ID No: 86. In some embodiments, a prime editor is a fusion protein that is encoded by a polynucleotide comprising a nucleotide sequence as set forth in any of SEQ ID NO: 79-82, 87-90, 94-95, 97-98, 100-103, 106-109, 112-115, 118-121, 123, 124, 126, 127, 129, 130, 132, 133, 135, 136, 138, 139, 144, 145, 147, 148, 150, 151, 153, 154, 156, 157, 159, 160, 162, 163, 165, 166, 168, 169, 171, 172, 174, 175, 177, 178, 180, 181, 183, 184, 186, 187, 189, 190, 192, 193, 195, 196, 198, 199, 201, 202, 204, 205, 207, 208, 210, 211, 213, 214, 216, 217, 219, 220, 222, 223, 225, 226, 228, 229, 231, 232, 233, 234, 241, 242, 274-285, and 592-595. In some embodiments, a prime editor is a fusion protein that is encoded by a polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 79- 82, 87-90, 274-285, or 592-595.

Prime editing guide RNAs (PEgRNAs)

[0322] The term "prime editing guide RNA", or "PEgRNA", refers to a guide polynucleotide that comprises one or more intended nucleotide edits for incorporation into a double stranded target polynucleotide, *e.g.*, double stranded target DNA. In some embodiments, the PEgRNA associates with and directs a prime editor to incorporate the one or more intended nucleotide edits into the double stranded target DNA, *e.g.*, a target gene via prime editing. "Nucleotide edit" or "intended nucleotide edit" refers to a specified deletion of one or more nucleotides at one specific position, insertion of one or more nucleotides at one specific position, substitution of a single nucleotide, or other alterations at one specific position to be incorporated into the sequence of the double stranded target DNA, *e.g.*, a target gene. Intended nucleotide edit may refer to the edit on the editing template as compared to the sequence on the target strand of the double stranded target DNA, *e.g.*, a target gene, or may refer to the edit encoded by the editing template on the newly synthesized single stranded DNA that replaces the editing target sequence, as compared to the editing target sequence. In some embodiments, a PEgRNA comprises a spacer sequence that is complementary or substantially complementary to a search target sequence on a target strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the PEgRNA comprises a gRNA core that associates with a DNA binding domain, *e.g.*, a CRISPR-Cas protein domain, of a prime editor. In some embodiments, the PEgRNA further comprises an extended nucleotide sequence comprising one or more intended nucleotide edits compared to the endogenous sequence of the double stranded target DNA, *e.g.*, a target gene, wherein the extended nucleotide sequence may be referred to as an extension arm.

[0323] In certain embodiments, the extension arm comprises a primer binding site sequence (PBS) that can initiate target-primed DNA synthesis. In some embodiments, the PBS is complementary or substantially complementary to a free 3' end on the edit strand of the double stranded target DNA, *e.g.*, a target gene at a nick site generated by the prime editor. In some embodiments, the extension arm further comprises an editing template that comprises one or more intended nucleotide edits to be incorporated in the double stranded target DNA, *e.g.*, a target gene by prime editing. In some embodiments, the editing template is a template for an RNA-dependent DNA polymerase domain or polypeptide of the prime editor, for example, a reverse transcriptase domain. The reverse transcriptase editing template may also be referred to herein as an RT template, or RTT. In some embodiments, the editing template comprises partial complementarity to an editing target sequence in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the editing template comprises substantial or partial complementarity to the editing target sequence except at the position of the intended nucleotide edits to be incorporated into the double stranded target DNA, *e.g.*, a target gene. An exemplary architecture of a PEgRNA including its components is as demonstrated in **FIG. 2**.

[0324] In some embodiments, a PEgRNA includes only RNA nucleotides and forms an RNA polynucleotide. In some embodiments, a PEgRNA is a chimeric polynucleotide that includes both RNA and DNA nucleotides. For example, a PEgRNA can include DNA in the spacer sequence, the gRNA core, or the extension arm. In some embodiments, a PEgRNA comprises DNA in the spacer sequence. In some embodiments, the entire spacer sequence of a PEgRNA is a DNA sequence. In some embodiments, the PEgRNA comprises DNA in the gRNA core, for example, in a stem region of the gRNA core. In some embodiments, the PEgRNA comprises DNA in the extension arm, for example, in the editing template. An editing template that comprises a DNA sequence may serve as a DNA synthesis template for a DNA polymerase in a prime editor, for example, a DNA-dependent DNA polymerase. Accordingly, the PEgRNA may be a chimeric polynucleotide that comprises RNA in the spacer, gRNA core, and/or the PBS sequences and DNA in the editing template.

[0325] Components of a PEgRNA may be arranged in a modular fashion. In some embodiments, the spacer and the extension arm comprising a primer binding site sequence (PBS) and an editing template, *e.g.*, a reverse transcriptase template (RTT), can be interchangeably located in the 5' portion of the PEgRNA, the 3' portion of the PEgRNA, or in the middle of the gRNA core. In some embodiments, a PEgRNA comprises a PBS and an editing template sequence in 5' to 3' order. In some embodiments, the gRNA core of a PEgRNA of this disclosure may be located in between a spacer and an extension arm of the PEgRNA. In some embodiments, the gRNA core of a PEgRNA may be located at the 3' end of a spacer. In some embodiments, the gRNA core of a PEgRNA may be located at the 5' end of a spacer. In some embodiments, the gRNA core of a PEgRNA may be located at the 3' end of an extension arm. In some embodiments, the gRNA core of a PEgRNA may be located at the 5' end of an extension arm. In some embodiments, the PEgRNA comprises, from 5' to 3': a spacer, a gRNA core, and an extension arm. In some embodiments, the PEgRNA comprises, from 5' to 3': a spacer, a gRNA core, an editing template, and a PBS. In some embodiments, the PEgRNA comprises, from 5' to 3': an extension arm, a spacer, and a gRNA core. In some embodiments, the PEgRNA comprises, from 5' to 3': an editing target, a PBS, a spacer, and a gRNA core.

[0326] In some embodiments, a PEgRNA comprises a single polynucleotide molecule that comprises the spacer sequence, the gRNA core, and the extension arm. In some embodiments, a PEgRNA comprises multiple polynucleotide molecules, for example, two polynucleotide molecules. In some embodiments, a PEgRNA comprise a first polynucleotide molecule that comprises the spacer and a portion of the gRNA core, and a second polynucleotide molecule that comprises the rest of the gRNA core and the extension arm. In some embodiments, the gRNA core portion in the first polynucleotide molecule and the gRNA core portion in the second polynucleotide molecule are at least partly complementary to each other. In some embodiments, the PEgRNA may comprise a first polynucleotide comprising the spacer and a first portion of a gRNA core comprising, which may be also be referred to as a crRNA. In some embodiments, the PEgRNA comprise a second polynucleotide comprising a second portion of the gRNA core and the extension arm, wherein the second portion of the gRNA core may also be referred to as a trans-activating crRNA, or tracr RNA. In some embodiments, the crRNA portion and the tracr RNA portion of the gRNA core are at least partially complementary to each other. In some embodiments, the partially complementary portions of the crRNA and the tracr RNA form a lower stem, a bulge, and an upper stem, as exemplified in **FIG. 4**.

[0327] In some embodiments, a spacer sequence comprises a region that has substantial complementarity to a search target sequence on the target strand of a double stranded target DNA, *e.g.* an *AT7B* gene. In some embodiments, the spacer sequence of a PEgRNA is identical or substantially identical to a protospacer sequence on the edit strand of the double stranded target DNA, *e.g.*, a target gene (except that the protospacer sequence comprises thymine and the spacer sequence may comprise uracil). In some embodiments, the spacer sequence is at least about 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to a search target sequence in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the spacer comprises is substantially complementary to the search target sequence.

[0328] In some embodiments, the length of the spacer varies from at least 10 nucleotides to 100 nucleotides. For examples, a spacer may be at least 10 nucleotides, at least 11 nucleotides, at least 12 nucleotides, at least 13 nucleotides, at least 14 nucleotides, at least 15 nucleotides, at least 16 nucleotides, at least 17 nucleotides, at least 18 nucleotides, at least 19 nucleotides, at least 20 nucleotides, at least 30 nucleotides, at least 40 nucleotides, at least 50 nucleotides, at least 60 nucleotides, at least 70 nucleotides, at least 80 nucleotides, at least 90 nucleotides, at least 100 nucleotides. In some embodiments, the spacer is 16 nucleotides, 17 nucleotides, 18 nucleotides, 19 nucleotides, 20 nucleotides, 21 nucleotides, 22 nucleotides, 23 nucleotides, 24 nucleotides, or 25 nucleotides in length. In some embodiments, the spacer is from 15 nucleotides to 30 nucleotides in length, 15 to 25 nucleotides in length, 18 to 22 nucleotides in length, 10 to 20 nucleotides in length, 20 to 30 nucleotides in length, 30 to 40 nucleotides in length, 40 to 50 nucleotides in length, 50 to 60 nucleotides in length, 60 to 70 nucleotides in length, 70 to 80 nucleotides in length, or 90 nucleotides to 100 nucleotides in length. In some embodiments, the spacer is 20 nucleotides in length. In some embodiments, the spacer is 17 to 18 nucleotides in length.

[0329] As used herein in a PEgRNA or a nick guide RNA sequence, or fragments thereof such as a spacer, PBS, or RTT sequence, unless indicated otherwise, it should be appreciated that the letter "T" or "thymine" indicates a nucleobase in a DNA sequence that encodes the PEgRNA or guide RNA sequence, and is intended to refer to an uracil (U) nucleobase of the PEgRNA or guide RNA or any chemically modified uracil nucleobase known in the art, such as 5-methoxyuracil.

[0330] The extension arm of a PEgRNA may comprise a primer binding site (PBS) and an editing template (*e.g.*, an RTT). The extension arm may be partially complementary to the spacer. In some embodiments, the editing template (*e.g.*, RTT) is partially complementary to the spacer. In some embodiments, the editing template (*e.g.*, RTT) and the primer binding site (PBS) are each partially complementary to the spacer.

[0331] An extension arm of a PEgRNA may comprise a primer binding site sequence (PBS, or PBS sequence) that hybridizes with a free 3' end of a single stranded DNA in the double stranded target DNA, *e.g.*, a target gene generated by nicking with a prime editor. The length of the PBS sequence may vary depending on, *e.g.*, the prime editor components, the search target sequence and other components of the

PEgRNA. In some embodiments, the length of the primer binding site (PBS) varies from at least 2 nucleotides to 50 nucleotides. For examples, a primer binding site (PBS) may be at least 2 nucleotides, at least 3 nucleotides, at least 4 nucleotides, at least 5 nucleotides, at least 6 nucleotides, at least 7 nucleotides, at least 8 nucleotides, at least 9 nucleotides, at least 10 nucleotides, at least 11 nucleotides, at least 12 nucleotides, at least 13 nucleotides, at least 14 nucleotides, at least 15 nucleotides, at least 16 nucleotides, at least 17 nucleotides, at least 18 nucleotides, at least 19 nucleotides, at least 20 nucleotides, at least 30 nucleotides, at least 40 nucleotides, or at least 50 nucleotides in length. In some embodiments, the PBS is at least 6 nucleotides in length. In some embodiments, the PBS is about 4 to 16 nucleotides, about 6 to 16 nucleotides, about 6 to 18 nucleotides, about 6 to 20 nucleotides, about 8 to 20 nucleotides, about 10 to 20 nucleotides, about 12 to 20 nucleotides, about 14 to 20 nucleotides, about 16 to 20 nucleotides, or about 18 to 20 nucleotides in length. In some embodiments, the PBS is about 7 to 15 nucleotides in length. In some embodiments, the PBS is 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides in length. In some embodiments, the PBS is 8, 9, 10, 11, 12, 13, or 14 nucleotides in length.

[0332] The PBS may be complementary or substantially complementary to a DNA sequence in the edit strand of the double stranded target DNA, *e.g.*, a target gene. By annealing with the edit strand at a free hydroxy group, *e.g.,* a free 3' end generated by prime editor nicking, the PBS may initiate synthesis of a new single stranded DNA encoded by the editing template at the nick site. In some embodiments, the PBS is at least about 70%, 75%, 80%, 85%, 90%, 95%, or 100% complementary to a region of the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the PBS is perfectly complementary, or 100% complementary, to a region of the edit strand of the double stranded target DNA, *e.g.*, a target gene.

[0333] An extension arm of a PEgRNA may comprise an editing template that serves as a DNA synthesis template for the DNA polymerase in a prime editor during prime editing.

[0334] The length of an editing template may vary depending on, *e.g.*, the prime editor components, the search target sequence, and other components of the PEgRNA. In some embodiments, the editing template serves as a DNA synthesis template for a reverse transcriptase, and the editing template is referred to as a reverse transcription editing template (RTT).

[0335] The editing template (*e.g.*, RTT), in some embodiments, is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length. In some embodiments, the RTT is 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length. In some embodiments, the RTT is 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides in length.

[0336] In some embodiments, the editing template (*e.g.*, RTT) sequence is about 70%, 75%, 80%, 85%, 90%, 95%, or 99% complementary to the editing target sequence on the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the editing template sequence (*e.g.*, RTT) is substantially complementary to the editing target sequence. In some embodiments, the editing template sequence (*e.g.*, RTT) is complementary to the editing target sequence except at positions of the intended nucleotide edits to be incorporated int the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the editing template comprises a nucleotide sequence comprising about 85% to about 95% complementarity to an editing target sequence in the edit strand in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the editing template comprises 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%, or about 99% complementarity to an editing target sequence in the edit strand of the double stranded target DNA, *e.g.*, a target gene.

[0337] An intended nucleotide edit in an editing template of a PEgRNA may comprise various types of alterations as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the nucleotide edit is a single nucleotide substitution as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the nucleotide edit is a deletion as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the nucleotide edit is an insertion as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises one to ten intended nucleotide edits as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises one or more intended nucleotide edits as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises two or more intended nucleotide edits as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises three or more intended nucleotide edits as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises four or more, five or more, or six or more intended nucleotide edits as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises two single nucleotide substitutions, insertions, deletions, or any combination thereof, as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises three single nucleotide substitutions, insertions, deletions, or any combination thereof, as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, the editing template comprises four, five, or six single nucleotide substitutions, insertions, deletions, or any combination thereof, as compared to the double stranded target DNA, *e.g.*, a target gene sequence. In some embodiments, a nucleotide substitution comprises an adenine (A)-to-thymine (T) substitution. In some embodiments, a nucleotide substitution comprises an A-to-guanine (G) substitution. In some embodiments, a nucleotide substitution comprises an A-to-cytosine (C) substitution. In some embodiments, a nucleotide substitution comprises a T-A substitution. In some embodiments, a nucleotide substitution comprises a T-G substitution. In some embodiments, a nucleotide substitution comprises a T-C substitution. In some embodiments, a nucleotide substitution comprises a G-to-A substitution. In some embodiments, a nucleotide substitution comprises a G-to-T substitution. In some embodiments, a nucleotide substitution comprises a G-to-C substitution. In some embodiments, a nucleotide substitution comprises a C-to-A substitution. In some embodiments, a nucleotide substitution comprises a C-to-T substitution. In some embodiments, a nucleotide substitution comprises a C-to-G substitution.

[0338] In some embodiments, a nucleotide insertion is at least 5 nucleotides, at least 6 nucleotides, at least 7 nucleotides, at least 8 nucleotides, at least 9 nucleotides, at least 10 nucleotides, at least 11 nucleotides, at least 12 nucleotides, at least 13 nucleotides, at least 14 nucleotides, at least 15 nucleotides, at least 16 nucleotides, at least 17 nucleotides, at least 18 nucleotides, at least 19 nucleotides, or at least 20 nucleotides in length. In some embodiments, a nucleotide insertion is from 1 to 2 nucleotides, from 1 to 3 nucleotides, from 1 to 4 nucleotides, from 1 to 5 nucleotides, form 2 to 5 nucleotides, from 3 to 5 nucleotides, from 3 to 6 nucleotides, from 3 to 8 nucleotides, from 4 to 9 nucleotides, from 5 to 10 nucleotides, from 6 to 11 nucleotides, from 7 to 12 nucleotides, from 8 to 13 nucleotides, from 9 to 14 nucleotides, from 10 to 15 nucleotides, from 11 to 16 nucleotides, from 12 to 17 nucleotides, from 13 to 18 nucleotides, from 14 to 19 nucleotides, from 15 to 20 nucleotides in length. In some embodiments, a nucleotide insertion is a single nucleotide insertion. In some embodiments, a nucleotide insertion comprises insertion of two nucleotides.

[0339] The editing template of a PEgRNA may comprise one or more intended nucleotide edits, compared to the double stranded target DNA, *e.g.*, a target gene, to be edited. Position of the intended nucleotide edit(s) relevant to other components of the PEgRNA, or to particular nucleotides (*e.g.*, mutations) in the double stranded target DNA, *e.g.*, a target gene, may vary. In some embodiments, the nucleotide edit is in a region of the PEgRNA corresponding to or homologous to the protospacer sequence. In some embodiments, the nucleotide edit is in a region of the PEgRNA corresponding to a region of the double stranded target DNA outside of the protospacer sequence.

[0340] In some embodiments, the position of a nucleotide edit incorporation in the double stranded target DNA, *e.g.*, a target gene may be determined based on position of the protospacer adjacent motif (PAM). For instance, the intended nucleotide edit may be installed in a sequence corresponding to the protospacer adjacent motif (PAM) sequence. In some embodiments, a nucleotide edit in the editing template is at a position corresponding to the 5’ most nucleotide of the PAM sequence. In some embodiments, a nucleotide edit in the editing template is at a position corresponding to the 3’ most nucleotide of the PAM sequence. In some embodiments, position of an intended nucleotide edit in the editing template may be referred to by aligning the editing template with the partially complementary edit strand of the double stranded target DNA, *e.g.*, a target gene, and referring to nucleotide positions on the editing strand where the intended nucleotide edit is incorporated. In some embodiments, a nucleotide edit is incorporated at a position corresponding to about 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides upstream of the 5’ most nucleotide of the PAM sequence in the edit strand of the double stranded target DNA, *e.g.*, a target gene. By 0 nucleotide upstream or downstream of a reference position, it is meant that the intended nucleotide is immediately upstream or downstream of the reference position. In some embodiments, a nucleotide edit is incorporated at a position corresponding to about 0 to 2 nucleotides, 0 to 4 nucleotides, 0 to 6 nucleotides, 0 to 8 nucleotides, 0 to 10 nucleotides, , 2 to 4 nucleotides, 2 to 6 nucleotides, 2 to 8 nucleotides, 2 to 10 nucleotides, 2 to 12 nucleotides, 4 to 6 nucleotides, 4 to 8 nucleotides, 4 to 10 nucleotides, 4 to 12 nucleotides, 4 to 14 nucleotides, 6 to 8 nucleotides, 6 to 10 nucleotides, 6 to 12 nucleotides, 6 to 14 nucleotides, 6 to16 nucleotides, 8 to 10 nucleotides, 8 to 12 nucleotides, 8 to 14 nucleotides, 8 to 16 nucleotides, 8 to 18 nucleotides, 10 to 12 nucleotides, 10 to 14 nucleotides, 10 to 16 nucleotides, 10 to 18 nucleotides, 10 to 20 nucleotides, 12 to 14 nucleotides, 12 to 16 nucleotides, 12 to 18 nucleotides, 12 to 20 nucleotides, 12 to 22 nucleotides, 14 to 16 nucleotides, 14 to 18 nucleotides, 14 to 20 nucleotides, 14 to 22 nucleotides, 14 to 24 nucleotides, 16 to 18 nucleotides, 16 to 20 nucleotides, 16 to 22 nucleotides, 16 to 24 nucleotides, 16 to 26 nucleotides, 18 to 20 nucleotides, 18 to 22 nucleotides, 18 to 24 nucleotides, 18 to 26 nucleotides, 18 to 28 nucleotides, 20 to 22 nucleotides, 20 to 24 nucleotides, 20 to 26 nucleotides, 20 to 28 nucleotides, or 20 to 30 nucleotides upstream of the 5' most nucleotide of the PAM sequence. In some embodiments, the nucleotide edit is incorporated at a position corresponding to 3 nucleotides upstream of the 5' most nucleotide of the PAM sequence. In some embodiments, the nucleotide edit in is incorporated at a position corresponding to 4 nucleotides upstream of the 5' most nucleotide of the PAM sequence. In some embodiments, the nucleotide edit is incorporated at a position corresponding to 5 nucleotides upstream of the 5' most nucleotide of the PAM sequence. In some embodiments, the nucleotide edit in the editing template is at a position corresponding to 6 nucleotides upstream of the 5' most nucleotide of the PAM sequence.

[0341] In some embodiments, an intended nucleotide edit is incorporated at a position corresponding to about 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 nucleotides downstream of the 5' most nucleotide of the PAM sequence in the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, a nucleotide edit is incorporated at a position corresponding to about 0 to 2 nucleotides, 0 to 4 nucleotides, 0 to 6 nucleotides, 0 to 8 nucleotides, 0 to 10 nucleotides, , 2 to 4 nucleotides, 2 to 6 nucleotides, 2 to 8 nucleotides, 2 to 10 nucleotides, 2 to 12 nucleotides, 4 to 6 nucleotides, 4 to 8 nucleotides, 4 to 10 nucleotides, 4 to 12 nucleotides, 4 to 14 nucleotides, 6 to 8 nucleotides, 6 to 10 nucleotides, 6 to 12 nucleotides, 6 to 14 nucleotides, 6 to16 nucleotides, 8 to 10 nucleotides, 8 to 12 nucleotides, 8 to 14 nucleotides, 8 to 16 nucleotides, 8 to 18 nucleotides, 10 to 12 nucleotides, 10 to 14 nucleotides, 10 to 16 nucleotides, 10 to 18 nucleotides, 10 to 20 nucleotides, 12 to 14 nucleotides, 12 to 16 nucleotides, 12 to 18 nucleotides, 12 to 20 nucleotides, 12 to 22 nucleotides, 14 to 16 nucleotides, 14 to 18 nucleotides, 14 to 20 nucleotides, 14 to 22 nucleotides, 14 to 24 nucleotides, 16 to 18 nucleotides, 16 to 20 nucleotides, 16 to 22 nucleotides, 16 to 24 nucleotides, 16 to 26 nucleotides, 18 to 20 nucleotides, 18 to 22 nucleotides, 18 to 24 nucleotides, 18 to 26 nucleotides, 18 to 28 nucleotides, 20 to 22 nucleotides, 20 to 24 nucleotides, 20 to 26 nucleotides, 20 to 28 nucleotides, or 20 to 30 nucleotides downstream of the 5' most nucleotide of the PAM sequence. In some embodiments, a nucleotide edit is incorporated at a position corresponding to 3 nucleotides downstream of the 5' most nucleotide of the PAM sequence. In some embodiments, a nucleotide edit is incorporated at a position corresponding to 4 nucleotides downstream of the 5' most nucleotide of the PAM sequence. In some embodiments, a nucleotide edit is incorporated at a position corresponding to 5 nucleotides downstream of the 5' most nucleotide of the PAM sequence. In some embodiments, a nucleotide edit is incorporated at a position corresponding to 6 nucleotides downstream of the 5' most nucleotide of the PAM sequence. By "upstream" and "downstream" it is intended to define relevant positions at least two regions or sequences in a nucleic acid molecule orientated in a 5′-to-3′ direction. For example, a first sequence is upstream of a second sequence in a DNA molecule where the first sequence is positioned 5' to the second sequence. Accordingly, the second sequence is downstream of the first sequence.

[0342] When referred to in the PEgRNA, positions of the one or more intended nucleotide edits may be referred to relevant to components of the PEgRNA. For example, an intended nucleotide edit may be 5' or 3' to the PBS. In some embodiments, a PEgRNA comprises the structure, from 5' to 3': a spacer, a gRNA core, an editing template, and a PBS. In some embodiments, the intended nucleotide edit is 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or 40 base pairs upstream to the 5' most nucleotide of the PBS. In some embodiments, the intended nucleotide edit is 0 to 2 base pairs, 0 to 4 base pairs, 0 to 6 base pairs, 0 to 8 base pairs, 0 to 10 base pairs, 2 to 4 base pairs, 2 to 6 base pairs, 2 to 8 base pairs, 2 to 10 base pairs, 2 to 12 base pairs, 4 to 6 base pairs, 4 to 8 base pairs, 4 to 10 base pairs, 4 to 12 base pairs, 4 to 14 base pairs, 6 to 8 base pairs, 6 to 10 base pairs, 6 to 12 base pairs, 6 to 14 base pairs, 6 to16 base pairs, 8 to 10 base pairs, 8 to 12 base pairs, 8 to 14 base pairs, 8 to 16 base pairs, 8 to 18 base pairs, 10 to 12 base pairs, 10 to 14 base pairs, 10 to 16 base pairs, 10 to 18 base pairs, 10 to 20 base pairs, 12 to 14 base pairs, 12 to 16 base pairs, 12 to 18 base pairs, 12 to 20 base pairs, 12 to 22 base pairs, 14 to 16 base pairs, 14 to 18 base pairs, 14 to 20 base pairs, 14 to 22 base pairs, 14 to 24 base pairs, 16 to 18 base pairs, 16 to 20 base pairs, 16 to 22 base pairs, 16 to 24 base pairs, 16 to 26 base pairs, 18 to 20 base pairs, 18 to 22 base pairs, 18 to 24 base pairs, 18 to 26 base pairs, 18 to 28 base pairs, 20 to 22 base pairs, 20 to 24 base pairs, 20 to 26 base pairs, 20 to 28 base pairs, or 20 to 30 base pairs upstream to the 5' most nucleotide of the PBS.

[0343] The corresponding positions of the intended nucleotide edit incorporated in the double stranded target DNA, *e.g.*, a target gene may also be referred to based on the nicking position generated by a prime editor based on sequence homology and complementarity. For example, in embodiments, the distance between the nucleotide edit to be incorporated into the double stranded target DNA, *e.g.*, a target gene, and the nick generated by the prime editor may be determined when the spacer hybridizes with the search target sequence and the extension arm hybridizes with the editing target sequence. In certain embodiments, the position of the nucleotide edit can be in any position downstream of the nick site on the edit strand (or the PAM strand) generated by the prime editor, such that the distance between the nick site and the intended nucleotide edit is 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length. In some embodiments, the position of the nucleotide edit is 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides upstream of the nick site on the edit strand. In some embodiments, the position of the nucleotide edit is 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides downstream of the nick site on the edit strand. In some embodiments, the position of the nucleotide edit is 0 base pairs from the nick site on the edit strand, that is, the editing position is at the same position as the nick site. As used herein, the distance between the nick site and the nucleotide edit, for example, where the nucleotide edit comprises an insertion or deletion, refers to the 5' most position of the nucleotide edit for a nick that creates a 3' free end on the edit strand (i.e., the "near position" of the nucleotide edit to the nick site). Similarly, as used herein, the distance between the nick site and a PAM position edit, for example, where the nucleotide edit comprises an insertion, deletion, or substitution of two or more contiguous nucleotides, refers to the 5' most position of the nucleotide edit and the 5' most position of the PAM sequence.

[0344] In some embodiments, the editing template extends beyond a nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. For example, in some embodiments, the editing template comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 base pairs 3' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 30 base pairs 3' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 25 base pairs 3' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 20 base pairs 3' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 30 base pairs 5' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 25 base pairs 5' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence. In some embodiments, the editing template comprises at least 4 to 20 base pairs 5' to the nucleotide edit to be incorporated to the double stranded target DNA, *e.g.*, a target gene, sequence.

[0345] In some embodiments, the editing template comprises an adenine at the first nucleobase position (*e.g.*, for a PEgRNA following 5'-spacer-gRNA core-RTT-PBS-3' orientation, the 5' most nucleobase is the "first base"). In some embodiments, the editing template comprises a guanine at the first nucleobase position (*e.g.*, for a PEgRNA following 5'-spacer-gRNA core-RTT-PBS-3' orientation, the 5' most nucleobase is the "first base"). In some embodiments, the editing template comprises an uracil at the first nucleobase position (*e.g.*, for a PEgRNA following 5'-spacer-gRNA core-RTT-PBS-3' orientation, the 5' most nucleobase is the "first base"). In some embodiments, the editing template comprises a cytosine at the first nucleobase position (*e.g.*, for a PEgRNA following 5'-spacer-gRNA core-RTT-PBS-3' orientation, the 5' most nucleobase is the "first base"). In some embodiments, the editing template does not comprise a cytosine at the first nucleobase position (*e.g.*, for a PEgRNA following 5'-spacer-gRNA core-RTT-PBS-3' orientation, the 5' most nucleobase is the "first base").

[0346] The editing template of a PEgRNA may encode a new single stranded DNA (*e.g.* by reverse transcription) to replace a target sequence in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the editing target sequence in the edit strand of the double stranded target DNA, *e.g.*, a target gene is replaced by the newly synthesized strand, and the nucleotide edit(s) are incorporated in the region of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the newly synthesized DNA strand replaces the editing target sequence in the double stranded target DNA, *e.g.*, a target gene, wherein the editing target sequence (or the endogenous sequence complementary to the editing target sequence on the target strand of the target gene) comprises a mutation compared to a wild-type sequence of the same gene, wherein incorporation of the one or more intended nucleotide edits corrects the mutation.

[0347] A guide RNA core (also referred to herein as the gRNA core, gRNA scaffold, or gRNA backbone sequence) of a PEgRNA may contain a polynucleotide sequence that binds to a DNA binding domain (*e.g.*, Cas9) of a prime editor. The gRNA core may interact with a prime editor as described herein, for example, by association with a DNA binding domain, such as a DNA nickase of the prime editor.

[0348] One of skill in the art will recognize that different prime editors having different DNA binding domains from different DNA binding proteins may require different gRNA core sequences specific to the DNA binding protein. In some embodiments, the gRNA core is capable of binding to a Cas9-based prime editor. In some embodiments, the gRNA core is capable of binding to a Cpf1-based prime editor. In some embodiments, the gRNA core is capable of binding to a Cas12b-based prime editor.

[0349] In some embodiments, the gRNA core comprises regions and secondary structures involved in binding with specific CRISPR Cas proteins. For example, in a Cas9 based prime editing system, the gRNA core of a PEgRNA may comprise one or more regions of a base paired "lower stem" adjacent to the spacer sequence and a base paired "upper stem" following the lower stem, where the lower stem and upper stem may be connected by a "bulge" comprising unpaired RNAs. The gRNA core may further comprise a "nexus" distal from the spacer sequence, followed by a hairpin structure, *e.g.*, at the 3' end, as exemplified in **FIG. 4**. In some embodiments, the gRNA core comprises modified nucleotides as compared to a wild-type gRNA core in the lower stem, upper stem, and/or the hairpin. For example, nucleotides in the lower stem, upper stem, an/or the hairpin regions may be modified, deleted, or replaced. In some embodiments, RNA nucleotides in the lower stem, upper stem, an/or the hairpin regions may be replaced with one or more DNA sequences. In some embodiments, the gRNA core comprises unmodified or wild-type RNA sequences in the nexus and/or the bulge regions. In some embodiments, the gRNA core does not include long stretches of A-T pairs, for example, a GUUUU-AAAAC pairing element.

[0350] In some embodiments, the gRNA core comprises the sequence: GUUUGAGAGCUAGAAAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUCC (SEQ ID NO: 556), or GUUUAAGAGCUAUGCUGGAAACAGCAUAGCAAGUUUAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC(SEQ ID NO: 557) In some embodiments, the gRNA core comprises the sequence GUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC(SEQ ID NO: 558). Any gRNA core sequences known in the art are also contemplated in the prime editing compositions described herein.

[0351] A PEgRNA may also comprise optional modifiers, *e.g.*, 3′ end modifier region and/or an 5′ end modifier region. In some embodiments, a PEgRNA comprises at least one nucleotide that is not part of a spacer, a gRNA core, or an extension arm. The optional sequence modifiers could be positioned within or between any of the other regions shown, and not limited to being located at the 3′ and 5′ ends. In certain embodiments, the PEgRNA comprises secondary RNA structure, such as, but not limited to, aptamers, hairpins, stem/loops, toeloops, and/or RNA-binding protein recruitment domains (*e.g.*, the MS2 aptamer which recruits and binds to the MS2cp protein). In some embodiments, a PEgRNA comprises a short stretch of uracil at the 5' end or the 3' end. For example, in some embodiments, a PEgRNA comprisng a 3' extension arm comprises a "UUU" sequence at the 3' end of the extension arm. In some embodiments, a PEgRNA comprises a toeloop sequence at the 3' end. In some embodiments, the PEgRNA comprises a 3' extension arm and a toeloop sequence at the 3' end of the extension arm. In some embodiments, the PEgRNA comprises a 5' extension arm and a toeloop sequence at the 5' end of the extension arm. In some embodiments, the PEgRNA comprises a toeloop element having the sequence 5'-GAAANNNNN-3', wherein N is any nucleobase. In some embodiments, the secondary RNA structure is positioned within the spacer. In some embodiments, the secondary structure is positioned within the extension arm. In some embodiments, the secondary structure is positioned within the gRNA core. In some embodiments, the secondary structure is positioned between the spacer and the gRNA core, between the gRNA core and the extension arm, or between the spacer and the extension arm. In some embodiments, the secondary structure is positioned between the PBS and the editing template. In some embodiments the secondary structure is positioned at the 3' end or at the 5' end of the PEgRNA. In some embodiments, the PEgRNA comprises a transcriptional termination signal at the 3′ end of the PEgRNA. In addition to secondary RNA structures, the PEgRNA may comprise a chemical linker or a poly(N) linker or tail, where "N" can be any nucleobase. In some embodiments, the chemical linker may function to prevent reverse transcription of the gRNA core.

[0352] The 3' end sequence and the 5' end sequence of a PEgRNA can be any one of the functional components of the PEgRNA and can comprise any sequence known in the art. In some embodiments, the PEgRNA comprises an extension arm at the 3' end. For example, the PEgRNA may comprise the structure, from 5' to 3': a spacer, a gRNA core, an editing template (*e.g.*, RTT), and a PBS. In some embodiments, the PEgRNA comprises a gRNA core at the 3' end. For example, the PEgRNA may comprise the structure, from 5' to 3': an editing template (*e.g.*, RTT), a PBS, a spacer, and a gRNA core. In some embodiments, the PEgRNA comprises a specific nucleotide sequence at the 3' end. In some embodiments, the three 3' most nucleotides of the PEgRNA are 5'-UUU-3'. In some embodiments, the four 3' most nucleotides of the PEgRNA are 5'-UUUU-3'. In some embodiments, the three 3' most nucleotides of the PEgRNA are not 5'-UUU-3'In some embodiments, the four 3' most nucleotides of the PEgRNA are not 5'-UUUU-3'. In some embodiments, the PEgRNA does not comprise two consecutive uracils in the three 3' most nucleotides. In some embodiments, the PEgRNA does not comprise two consecutive uracils in the four 3' most nucleotides. In some embodiments, the PEgRNA does not comprise a uracil in the four 3' most nucleotides. In some embodiments, the PEgRNA does not comprise a uracil in the three 3' most nucleotides. In some embodiments, the PEgRNA is chemically synthesized.

[0353] In some embodiments, a prime editing system or composition further comprises a nick guide polynucleotide, such as a nick guide RNA (ngRNA). Without wishing to be bound by any particular theory, the non-edit strand of a double stranded target DNA in the double stranded target DNA, *e.g.*, a target gene may be nicked by a CRISPR-Cas nickase directed by an ngRNA. In some embodiments, the nick on the non-edit strand directs endogenous DNA repair machinery to use the edit strand as a template for repair of the non-edit strand, which may increase efficiency of prime editing. In some embodiments, the non-edit strand is nicked by a prime editor localized to the non-edit strand by the ngRNA. Accordingly, also provided herein are PEgRNA systems comprising at least one PEgRNA and at least one ngRNA.

[0354] In some embodiments, the ngRNA is a guide RNA which contains a variable spacer sequence and a guide RNA scaffold or core region that interacts with the DNA binding domain, *e.g.* Cas9 of the prime editor. In some embodiments, the ngRNA comprises a spacer sequence (referred to herein as an ng spacer, or a second spacer) that is substantially complementary to a second search target sequence (or ng search target sequence), which is located on the edit strand, or the non-target strand. Thus, in some embodiments, the ng search target sequence recognized by the ng spacer and the search target sequence recognized by the spacer sequence of the PEgRNA are on opposite strands of the double stranded target DNA of double stranded target DNA, *e.g.*, a target gene. A prime editing system or complex comprising a ngRNA may be referred to as a "PE3" prime editing system, PE3 prime editing compositions or PE3 prime editing complex.

[0355] In some embodiments, the ng search target sequence is located on the non-target strand, within 10 nucleotides to 100 nucleotides of an intended nucleotide edit incorporated by the PEgRNA on the edit strand. In some embodiments, the ng target search target sequence is within 10 bp, 20 bp, 30 bp, 40 bp, 50 bp, 60 bp, 70 bp, 80 bp, 90 bp, 91 bp, 92 bp, 93 bp, 94 bp, 95 bp, 96 bp, 97 bp, 98 bp, 99 bp, or 100 bp of an intended nucleotide edit incorporated by the PEgRNA on the edit strand. In some embodiments, the 5' ends of the ng search target sequence and the PEgRNA search target sequence are within 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 bp apart from each other. In some embodiments, the 5' ends of the ng search target sequence and the PEgRNA search target sequence are within 10 bp, 20 bp, 30 bp, 40 bp, 50 bp, 60 bp, 70 bp, 80 bp, 90 bp, 91 bp, 92 bp, 93 bp, 94 bp, 95 bp, 96 bp, 97 bp, 98 bp, 99 bp, or 100 bp apart from each other.

[0356] In some embodiments, an ng spacer sequence is complementary to, and may hybridize with the second search target sequence only after an intended nucleotide edit has been incorporated on the edit strand, by the editing template of a PEgRNA. Such a prime editing system maybe referred to as a "PE3b" prime editing system or composition. In some embodiments, the ngRNA comprises a spacer sequence that matches only the edit strand after incorporation of the nucleotide edits, but not the endogenous double stranded target DNA, *e.g.*, a target gene sequence on the edit strand. Accordingly, in some embodiments, an intended nucleotide edit is incorporated within the ng search target sequence. In some embodiments, the intended nucleotide edit is incorporated within about 1-10 nucleotides of the position corresponding to the PAM of the ng search target sequence.

[0357] A PEgRNA and/or an ngRNA of this disclosure, in some embodiments, may include modified nucleotides, *e.g.*, chemically modified DNA or RNA nucleobases, and may include one or more nucleobase analogs (*e.g.*, modifications which might add functionality, such as temperature resilience). In some embodiments, PEgRNAs and/or ngRNAs as described herein may be chemically modified. The phrase "chemical modifications," as used herein, can include modifications which introduce chemistries which differ from those seen in naturally occurring DNA or RNAs, for example, covalent modifications such as the introduction of modified nucleotides, (*e.g.*, nucleotide analogs, or the inclusion of pendant groups which are not naturally found in DNA or RNA molecules).

[0358] In some embodiments, the PEgRNAs and/or ngRNAs provided in this disclosure may have undergone a chemical or biological modifications. Modifications may be made at any position within a PEgRNA or ngRNA, and may include modification to a nucleobase or to a phosphate backbone of the PEgRNA or ngRNA. In some embodiments, chemical modifications can be structure guided modifications. In some embodiments, a chemical modification is at the 5' end and/or the 3' end of a PEgRNA. In some embodiments, a chemical modification is at the 5' end and/or the 3' end of a ngRNA. In some embodiments, a chemical modification may be within the spacer sequence, the extension arm, the editing template sequence, or the primer binding site of a PEgRNA. In some embodiments, a chemical modification may be within the spacer sequence or the gRNA core of a PEgRNA or a ngRNA. In some embodiments, a chemical modification may be within the 3' most nucleotides of a PEgRNA or ngRNA. In some embodiments, a chemical modification may be within the 3' most end of a PEgRNA or ngRNA. In some embodiments, a chemical modification may be within the 5' most end of a PEgRNA or ngRNA. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 3 contiguous chemically modified nucleotides at the 3′ end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, or 5 or more chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, or 5 more chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, or 3 or more chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, or 3 more chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more contiguous chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more contiguous chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, or 5 contiguous chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, or 5 contiguous chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, or 3 contiguous chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, or 3 contiguous chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 3 contiguous chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, or more chemically modified nucleotides near the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 3 contiguous chemically modified nucleotides at the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 3 contiguous chemically modified nucleotides at the 5' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, or more chemically modified nucleotides near the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, or more contiguous chemically modified nucleotides near the 3' end. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, or more chemically modified nucleotides near the 3' end, where the 3' most nucleotide is not modified, and the 1, 2, 3, 4, 5, or more chemically modified nucleotides precede the 3' most nucleotide in a 5'-to-3' order. In some embodiments, a PEgRNA or ngRNA comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 or more chemically modified nucleotides near the 3' end, where the 3' most nucleotide is not modified, and the 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 or more chemically modified nucleotides precede the 3' most nucleotide in a 5'-to-3' order.

[0359] In some embodiments, a PEgRNA or ngRNA comprises one or more chemical modified nucleotides in the gRNA core. As exemplified in **FIG. 4**, the gRNA core of a PEgRNA may comprise one or more regions of a base paired lower stem, a base paired upper stem, where the lower stem and upper stem may be connected by a bulge comprising unpaired RNAs. The gRNA core may further comprise a nexus distal from the spacer sequence. In some embodiments, the gRNA core comprises one or more chemically modified nucleotides in the lower stem, upper stem, and/or the hairpin regions. In some embodiments, all of the nucleotides in the lower stem, upper stem, and/or the hairpin regions are chemically modified.

[0360] A chemical modification to a PEgRNA or ngRNA can comprise a 2′-O-thionocarbamate-protected nucleoside phosphoramidite, a 2′-O-methyl (M), a 2′-O-methyl 3′phosphorothioate (MS), or a 2′-O-methyl 3′thioPACE (MSP), or any combination thereof. In some embodiments, a chemical modification to a PEgRNA or ngRNA comprises a nucleotide sugar modification. In some embodiments, the chemical modification comprises a 2'O-C1-4alkyl modification. In some embodiments, the chemical modification comprises a 2'-O-C1-3alkyl modification. In some embodiments, the chemical modification comprises a 2'-O-methyl (2'-OMe), 2'-deoxy (2'-H), a, for example, 2'-fluoro (2'-F), 2'-methoxyethyl (2'-MOE), 2′-amino ("2′-NH2"), or 2′-arabinosyl ("2′-arabino"), 2′-F-arabinosyl ("2′-F-arabino") modification. In some embodiments, a chemically modification to a PEgRNA and/or ngRNA comprises an internucleotide linkage modification. In some embodiments, the internucleotide linkage is a phosphorothioate ("PS"), phosphonocarboxylate (P(CH2)nCOOR), phosphoroacetate (PACE), (P(CH2COO−)) thiophosphonocarboxylate ((S)P(CH2)nCOOR), thiophosphonoacetate (thioPACE), ((S)P(CH2COO−)), alkylphosphonate (P(C1-3alkyl) such as methylphosphonate —P(CH3), boranophosphonate (P(BH3)), or phosphorodithioate (P(S)2) modification. In some embodiments, the chemically modified PEgRNA or ngRNA is a 2′-O-methyl (M) RNA, a 2′-O-methyl 3′phosphorothioate

(MS) RNA, a 3'thioPACE RNA, a 2′-O-methyl 3′thioPACE (MSP) RNA, a 2'-F RNA, or a RNA having any other chemical modifications known in the art, or any combination thereof. A chemical modification may also include, for example, the incorporation of non-nucleotide linkages or modified nucleotides into the PEgRNA and/or ngRNA (*e.g.*, modifications to one or both of the 3' and 5' ends of a guide RNA molecule). Such modifications can include the addition of bases to an RNA sequence, complexing the RNA with an agent (*e.g.*, a protein or a complementary nucleic acid molecule), and inclusion of elements which change the structure of an RNA molecule (*e.g.*, which form secondary structures).

[0361] In some embodiments, the PEgRNA comprises the sequence of 5'-mXmXmXmXmX-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mXmXmXmXmX-3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the "rest of extension arm sequence" represent the unmodified nucleotides of the extension arm sequence. As used herein in the context of a PEgRNA sequence or guide RNA sequence chemical modification, "m" stands for a 2'-O-methyl modification.

[0362] In some embodiments, the PEgRNA comprises the sequence of 5'-mX*mX*mX*mX*mX*-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX*mX*mX*mX*mX*-3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the "rest of extension arm sequence" represent the unmodified nucleotides of the extension arm sequence. As used herein in the context of a PEgRNA sequence or guide RNA sequence chemical modification, "*" stands for a phosphorothioate linkage.

[0363] In some embodiments, the PEgRNA comprises the sequence of 5'-mXmXmXmX-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mXmXmXmX-3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the "rest of extension arm sequence" represent the unmodified nucleotides of the extension arm sequence.

[0364] In some embodiments, the PEgRNA comprises the sequence of 5'-mX*mX*mX*mX*-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX*mX*mX*mX*-3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the "rest of extension arm sequence" represent the unmodified nucleotides of the extension arm sequence.

[0365] In some embodiments, the PEgRNA comprises the sequence of 5'-mXmXmXmXmX-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mXmXmXmXmX-3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the "rest of extension arm sequence" represent the unmodified nucleotides of the extension arm sequence.

[0366] In some embodiments, the PEgRNA comprises the sequence of 5'-mX*mX*mX*- rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX*mX*mX* -3', wherein X is any nucleotide, wherein the "rest of spacer sequence" represent the unmodified nucleotides of the spacer sequence, wherein the “rest of extension arm sequence” represent the unmodified nucleotides of the extension arm sequence.

[0367] In some embodiments, the PEgRNA comprises the sequence of 5’-mXmX-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mXmX-3’, wherein X is any nucleotide, wherein the “rest of spacer sequence” represent the unmodified nucleotides of the spacer sequence, wherein the “rest of extension arm sequence” represent the unmodified nucleotides of the extension arm sequence.

[0368] In some embodiments, the PEgRNA comprises the sequence of 5’-mX*mX* -[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX*mX* -3’, wherein X is any nucleotide, wherein the “rest of spacer sequence” represent the unmodified nucleotides of the spacer sequence, wherein the “rest of extension arm sequence” represent the unmodified nucleotides of the extension arm sequence.

[0369] In some embodiments, the PEgRNA comprises the sequence of 5’-mX-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX-3’, wherein X is any nucleotide, wherein the “rest of spacer sequence” represent the unmodified nucleotides of the spacer sequence, wherein the “rest of extension arm sequence” represent the unmodified nucleotides of the extension arm sequence.

[0370] In some embodiments, the PEgRNA comprises the sequence of 5’-mX*-[rest of spacer sequence-gRNA core – rest of extension arm sequence]-mX*-3’, wherein X is any nucleotide, wherein the “rest of spacer sequence” represent the unmodified nucleotides of the spacer sequence, wherein the “rest of extension arm sequence” represent the unmodified nucleotides of the extension arm sequence.

[0371] In some embodiments, the PEgRNA comprises the sequence of 5’-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGCACmU*mU*mU*U -3’ (SEQ ID NO: 559).

[0372] In some embodiments, the PEgRNA comprises the sequence of 5’-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGCACUUUU -3’(SEQ ID NO: 560).

[0373] In some embodiments, the PEgRNA comprises the sequence of 5’-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGCAC -3’(SEQ ID NO: 561).

[0374] In some embodiments, the PEgRNA comprises the sequence of 5’-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGmC*mA*mC* -3’(SEQ ID NO: 562).

[0375] In some embodiments, the PEgRNA comprises the sequence of 5’-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGU

CCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGCAC -3'(SEQ ID NO: 563).

[0376] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCmU*mU*mU*U -3'(SEQ ID NO: 564).

[0377] In some embodiments, the ngRNA comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCUUUU -3'(SEQ ID NO: 565).

[0378] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGC -3'(SEQ ID NO: 566).

[0379] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGmU*mG*mC* -3'(SEQ ID NO: 567).

[0380] In some embodiments, the ngRNA comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGC -3'(SEQ ID NO: 568).

[0381] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACmU*mU*mU*U -3'(SEQ ID NO: 569).

[0382] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACUUUU -3'(SEQ ID NO: 570).

[0383] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCAC -3'(SEQ ID NO: 571).

[0384] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGmC*mA*mC* -3'(SEQ ID NO: 572).

[0385] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGU

CCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCAC -3'(SEQ ID NO: 573).

[0386] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U -3'(SEQ ID NO: 574).

[0387] In some embodiments, the ngRNA comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3'(SEQ ID NO: 575).

[0388] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 576).

[0389] In some embodiments, the ngRNA comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGmU*mG*mC* -3'(SEQ ID NO: 577).

[0390] In some embodiments, the ngRNA comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 578).

[0391] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACmU*mU*mU*U -3'(SEQ ID NO: 579).

[0392] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACUUUU -3'(SEQ ID NO: 580).

[0393] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC -3'(SEQ ID NO: 581).

[0394] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGmC*mA*mC* -3'(SEQ ID NO: 582).

[0395] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGU

CCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC-3'(SEQ ID NO: 583).

[0396] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U -3'(SEQ ID NO: 574).

[0397] In some embodiments, the nick guide RNA (ngRNA) coprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3'(SEQ ID NO: 575).

[0398] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 576).

[0399] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGmU*mG*mC -3'(SEQ ID NO: 577).

[0400] In some embodiments, the nick guide RNA (ngRNA) coprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 578).

[0401] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACmU*mU*mU*U -3'(SEQ ID NO: 579).

[0402] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACUUUU -3'(SEQ ID NO: 580).

[0403] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC -3' (SEQ ID NO: 581).

[0404] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGmC*mA*mC* -3'(SEQ ID NO: 582).

[0405] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC-3'(SEQ ID NO: 583).

[0406] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U -3'(SEQ ID NO: 574).

[0407] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3'(SEQ ID NO: 575).

[0408] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 576).

[0409] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGmU*mG*mC* -3'(SEQ ID NO: 577).

[0410] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 578).

[0411] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACmU*mU*mU*U -3'(SEQ ID NO: 579).

[0412] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACUUUU -3'(SEQ ID NO: 580).

[0413] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC -3'(SEQ ID NO: 581).

[0414] In some embodiments, the PEgRNA comprises the sequence of 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGmC*mA*mC* -3'(SEQ ID NO: 582).

[0415] In some embodiments, the PEgRNA comprises the sequence of 5'-CAUGGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCAC -3'(SEQ ID NO: 583).

[0416] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U -3'(SEQ ID NO: 574).

[0417] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU -3'(SEQ ID NO: 575).

[0418] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC -3'(SEQ ID NO: 576).

[0419] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGmU*mG*mC* -3'(SEQ ID NO: 577).

[0420] In some embodiments, the nick guide RNA (ngRNA) comprises the sequence of 5'-CCUUGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGC-3'(SEQ ID NO: 578).

[0421] In some embodiments, the DNA encoding the PEgRNA comprises the sequence of 5'-GCATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCAGACTTCTCCACAGGAGTCAGGTGCACTTTTTTT -3'(SEQ ID NO: 584).

[0422] In some embodiments, the DNA encoding the PEgRNA comprises the sequence of 5'-GCATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCAGACTTCTCTACAGGAGTCAGGTGCACTTTTTTT -3'(SEQ ID NO: 585).

[0423] In some embodiments, the DNA encoding the nick guide RNA (ngRNA) comprises the sequence of 5'-GCCTTGATACCAACCTGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCTTTTTTT -3'(SEQ ID NO: 586).

Prime Editing Compositions

[0424] Disclosed herein, in some embodiments, are compositions, systems, and methods using a prime editing composition. The term "prime editing composition" or "prime editing system" refers to compositions involved in the method of prime editing as described herein. A prime editing composition may include a prime editor, *e.g.*, a prime editor fusion protein, and a PEgRNA. A prime editing composition may further comprise additional elements, such as second strand nicking ngRNAs. Components of a prime editing composition may be combined to form a complex for prime editing, or may be kept separately, *e.g.*, for administration purposes. In some embodiments, a prime editing composition comprises a prime editor fusion protein complexed with a PEgRNA and optionally complexed with a ngRNA. In some embodiments, the prime editing composition comprises a prime editor comprising a DNA binding domain and a DNA polymerase domain associated with each other through a PEgRNA. For example, the prime editing composition may comprise a prime editor comprising a DNA binding domain and a DNA polymerase domain linked to each other by an RNA-protein recruitment aptamer RNA sequence, which is linked to a PEgRNA. In some embodiments, a prime editing composition comprises a PEgRNA and a polynucleotide, a polynucleotide construct, or a vector that encodes a prime editor fusion protein. In some embodiments, a prime editing composition comprises a PEgRNA, a ngRNA, and a polynucleotide, a polynucleotide construct, or a vector that encodes a prime editor fusion protein. In some embodiments, a prime editing composition comprises multiple polynucleotides, polynucleotide constructs, or vectors, each of which encodes one or more prime editing composition components. In some embodiments, the PEgRNA of a prime editing composition is associated with the DNA binding domain, *e.g.*, a Cas9 nickase, of the prime editor. In some embodiments, the PEgRNA of a prime editing composition complexes with the DNA binding domain of a prime editor and directs the prime editor to the target DNA.

[0425] In some embodiments, a prime editing composition comprises one or more polynucleotides that encode prime editor components and/or PEgRNA or ngRNAs. In some embodiments, a prime editing composition comprises a polynucleotide encoding a fusion protein comprising a DNA binding domain and a DNA polymerase domain. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a fusion protein comprising a DNA binding domain and a DNA polymerase domain, and (ii) a PEgRNA or a polynucleotide encoding the PEgRNA. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a fusion protein comprising a DNA binding domain and a DNA polymerase domain, (ii) a PEgRNA or a polynucleotide encoding the PEgRNA, and (iii) an ngRNA or a polynucleotide encoding the ngRNA. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a DNA binding domain of a prime editor, *e.g.*, a Cas9 nickase, (ii) a polynucleotide encoding a DNA polymerase domain of a prime editor, *e.g.*, a reverse transcriptase, and (iii) a PEgRNA or a polynucleotide encoding the PEgRNA. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a DNA binding domain of a prime editor, *e.g.*, a Cas9 nickase, (ii) a polynucleotide encoding a DNA polymerase domain of a prime editor, *e.g.*, a reverse transcriptase, (iii) a PEgRNA or a polynucleotide encoding the PEgRNA, and (iv) an ngRNA or a polynucleotide encoding the ngRNA. In some embodiments, the polynucleotide encoding the DNA biding domain or the polynucleotide encoding the DNA polymerase domain further encodes an additional polypeptide domain, *e.g.*, an RNA-protein recruitment domain, such as a MS2 coat protein domain. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a N-terminal half of a prime editor fusion protein and an intein-N and (ii) a polynucleotide encoding a C-terminal half of a prime editor fusion protein and an intein-C. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a N-terminal half of a prime editor fusion protein and an intein-N (ii) a polynucleotide encoding a C-terminal half of a prime editor fusion protein and an intein-C, (iii) a PEgRNA or a polynucleotide encoding the PEgRNA, and/or (iv) an ngRNA or a polynucleotide encoding the ngRNA. In some embodiments, a prime editing composition comprises (i) a polynucleotide encoding a N-terminal portion of a DNA binding domain and an intein-N, (ii) a polynucleotide encoding a C-terminal portion of the DNA binding domain, an intein-C, and a DNA polymerase domain. In some embodiments, the DNA binding domain is a Cas protein domain, *e.g.*, a Cas9 nickase. In some embodiments, the prime editing composition comprises (i) a polynucleotide encoding a N-terminal portion of a DNA binding domain and an intein-N, (ii) a polynucleotide encoding a C-terminal portion of the DNA binding domain, an intein-C, and a DNA polymerase domain, (iii) a PEgRNA or a polynucleotide encoding the PEgRNA, and/or (iv) a ngRNA or a polynucleotide encoding the ngRNA.

[0426] In some embodiments, a prime editing system comprises one or more polynucleotides encoding one or more prime editor polypeptides, wherein activity of the prime editing system can be temporally regulated by controlling the timing in which the vectors are delivered. For example, in some embodiments, a polynucleotide encoding the prime editor and a polynucleotide encoding a PEgRNA can be delivered simultaneously. For example, in some embodiments, a polynucleotide encoding the prime editor and a polynucleotide encoding a PEgRNA can be delivered sequentially.

Polynucleotides Encoding Prime Editor Components

[0427] Polynucleotides encoding prime editing composition components can be DNA, RNA, or any combination thereof. In some embodiments, a polynucleotide encoding a prime editing composition component is an expression construct. In some embodiments, a polynucleotide encoding a prime editing composition component is a vector. In some embodiments, the vector is a DNA vector. In some embodiments, the vector is a plasmid. In some embodiments, the vector is a virus vector, *e.g.*, a retroviral vector, adenoviral vector, lentiviral vector, herpesvirus vector, or an adeno-associated virus vector (AAV).

[0428] In some embodiments, polynucleotides encoding polypeptide components of a prime editing composition are codon optimized for improved expression. Codon optimization can refer to engineering a polynucleotide sequence for enhanced expression in a host cell of interest, by replacing at least one codon (*e.g.*, about or more than about 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more codons) of the native polynucleotide sequence with codons that are more frequently or most frequently used in the genes of that host cell while maintaining the native amino acid sequence. In some embodiments, codon optimization engineers a polynucleotide sequence for enhanced expression by altering GC content of the polynucleotide sequence to increase mRNA stability in the host cell.

[0429] In some embodiments, codon optimization minimizes tandem repeat codons or tandem repeat nucleobase runs that may impair gene construction or expression. Codon optimization may also include customizing transcriptional and translational control regions, inserting or removing protein trafficking sequences, removing or adding post translation modification sites in encoded proteins (*e.g.*, glycosylation sites), adding, removing or shuffling protein domains, inserting or deleting restriction sites, and/or modifying ribosome binding sites and mRNA degradation sites to enhance expression and proper folding of the prime editor polypeptide in the host cell.

[0430] In some embodiments, a polynucleotide encoding a prime editor polypeptide, *e.g.*, a DNA sequence or mRNA sequence, is codon optimized, e.g., for expression in a cell of a specific species. Various species exhibit particular bias for certain codons of a particular amino acid. In some embodiments, the polynucleotide can be optimized for increased expression in cells of a specific species, using a codon usage table. Codon usage tables are readily available to those skilled in the art, for example, in Nakamura, Y., *et al.* "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" Nucl. Acids Res. 28:292 (2000). Computer algorithms for codon optimizing a particular sequence for expression in a particular host cell are also available, such as GeneArt (Life Technologies), or DNA2.0 (Menlo Park, CA).

[0431] In some embodiments, a polynucleotide encoding a prime editor polypeptide, *e.g.,* a DNA sequence or mRNA sequence, is codon optimized for expression in a desired cell from specific species, *e.g.*, in bacterial cell, plant cell, insect cell, or mammalian cell. In some embodiments, the codon optimization is for expression in a eukaryotic cell. In some embodiments, the codon optimization is for expression in a mammalian cell. In some embodiments, the codon optimization is for expression in a human cell. In some embodiments, a polynucleotide encoding a prime editor polypeptide is codon optimized for expression in a desire cell type. In some embodiments, the codon optimization is for expression in a hematopoietic stem cell (HSC). In some embodiments, the codon optimization is for expression in a CD34$^+$ HSC. In some embodiments, the codon optimization is for expression in a human hematopoietic stem cell (HSC). In some embodiments, the codon optimization is for expression in a human CD34$^+$ HSC. In some embodiments, the codon optimization is for expression in a human CD34$^+$ hematopoietic stem progenitor cell (HSPC). In some embodiments, the codon optimization is for expression in hepatocytes, fibroblasts, keratinocytes, epithelial cells (*e.g.*, mammary epithelial cells, intestinal epithelial cells), endothelial cells, glial cells, neural cells, formed elements of the blood (*e.g.*, lymphocytes, bone marrow cells, hematopoietic stem progenitor cells), muscle cells and precursors of these somatic cell types. In some embodiments, the codon optimization is for expression in primary hepatocytes. In some embodiments, the codon optimization is for expression in pluripotent stem cells (iPSCs). In some embodiments, the codon optimization is for expression in neurons. In some embodiments, the codon optimization is for expression in basal ganglia. the codon optimization is for expression in epithelial cells from lung, liver, stomach, or intestine. the codon optimization is for expression in retinal cells.

[0432] In some embodiments, codon optimization engineers a polynucleotide sequence for enhanced expression by altering secondary structure to enhance expression in the host cell. “Secondary structure” refers to the three-dimensional form of local segments of a biopolymer, such as a polynucleotide. In some embodiments, a secondary structure may be formed in a polynucleotide molecule, *e.g.*, a DNA or an RNA molecule. In some embodiments, a secondary structure in a polynucleotide is formed by base pairing of complementary nucleotide sequences within a single polynucleotide molecule. In some embodiments, a secondary structure in a polynucleotide comprises one or more double-stranded regions through base pairing of complementary nucleotide sequences within a single polynucleotide molecule. In some embodiments, the secondary structure of a polynucleotide, *e.g.,* a DNA or mRNA, comprises a hairpin, a stem, a loop, a tetraloop, a pseudoknot, a stem-loop, or any combination thereof. In some embodiments, when a polynucleotide contains an altered secondary structure as compared to a reference polynucleotide, the polynucleotide has a reduced or increased degree of secondary structure compared to the reference polynucleotide. Degree of secondary structure can be measured by the percentage of nucleotides of a polynucleotide that form complementary base pairs within the same polynucleotide.

[0433] In some embodiments, an optimized polynucleotide sequence, *e.g.*, a mRNA encoding a prime editor fusion protein, exhibits an increased degree of secondary structure compared to a reference polynucleotide sequence, *e.g.*, an unaltered reference mRNA encoding a PE protein. In some embodiments, a reference sequence is a wild-type polynucleotide sequence encoding all or a portion of a prime editor protein. In some embodiments, a reference sequence is a polynucleotide sequence encoding a functional variant of all or a portion of a prime editor protein, the reference sequence being altered from the wild type polynucleotide sequence only to encode one or more amino acid substitutions in of the functional variant. An exemplary reference polynucleotide sequence encoding the PE protein is provided in SEQ ID NOs: 26, 27, 32, 33. In some embodiments, a codon optimized polynucleotide sequence exhibits a reduced degree of secondary structure compared to a reference polynucleotide sequence. In some embodiments, a codon optimized polynucleotide comprises a reduced number of inverted repeat motifs compared to a reference polynucleotide sequence. In some embodiments, a codon optimized polynucleotide sequence exhibits an increased degree of secondary structure compared to a reference polynucleotide sequence. In some embodiments, a codon optimized polynucleotide comprises an increased number of inverted repeat motifs compared to a reference polynucleotide sequence.

[0434] In some embodiments, a codon optimized polynucleotide exhibits an altered degree of secondary structure in a specific portion as compared to a reference polynucleotide sequence. In some embodiments, a codon optimized polynucleotide exhibits a reduced degree of secondary structure in a specific portion as compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits an altered degree of secondary structure in an open reading frame (ORF) compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits a reduced degree of secondary structure in a ribosome binding site at the 5' region of an ORF compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits a reduced degree of secondary structure at the N terminus of the ORF compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits a reduced degree of secondary structure at the C terminus of the ORF compared to a reference polynucleotide sequence. In some embodiments, a codon optimized polynucleotide sequence exhibits an increased secondary structure in a specific portion as compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits an increased degree of secondary structure in an open reading frame (ORF) compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits an increased degree of secondary structure at the N terminus of the ORF compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide exhibits an increased degree of secondary structure at the C terminus of the ORF compared to a reference polynucleotide sequence. In some embodiments, the codon optimized polynucleotide (*e.g.* mRNA) that encodes a prime editor polypeptide exhibits an increased degree of secondary structure compared to a reference coding sequence, *e.g.*, of a SpCas9 or a M-MLV RT. In some embodiments, the codon optimized polynucleotide (*e.g.* mRNA) that encodes a prime editor polypeptide exhibits an increased secondary structure in an open reading frame (ORF) compared to the reference coding sequence, *e.g.*, of a SpCas9 or a M-MLV RT. In some embodiments, the codon optimized polynucleotide (*e.g.*, mRNA) that encodes a prime editor polypeptide exhibits secondary structure(s) that increase stability of the polynucleotide. In some embodiments, the codon optimized polynucleotide (*e.g.*, mRNA) that encodes a prime editor polypeptide exhibits secondary structure(s) that increase initiation of polypeptide synthesis at or from an initiation codon. In some embodiments, the codon optimized polynucleotide (*e.g.*, mRNA) that encodes a prime editor polypeptide exhibits secondary structure(s) that inhibit or reduce of the amount of polypeptide translated from any ORF within the polynucleotide other than the full ORF, thereby increasing translational fidelity of the prime editor polypeptide. In some embodiments, the secondary structure improves stability of the polynucleotide, *e.g.*, mRNA, or a mRNA encoded by the polynucleotide. In some embodiments, the secondary structure improves thermostability of the polynucleotide, *e.g.*, mRNA, or a mRNA encoded by the polynucleotide.

[0435] Optimized polynucleotides that encode prime editor polypeptide or components are provided.

[0436] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of SEQ ID NO: 627 or SEQ ID NO: 629 (e.g., a DNA polynucleotide) or to the nucleic acid sequence of SEQ ID NO: 628, or SEQ ID NO: 630 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of SEQ ID NO: 627, or SEQ ID NO: 629 or from the group consisting of SEQ ID NO: 628, or SEQ ID NO: 630.

[0437] In some embodiments, a prime editor comprises a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs. 28, 41, 50, 59, 68, 83, 91, 245, or 257 (e.g., a DNA polynucleotide) or to the nucleic acid sequence of SEQ ID NOs: 29, 42, 51, 60, 69, 84, 92, 246, or 258 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of any of SEQ ID NOs. 28, 41, 50, 59, 68, 83, 91, 245, or 257 (e.g., a DNA polynucleotide) or from the group consisting of any of SEQ ID NOs. 29, 42, 51, 60, 69, 84, 92, 246, or 258 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises a DNA polymerase domain that is encoded by a polynucleotide that is codon optimized. In some embodiments, a prime editor comprises a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs. 83 or 91, (e.g., a DNA polynucleotide) or to the nucleic acid sequence of SEQ ID NOs: 84 or 92 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of any of SEQ ID NOs. 83 or 91 (e.g., a DNA polynucleotide) or from the group consisting of any of SEQ ID NOs. 84 or 92 (e.g., an RNA polynucleotide).

[0438] In some embodiments, a prime editor comprises a linker that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs: 235, 247, 259, 633, or 635(e.g., a DNA polynucleotide) or to the nucleic acid sequence selected from any of SEQ ID NO: 236, 248, 260, 634, or 636 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises a linker that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 235, 247, 259, 633, or 635 or from the group consisting of SEQ ID NO:236, 248, 260, 634, or 636. In some embodiments, a prime editor comprises a linker that is encoded by a polynucleotide that is codon optimized.

[0439] In some embodiments, a prime editor comprises one or more NLS that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs: 239, 251, 263, 631, or 637 (e.g., a DNA polynucleotide) or to a nucleic acid sequence of SEQ ID NO: 240, 252, 264, 632, or 638 (e.g., an RNA polynucleotide). In some embodiments, a prime editor comprises one or more NLS that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 239, 251, 263, 631, or 637 or from the group consisting of SEQ ID NO: 240, 252, 264, 632, or 638. In some embodiments, a prime editor comprises an NLS that is encoded by a polynucleotide that is codon optimized.

[0440] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to the nucleic acid sequence of SEQ ID NO: 627 or SEQ ID NO: 629 (e.g., a DNA polynucleotide) or to the nucleic acid sequence of SEQ ID NO: 628, or SEQ ID NO: 630 (e.g., an RNA polynucleotide) and further comprises a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs. 28, 41, 50, 59, 68, 83, 91, 245, or 257 (e.g., a DNA polynucleotide) or to the nucleic acid sequence of SEQ ID NOs: 29, 42, 51, 60, 69, 84, 92, 246, or 258 (e.g., an RNA polynucleotide) optionally wherein the prime editor further comprises a linker that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs: 235, 247, 259, 633, or 635(e.g., a DNA polynucleotide) or to the nucleic acid sequence selected from any of SEQ ID NO: 236, 248, 260, 634, or 636 (e.g., an RNA polynucleotide), optionally wherein the prime editor further comprises a NLS that is encoded by a polynucleotide comprising a nucleic acid sequence that is at least about 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from any of SEQ ID NOs: 239, 251, 263, 631, or 637 (e.g., a DNA polynucleotide) or to a nucleic acid sequence of SEQ ID NO: 240, 252, 264, 632, or 638 (e.g., an RNA polynucleotide).

[0441] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of SEQ ID NO: 627, or SEQ ID NO: 629 or from the group consisting of SEQ ID NO: 628, or SEQ ID NO: 630, further comprising a a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of any of SEQ ID NOs. 28, 41, 50, 59, 68, 83, 91, 245, or 257 (e.g., a DNA polynucleotide) or from the group consisting of any of SEQ ID NOs. 29, 42, 51, 60, 69, 84, 92, 246, or 258 (e.g., an RNA polynucleotide), optionally wherein the prime editor further comprises a linker that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 235, 247, 259, 633, or 635 or from the group consisting of SEQ ID NO:236, 248, 260, 634, or 636, optionally wherein the prime editor further comprises one or more NLS that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 239, 251, 263, 631, or 637 or from the group consisting of SEQ ID NO: 240, 252, 264, 632, or 638.

[0442] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence is selected from the group consisting of SEQ ID NO: 627, or SEQ ID NO: 629 (e.g., a DNA polynucleotide) or from the group consisting of SEQ ID NO: 628, or SEQ ID NO: 630, (e.g., a RNA polynucleotide) further comprising a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence that is selected from the group consisting of any of SEQ ID NOs. 83, 91, 245, or 257(e.g., a DNA polynucleotide) or from the group consisting of SEQ ID NO: 84, 92, 246, or 258, (e.g., a RNA polynucleotide) optionally wherein the prime editor further comprises a a linker that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 235, 247, 259, 633, or 635 or from the group consisting of SEQ ID NO:236, 248, 260, 634, or 636, optionally wherein the prime editor further comprises one or more NLS that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 239, 251, 263, 631, or 637 or from the group consisting of SEQ ID NO: 240, 252, 264, 632, or 638.

[0443] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NO: 627, (e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 629 (e.g., an RNA polynucleotide) further comprising a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NO. 83 (e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 84 (e.g., a RNA polynucleotide) optionally wherein the prime editor further comprises a linker that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 633, or 635 or from the group consisting of SEQ ID NO: 634, or 636, optionally wherein the prime editor further comprises one or more NLS that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 631, or 637 or from the group consisting of SEQ ID NO: 632, or 638.

[0444] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NO: 629, (e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 630 (e.g., an RNA polynucleotide) further comprising a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NO. 91 (e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 92 (e.g., a RNA polynucleotide) optionally wherein the prime editor further comprises a linker that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 633, or 635 or from the group consisting of SEQ ID NO: 634, or 636, optionally wherein the prime editor further comprises one or more NLS that is encoded by a polynucleotide that is selected from the group consisting of SEQ ID NO: 631, or 637 or from the group consisting of SEQ ID NO: 632, or 638.

[0445] In some embodiments, a prime editor comprises a DNA binding domain (e.g., a Cas9) that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NO: 627 or 629, (e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 628 or 630 (e.g., an RNA polynucleotide) further comprising a DNA polymerase domain that is encoded by a polynucleotide comprising a nucleic acid sequence as set forth in SEQ ID NOs. 83 or 91(e.g., a DNA polynucleotide) or as set forth in SEQ ID NO: 84 or 92 (e.g., a RNA polynucleotide) optionally wherein the prime editor further comprises a linker that is encoded by a polynucleotide that is selected a sequence as set forth in SEQ ID NO: 233, or as set forth in SEQ ID NO:236, optionally wherein the prime editor further comprises one or more NLS that is encoded by a polynucleotide as set forth in SEQ ID NO: 239, 631, or 637 or as set forth in SEQ ID NO: 240.

[0446] In some embodiments, a prime editing composition comprises a polynucleotide that encodes a prime editor that comprises an amino acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of the sequences set forth in SEQ ID NO: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, or 625. In some embodiments, a prime editing composition comprises a polynucleotide that encodes a prime editor that comprises an amino acid sequence selected from any one of SEQ ID NOs: 25, 34, 35, 43, 44, 52, 53, 61, 62, 63, 70-78, 85, 86, 93, 96, 99, 104, 105, 110, 111, 116, 117, 122, 125, 128, 131, 134, 137, 140, 143, 146, 149, 152, 155, 158, 161, 164, 170, 176, 179, 182, 185, 188, 191, 194, 197, 200, 203, 206, 209, 212, 215, 218, 221, 224, 227, 230, 620, 622, 624, or 625 (Tables 15-66). In some embodiments, the polynucleotide encoding a prime editor is a DNA polynucleotide. In some embodiments, the polynucleotide encoding a prime editor is an RNA polynucleotide (e.g., a mRNA). In some embodiments, a polynucleotide (e.g., a DNA polynucleotide) encoding a prime editor comprises a nucleic acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of the sequences set forth in 26, 30, 32, 34, 37, 39, 46, 48, 55, 57, 64, 66, 79, 81, 87, 89, 94, 97, 100, 102, 106, 108, 112, 114, 118, 120, 123, 126, 129, 132, 135, 138, 141, 144, 147, 150, 153, 156, 159, 162, 165, 168, 171, 174, 177, 180, 183, 186, 189, 192, 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 233, 241, 243, 253, 255, 263, or 265(Tables 15-66) or to one of the sequences set forth in SEQ ID NO: 27, 31, 33, 35, 38, 40, 47, 49, 56, 58, 65, 67, 79, 82, 88, 90, 95, 98, 101, 103, 107, 109, 113, 115, 119, 121, 124, 127, 130, 133, 136, 139, 142, 145, 148, 151, 154, 157, 160, 163, 166, 169, 172, 175, 178, 181, 184, 187, 190, 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 234, 242, 244, 254, 256, 264, or 266 (Tables 15-66). In some embodiments, a polynucleotide (e.g., a DNA polynucleotide) encoding a prime editor comprises a nucleic acid sequence that is selected from any one of SEQ ID NOs. 26, 30, 32, 34, 37, 39, 46, 48, 55, 57, 64, 66, 79, 81, 87, 89, 94, 97, 100, 102, 106, 108, 112, 114, 118, 120, 123, 126, 129, 132, 135, 138, 141, 144, 147, 150, 153, 156, 159, 162, 165, 168, 171, 174, 177, 180, 183, 186, 189, 192, 195, 198, 201, 204, 207, 210, 213, 216, 219, 222, 225, 228, 231, 233, 241, 243, 253, 255, 263, or 265(Tables 15-66) (e.g., a DNA polynucleotide) or is selected from any one of SEQ ID NOs. SEQ ID NO: 27, 31, 33, 35, 38, 40, 47, 49, 56, 58, 65, 67, 79, 82, 88, 90, 95, 98, 101, 103, 107, 109, 113, 115, 119, 121, 124, 127, 130, 133, 136, 139, 142, 145, 148, 151, 154, 157, 160, 163, 166, 169, 172, 175, 178, 181, 184, 187, 190, 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 234, 242, 244, 254, 256, 264, or 266 (Tables 15-66) (e.g., an RNA polynucleotide).

[0447] In some embodiments, a polynucleotide encoding a prime editor comprises a nucleic acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any one of the sequences set forth in SEQ ID NOs:79, 81, 87, 89, or 233(e.g., a DNA polynucleotide) or to any one of the sequences set forth in SEQ ID NOs:80, 82, 88, 90, or 234(e.g., an RNA polynucleotide).). In some embodiments, a polynucleotide (e.g., an RNA polynucleotide) encoding a prime editor comprises a nucleic acid sequence that is selected from any one of SEQ ID NOs: 79, 81, 87, 89, or 233 (e.g., a DNA polynucleotide) or is selected from any one of SEQ ID NO: 80, 82, 88, 90, or 234 (e.g., an RNA polynucleotide).

[0448] In some embodiments, a polynucleotide encoding a prime editor comprises a nucleic acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any of sequences set forth in SEQ ID NOs:79 or 81, (e.g., a DNA polynucleotide) or any of sequences set forth in SEQ ID NOs:80 or 82. In some embodiments, a polynucleotide (e.g., an RNA polynucleotide) encoding a prime editor comprises a nucleic acid sequence that is selected from any one of SEQ ID NOs: 79 or 81 (e.g., a DNA polynucleotide) or is selected from any one of SEQ ID NO: 80 or 82 (e.g., an RNA polynucleotide).

[0449] In some embodiments, a polynucleotide encoding a prime editor comprises a nucleic acid sequence that is at least about 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% identical to any of sequences set forth in SEQ ID NOs: 88 or 90, (e.g., a DNA polynucleotide) or any of sequences set forth in SEQ ID NOs:88 or 90. In some embodiments, a polynucleotide (e.g., an RNA polynucleotide) encoding a prime editor comprises a nucleic acid sequence that is selected from any one of SEQ ID NOs: 87 or 89, (e.g., a DNA polynucleotide) or is selected from any one of SEQ ID NO: 88 or 90 (e.g., an RNA polynucleotide).

[0450] In some embodiments, the polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos: 79, 80, 94, 95, 106, 107, 118, and 119. In some embodiments, the polynucleotide comprises a sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to a sequence selected from the group consisting of SEQ ID Nos: 79, 80, 94, 95, 106, 107, 118, and 119. In some embodiments, the polynucleotide comprises a sequence having at least 80%, at least 85%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% identity to a sequence selected from the group consisting of SEQ ID Nos: 79, 80, 94, 95, 106, 107, 118, and 119.

[0451] In some embodiments, the polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos: 87, 88, 97, 98, 100, 101, 112, and 113. In some embodiments, the polynucleotide comprises a sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to a sequence selected from the group consisting of SEQ ID Nos: 87, 88, 97, 98, 100, 101, 112, and 113. In some embodiments, the polynucleotide comprises a sequence having at least 80%, at least 85%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% identity to a sequence selected from the group consisting of SEQ ID Nos: 87, 88, 97, 98, 100, 101, 112, and 113.

[0452] In some embodiments, the polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos: 274-285 or 592-595. In some embodiments, the polynucleotide comprises a sequence having at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% identity to a sequence selected from the group consisting of SEQ ID Nos: 274-285 or 592-595. In some embodiments, the polynucleotide comprises a sequence having at least 80%, at least 85%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 99.9% identity to a sequence selected from the group consisting of SEQ ID Nos: 274-285 or 592-595.

[0453] In some embodiments, provided herein are prime editing compositions comprising one or more polynucleotides encoding one or more prime editor components. In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA binding domain. In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, e.g., a RT domain. In some embodiments, a prime editing composition comprises a polynucleotide, e.g., a fusion polynucleotide, that comprises the polynucleotide encoding a DNA binding domain and the polynucleotide encoding a DNA polymerase domain, e.g., the RT domain. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 412-555. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least 80% identity to a sequence corresponding to nucleotides 100-2130 of a sequence selected from the group consisting of SEQ ID Nos 412-555. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence corresponding to nucleotides 100-2130 of a sequence selected from the group consisting of SEQ ID Nos 412-555. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 83 or 84. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 83 or 84. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises the sequence of SEQ ID No 83 or 84.

[0454] In some embodiments, a prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 91 or 92. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID No 91 or 92. In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA polymerase domain, wherein the polynucleotide comprises the sequence of SEQ ID No 91 or 92.

[0455] In some embodiments, the prime editing composition comprises a polynucleotide encoding a DNA binding domain. In some embodiments, the polynucleotide encoding the DNA binding domain comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID Nos 627-630. In some embodiments, the polynucleotide encoding the DNA binding domain comprises the sequence of SEQ ID No 627, 628, 629, or 630.

[0456] In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprising a nucleic acid sequence comprising a first polynucleotide encoding a DNA binding domain, a second polynucleotide encoding a DNA polymerase domain, optionally further comprising a third polynucleotide encoding a linker and optionally further comprising a fourth polynucleotide encoding an NLS. In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprises a nucleic acid sequence comprising a first polynucleotide encoding a DNA polymerase domain, a second polynucleotide encoding a DNA binding domain, optionally further comprising a third polynucleotide domain encoding a linker and optionally further comprising a fourth polynucleotide domain encoding an NLS. In some embodiments, the third polynucleotide sequence is located between the first and the second polynucleotide sequence. In some embodiments, the sequence encoding the NLS (e.g., fourth polynucleotide) is at the 5' end terminus of the sequence encoding the DNA binding domain. In some embodiments, the sequence encoding the NLS (e.g., fourth polynucleotide) is at the 5' end terminus of the sequence encoding the DNA polymerase domain. In some embodiments, the sequence encoding the NLS (e.g., fourth polynucleotide) is at the 3' end terminus of the sequence encoding the DNA binding domain. In some embodiments, the sequence encoding the NLS (e.g., fourth polynucleotide) is at the 3' end terminus of the sequence encoding the DNA polymerase domain. In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprising a nucleic acid sequence comprises two or more nucleotide sequences that encode two or more NLSs. In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprising a nucleic acid sequence comprises two or more nucleotide sequences that encode two or more NLS at the 3' end. In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprising a nucleic acid sequence comprises two or more nucleotide sequences that encode two or more NLS at the 5' end. In some embodiments, a polynucleotide, e.g., a fusion polynucleotide encoding a prime editor comprising a nucleic acid sequence comprises at least two nucleotide sequences that encode at least one NLS at the 3' end and at least one NLS at the 5' end. In some embodiments, the NLS is encoded by a polynucleotide comprising a sequence as set forth in SEQ ID Nos 239, 240, 251, 252, 263, and 264

[0457]

[0458] In some embodiments, a prime editing composition comprises a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the first and the second polynucleotides are connected to form a fusion polynucleotide. In some embodiments, the first and the second polynucleotides are connected by a polynucleotide sequence that encodes a peptide linker. In some embodiments, the polynucleotide sequence that encodes a peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID Nos 235 or 236. In some embodiments, the polynucleotide sequence that encodes a peptide linker comprises the sequence of SEQ ID Nos 235 or 236. In some embodiments, the fusion polynucleotide comprises the first and the second polynucleotides from 5' to 3'. In some embodiments, the fusion polynucleotide comprises the first and the second polynucleotides from 3' to 5'. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, 229, 241, and 242. In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, 229, 241, and 242. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NOs: 81 or 82. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 81 or 82. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NOs: 241 or 242. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 241 or 242.

[0459] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, , 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232. In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NOs: 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, , 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NOs: 89 or 90. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 89 or 90. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NOs: 102 or 103. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 102 or 103. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NOs: 114 or 115. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 114 or 115.

[0460] In some embodiments, the first polynucleotide, the second polynucleotide, or the fusion polynucleotide further comprises a sequence encoding one or more nuclear localization signals (NLSs). In some embodiments, the sequence encoding the NLS is at the 5' end terminus of the first polynucleotide. In some embodiments, the sequence encoding the NLS is at the 3' end terminus of the first polynucleotide. In some embodiments, the sequence encoding the NLS is at the 5' end terminus of the second polynucleotide. In some embodiments, the sequence encoding the NLS is at the 3' end terminus of the second polynucleotide. In some embodiments, the sequence encoding the NLS is between the first and the second polynucleotides. In some embodiments, the first polynucleotide, the second polynucleotide, both comprise comprises two or more sequences that encode two or more NLSs. The prime editing composition of any one of preceding claims, wherein the first polynucleotide and the second polynucleotide are connected, and wherein the first polynucleotide comprises a sequence encoding a NLS at the 5' end and wherein the second polynucleotide comprises a sequence encoding a NLS at the 3' end.

[0461] In some embodiments, the first polynucleotide and the second polynucleotide are connected, and wherein the first polynucleotide comprises a sequence encoding two or more NLSs at the 5' end and/or wherein the second polynucleotide comprises a sequence encoding two or more NLSs at the 3' end. In some embodiments, the NLS or the two or more NLSs comprise a bipartite NLS (BPNLS). In some embodiments, the BPNLS is a bipartite SV40 NLS or a bipartite Xenopus nucleoplasmin NLS. In some embodiments, the BPNLS comprises an amino acid sequence selected from the group consisting of SEQ ID Nos 4-24. In some embodiments, the NLS is encoded by a polynucleotide comprising a sequence as set forth in SEQ ID Nos 239, 240, 251, 252, 263, and 264. In some embodiments, the sequence encoding the NLS comprises the sequence of SEQ ID No 239 or 240 and is connected to the 3' end of the second polynucleotide.

[0462] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 94, 95, 106,107, 118, 119, 233, and 234. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 79, 80, 94, 95, 106,107, 118, 119, 233, or 234.

[0463] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence of SEQ ID NO 79 or 80. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NO 79 or 80.

[0464] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 87, 88, 97,98, 100, 101, 112, and 113.

[0465] . In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NOs: 87, 88, 97,98, 100, 101, 112, or 113.

[0466] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the sequence of SEQ ID NO 87 or 88. In some embodiments, the fusion polynucleotide comprises the sequence of SEQ ID NO 87 or 88.

[0467] In some embodiments, the fusion polypeptide further comprises a stop codon at the 3' end. In some embodiments, the stop codon comprises a sequence selected from the group consisting of SEQ ID Nos 269-272. In some embodiments, the stop codon comprises a sequence selected from the group consisting of sequences UAA, UAG, UGA, and UAAUAGUGA. In some embodiments, the stop codon comprises a DNA or RNA sequence of any stop codon known in the art.

[0468] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 276-279. In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos 276-279. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 282-285.In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos 282-285.

[0469] In some embodiments, the fusion polynucleotide further comprises a 5’ untranslated region sequence (5’ UTR) or a 3’ untranslated region sequence (3’ UTR).

[0470] In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 274, 275, 592, and 593. In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos 274, 275, 592, and 593. In some embodiments, the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 280, 281, 594, or 595.In some embodiments, the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID Nos 280, 281, 594, or 595.

[0471] In some embodiments, the first polynucleotide, the second polynucleotide, or the fusion polynucleotide comprises DNA. In some embodiments, the first polynucleotide, the second polynucleotide, or the fusion polynucleotide comprises a regulatory element. In some embodiments, the regulatory element is a promoter. In some embodiments, the first polynucleotide, the second polynucleotide, or the fusion polynucleotide comprises comprise RNA. In some embodiments, the first polynucleotide, the second polynucleotide, or the fusion polynucleotide comprises comprise mRNA.

[0472] A polynucleotide, *e.g.*, a DNA or mRNA, that encodes a protein domain described herein can be obtained by chemically synthesizing the DNA, or by connecting synthesized partly overlapping oligoDNA short chains by utilizing the PCR method and the Gibson Assembly method to construct a DNA encoding the full length thereof. The advantage of constructing a full-length DNA by chemical synthesis or a combination of PCR method or Gibson Assembly method is that the codon to be used can be designed in CDS full-length according to the host into which the DNA is introduced. In the expression of a heterologous DNA, the protein expression level is expected to increase by converting the DNA sequence thereof to a codon highly frequently used in the host organism. As the data of codon use frequency in host to be used, for example, the genetic code use frequency database (http://www.kazusa.or.jp/codon/index.html) disclosed in the home page of Kazusa DNA Research Institute can be used, or documents showing the codon use frequency in each host may be referred to. By reference to the obtained data and the DNA sequence to be introduced, codons showing low use frequency in the host from among those used for the DNA sequence may be converted to a codon coding the same amino acid and showing high use frequency.

[0473] In some embodiments, a polynucleotide encoding a polypeptide component of a prime editing composition are operably linked to one or more expression regulatory elements, for example, a promoter, a 3' UTR, a 5' UTR, or any combination thereof. In some embodiments, a polynucleotide encoding a prime editing composition component is a messenger RNA (mRNA). In some embodiments, the mRNA comprises a Cap at the 5' end and/or a poly A tail at the 3' end.

Pharmaceutical compositions

[0474] Disclosed herein are pharmaceutical compositions comprising any of the prime editing composition components, for example, prime editors, fusion proteins, polynucleotides encoding prime editor polypeptides, PEgRNAs, ngRNAs, and/or prime editing complexes described herein.

[0475] The term "pharmaceutical composition", as used herein, refers to a composition formulated for pharmaceutical use. In some embodiments, the pharmaceutical composition further comprises a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical composition comprises additional agents, *e.g.*, for specific delivery, increasing half-life, or other therapeutic compounds.

[0476] In some embodiments, a pharmaceutically acceptable carrier comprises any vehicle, such as a liquid or solid filler, diluent, excipient, manufacturing aid (*e.g.*, lubricant, talc magnesium, calcium or zinc stearate, or steric acid), or solvent encapsulating material, involved in carrying or transporting the compound from one site (*e.g.*, the delivery site) of the body, to another site (*e.g.*, organ, tissue or portion of the body). A pharmaceutically acceptable carrier is "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the tissue of the subject (*e.g.*, physiologically compatible, sterile, physiologic pH, etc.) Formulations of the pharmaceutical compositions described herein can be prepared by any method known or hereafter developed in the art of pharmacology. In general, such preparatory methods include the step of bringing the active ingredient(s) into association with an excipient and/or one or more other accessory ingredients, and then, if necessary and/or desirable, shaping and/or packaging the product into a desired single- or multi-dose unit. Pharmaceutical formulations can additionally comprise a pharmaceutically acceptable excipient, which, as used herein, includes any and all solvents, dispersion media, diluents, or other liquid vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, solid binders, lubricants, and the like, as suited to the particular dosage form desired.

Methods of editing

[0477] The methods and compositions disclosed herein can be used to edit a double stranded target DNA, *e.g.*, a target gene of interest by prime editing.

[0478] In some embodiments, the prime editing method comprises contacting a double stranded target DNA, *e.g.*, a target gene, with a PEgRNA and a prime editor (PE) polypeptide described herein. In some embodiments, the double stranded target DNA, *e.g.*, a target gene is double stranded, and comprises two strands of DNA complementary to each other. In some embodiments, the contacting with a PEgRNA and the contacting with a prime editor are performed sequentially. In some embodiments, the contacting with a prime editor is performed after the contacting with a PEgRNA. In some embodiments, the contacting with a PEgRNA is performed after the contacting with a prime editor. In some embodiments, the contacting with a PEgRNA, and the contacting with a prime editor are performed simultaneously. In some embodiments, the PEgRNA and the prime editor are associated in a complex prior to contacting a double stranded target DNA, *e.g.*, a target gene.

[0479] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in binding of the PEgRNA to a target strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in binding of the PEgRNA to a search target sequence on the target strand of the double stranded target DNA, *e.g.*, a target gene upon contacting with the PEgRNA. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in binding of a spacer sequence of the PEgRNA to a search target sequence with the search target sequence on the target strand of the double stranded target DNA, *e.g.*, a target gene upon said contacting of the PEgRNA.

[0480] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in binding of the prime editor to the double stranded target DNA, *e.g.*, a target gene, *e.g.,* the double stranded target DNA, *e.g.*, a target gene, upon the contacting of the PE composition with the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the DNA binding domain of the PE associates with the PEgRNA. In some embodiments, the PE binds the double stranded target DNA, *e.g.*, a target gene, directed by the PEgRNA. Accordingly, in some embodiments, the contacting of the double stranded target DNA, *e.g.*, a target gene result in binding of a DNA binding domain of a prime editor of the double stranded target DNA, *e.g.*, a target gene, directed by the PEgRNA.

[0481] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in a nick in an edit strand of the double stranded target DNA, *e.g.*, a target gene, by the prime editor upon contacting with the double stranded target DNA, *e.g.*, a target gene, thereby generating a nicked on the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in a single-stranded DNA comprising a free 3′ end at the nick site of the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in a nick in the edit strand of the double stranded target DNA, *e.g.*, a target gene by a DNA binding domain of the prime editor, thereby generating a single-stranded DNA comprising a free 3′ end at the nick site. In some embodiments, the DNA binding domain of the prime editor is a Cas domain. In some embodiments, the DNA binding domain of the prime editor is a Cas9. In some embodiments, the DNA binding domain of the prime editor is a Cas9 nickase.

[0482] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition results in hybridization of the PEgRNA with the 3’ end of the nicked single-stranded DNA, thereby priming DNA polymerization by a DNA polymerase domain of the prime editor.

In some embodiments, the free 3' end of the single-stranded DNA generated at the nick site hybridizes to a primer binding site sequence (PBS) of the contacted PEgRNA, thereby priming DNA polymerization. In some embodiments, the DNA polymerization is reverse transcription catalyzed by a reverse transcriptase domain of the prime editor. In some embodiments, the method comprises contacting the double stranded target DNA, *e.g.*, a target gene with a DNA polymerase, *e.g.*, a reverse transcriptase, as a part of a prime editor fusion protein or prime editing complex (in *cis*), or as a separate protein (in *trans*).

[0483] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition generates an edited single stranded DNA that is coded by the editing template of the PEgRNA by DNA polymerase mediated polymerization from the 3' free end of the single-stranded DNA at the nick site. In some embodiments, the editing template of the PEgRNA comprises one or more intended nucleotide edits compared to endogenous sequence of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the intended nucleotide edits are incorporated in the double stranded target DNA, *e.g.*, a target gene, by excision of the 5' single stranded DNA of the edit strand of the double stranded target DNA, *e.g.*, a target gene generated at the nick site and DNA repair. In some embodiments, the intended nucleotide edits are incorporated in the double stranded target DNA, *e.g.*, a target gene by excision of the editing target sequence and DNA repair. In some embodiments, excision of the 5' single stranded DNA of the edit strand generated at the nick site is by a flap endonuclease. In some embodiments, the flap nuclease is FEN1. In some embodiments, the method further comprises contacting the double stranded target DNA, *e.g.*, a target gene with a flap endonuclease. In some embodiments, the flap endonuclease is provided as a part of a prime editor fusion protein. In some embodiments, the flap endonuclease is provided in *trans*.

[0484] In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene with the prime editing composition generates a mismatched heteroduplex comprising the edit strand of the double stranded target DNA, *e.g.*, a target gene that comprises the edited single stranded DNA, and the unedited target strand of the double stranded target DNA, *e.g.*, a target gene. Without being bound by theory, the endogenous DNA repair and replication may resolve the mismatched edited DNA to incorporate the nucleotide change(s) to form the desired edited double stranded target DNA, *e.g.*, a target gene.

[0485] In some embodiments, the method further comprises contacting the double stranded target DNA, *e.g.*, a target gene, with a nick guide (ngRNA) disclosed herein. In some embodiments, the ngRNA comprises a spacer that binds a second search target sequence on the edit strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the contacted ngRNA directs the PE to introduce a nick in the target strand of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the nick on the target strand (non-edit strand) results in endogenous DNA repair machinery to use the edit strand to repair the non-edit strand, thereby incorporating the intended nucleotide edit in both strand of the double stranded target DNA, *e.g.*, a target gene and modifying the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the ngRNA comprises a spacer sequence that is complementary to, and may hybridize with, the second search target sequence on the edit strand only after the intended nucleotide edit(s) are incorporated in the edit strand of the double stranded target DNA, *e.g.*, a target gene.

[0486] In some embodiments, the double stranded target DNA, *e.g.*, a target gene is contacted by the ngRNA, the PEgRNA, and the PE simultaneously. In some embodiments, the ngRNA, the PEgRNA, and the PE form a complex when they contact the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the double stranded target DNA, *e.g.*, a target gene is contacted with the ngRNA, the PEgRNA, and the prime editor sequentially. In some embodiments, the double stranded target DNA, *e.g.*, a target gene is contacted with the ngRNA and/or the PEgRNA after contacting the double stranded target DNA, *e.g.*, a target gene with the PE. In some embodiments, the double stranded target DNA, *e.g.*, a target gene is contacted with the ngRNA and/or the PEgRNA before contacting the double stranded target DNA, *e.g.*, a target gene with the prime editor.

[0487] In some embodiments, the double stranded target DNA, *e.g.*, a target gene, is in a cell. Accordingly, also provided herein are methods of modifying a cell.

[0488] In some embodiments, the prime editing method comprises introducing a PEgRNA, a prime editor, and/or a ngRNA into the cell that has the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the prime editing method comprises introducing into the cell that has the double stranded target DNA, *e.g.*, a target gene with a prime editing composition comprising a PEgRNA, a prime editor polypeptide, and/or a ngRNA. In some embodiments, the PEgRNA, the prime editor polypeptide, and/or the ngRNA form a complex prior to the introduction into the cell. In some embodiments, the PEgRNA, the prime editor polypeptide, and/or the ngRNA form a complex after the introduction into the cell. The prime editors, PEgRNA and/or ngRNAs, and prime editing complexes may be introduced into the cell by any delivery approaches described herein or any delivery approach known in the art, including ribonucleoprotein (RNPs), lipid nanoparticles (LNPs), viral vectors, non-viral vectors, mRNA delivery, and physical techniques such as cell membrane disruption by a microfluidics device. The prime editors, PEgRNA and/or ngRNAs, and prime editing complexes may be introduced into the cell simultaneously or sequentially.

[0489] In some embodiments, the prime editing method comprises introducing into the cell a PEgRNA or a polynucleotide encoding the PEgRNA, a prime editor polynucleotide encoding a prime editor polypeptide, and optionally an ngRNA or a polynucleotide encoding the ngRNA. In some embodiments, the method comprises introducing the PEgRNA or the polynucleotide encoding the PEgRNA, the polynucleotide encoding the prime editor polypeptide, and/or the ngRNA or the polynucleotide encoding the ngRNA into the cell simultaneously. In some embodiments, the method comprises introducing the PEgRNA or the polynucleotide encoding the PEgRNA, the polynucleotide encoding the prime editor polypeptide, and/or the ngRNA or the polynucleotide encoding the ngRNA into the cell sequentially. In some embodiments, the method comprises introducing the polynucleotide encoding the prime editor polypeptide into the cell before introduction of the PEgRNA or the polynucleotide encoding the PEgRNA and/or the ngRNA or the polynucleotide encoding the ngRNA. In some embodiments, the polynucleotide encoding the prime editor polypeptide is introduced into and expressed in the cell before introduction of the PEgRNA or the polynucleotide encoding the PEgRNA and/or the ngRNA or the polynucleotide encoding the ngRNA into the cell. In some embodiments, the polynucleotide encoding the prime editor polypeptide is introduced into the cell after the PEgRNA or the polynucleotide encoding the PEgRNA and/or the ngRNA or the polynucleotide encoding the ngRNA are introduced into the cell. The polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA, may be introduced into the cell by any delivery approaches described herein or any delivery approach known in the art, for example, by RNPs, LNPs, viral vectors, non-viral vectors, mRNA delivery, and physical delivery.

[0490] In some embodiments, the polynucleotide encoding the prime editor polypeptide, the polynucleotide encoding the PEgRNA, and/or the polynucleotide encoding the ngRNA integrate into the genome of the cell after being introduced into the cell. In some embodiments, the polynucleotide encoding the prime editor polypeptide, the polynucleotide encoding the PEgRNA, and/or the polynucleotide encoding the ngRNA are introduced into the cell for transient expression. Accordingly, also provided herein are cells modified by prime editing.

[0491] In some embodiments, the cell is a prokaryotic cell. In some embodiments, the cell is a eukaryotic cell. In some embodiments, the cell is a mammalian cell. In some embodiments, the cell is a non-human primate cell, bovine cell, porcine cell, rodent or mouse cell. In some embodiments, the cell is a human cell. In some embodiments, the cell is a primary cell. In some embodiments, the cell is a human primary cell. In some embodiments, the cell is a progenitor cell. In some embodiments, the cell is a human progenitor cell. In some embodiments, the cell is a hepatocyte. In some embodiments, the cell is a human hepatocyte. In some embodiments, the cell is a primary human hepatocyte derived from an induced human pluripotent stem cell (iPSC). In some embodiments, the cell is a hematopoietic stem cell (HSC). In some embodiments, the cell is a human HSC. In some embodiments, the cell is a human $CD34^+$ HSC. In some embodiments, the codon optimization is for expression in a human $CD34^+$ hematopoietic stem progenitor cell (HSPC).

[0492] In some embodiments, the double stranded target DNA, *e.g.*, a target gene edited by prime editing is in a chromosome of the cell. In some embodiments, the intended nucleotide edits incorporate in the chromosome of the cell and are inheritable by progeny cells. In some embodiments, the intended nucleotide edits introduced to the cell by the prime editing compositions and methods are such that the cell and progeny of the cell also include the intended nucleotide edits. In some embodiments, the cell is autologous, allogeneic, or xenogeneic to a subject. In some embodiments, the cell is from or derived from a subject. In some embodiments, the cell is from or derived from a human subject. In some embodiments, the cell is introduced back into the subject, *e.g.*, a human subject, after incorporation of the intended nucleotide edits by prime editing.

[0493] In some embodiments, the method provided herein comprises introducing the prime editor polypeptide or the polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA into a plurality or a population of cells that comprise the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the population of cells is of the same cell type. In some embodiments, the population of cells is of the same tissue or organ. In some embodiments, the population of cells is heterogeneous. In some embodiments, the population of cells is homogeneous. In some embodiments, the population of cells is from a single tissue or organ, and the cells are heterogeneous. In some embodiments, the introduction into the population of cells is *ex vivo*. In some embodiments, the introduction into the population of cells is *in vivo*, *e.g.*, into a human subject.

[0494] In some embodiments, the double stranded target DNA, *e.g.*, a target gene is in a genome of each cell of the population. In some embodiments, introduction of the prime editor polypeptide or the polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA results in incorporation of one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene in at least one of the cells in the population of cells. In some embodiments, introduction of the prime editor polypeptide or the polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA results in incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene in a plurality of the population of cells. In some embodiments, introduction of the prime editor polypeptide or the polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA results in incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene in each cell of the population of cells. In some embodiments, introduction of the prime editor polypeptide or the polynucleotide encoding the prime editor polypeptide, the PEgRNA or the polynucleotide encoding the PEgRNA, and/or the ngRNA or the polynucleotide encoding the ngRNA results in incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene in sufficient number of cells such that the disease or disorder is treated, prevented or ameliorated.

[0495] In some embodiments, editing efficiency of the prime editing compositions and method described herein can be measured by calculating the percentage of edited double stranded target DNA, *e.g.*, a target gene in a population of cells introduced with the prime editing composition. In some embodiments, the editing efficiency is determined after 1 hour, 2 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 4 days, 5 days, 7 days, 10 days, or 14 days of exposing a double stranded target DNA, *e.g.*, a target gene to a prime editing composition. In some embodiments, the population of cells introduced with the prime editing composition is *ex vivo*. In some embodiments, the population of cells introduced with the prime editing composition is *in vitro*. In some embodiments, the population of cells introduced with the prime editing composition is *in vivo*. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1%, at least about 5%, at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, or at least about 99% relative to a suitable control. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least 25% relative to a suitable control. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least 35% relative to a suitable control. In some embodiments, the prime editing method disclosed herein has an editing efficiency of at least 30% relative to a suitable control. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least 45% relative to a suitable control. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least 50% relative to a suitable control.

[0496] In some embodiments, the methods disclosed herein have an editing efficiency of at least about 1%, at least about 5%, at least about 7.5%, at least about 10%, at least about 15%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% of editing in a primary cell relative to a suitable control primary cell.

[0497] In some embodiments, the methods disclosed herein have an editing efficiency of at least about 5%, at least about 7.5%, at least about 10%, at least about 15%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% of editing in a hepatocyte relative to a corresponding control hepatocyte. In some embodiments, the hepatocyte is a human hepatocyte.

[0498] In some embodiments, the methods disclosed herein have an editing efficiency of at least about 5%, at least about 7.5%, at least about 10%, at least about 15%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% of editing in a hematopoietic stem cell (HSC) relative to a corresponding control HSC. In some embodiments, the HSC is a human HSC.

[0499] In some embodiments, the methods disclosed herein having an increased editing efficiency by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 110%, at least 120%, at least 130%, at least 140%, at least 150%, at least 160%, at least 170%, at least 180%, at least 190%, at least 200%, at least 210%, at least 220%, at least 230%, at least 240%, at least 250%, at least 260%, at least 270%, at least 280%, at least 290%, at least 300% or more compared to prime editing with a prime editor having the sequence of SEQ ID NO: 25 and/or encoded by SEQ ID NO: 26. In some embodiments, the methods disclosed herein having an increased editing efficiency by at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 110%, at least 120%, at least 130%, at least 140%, at least 150%, at least 160%, at least 170%, at least 180%, at least 190%, at least 200%, at least 210%, at least 220%, at least 230%, at least 240%, at least 250%, at least 260%, at least 270%, at least 280%, at least 290%, at least 300% or more compared to prime editing with a prime editor having the sequence of SEQ ID NO: 25 and/or encoded by SEQ ID NO: 26. In some embodiments, the increased editing efficiency is in a human cell. In some embodiments, the increased editing efficiency is in a primary cell. In some embodiments, the increased editing efficiency is in a human primary cell. In some embodiments, the increased editing efficiency is in a progenitor cell. In some embodiments, the increased editing efficiency is in a human progenitor cell. In some embodiments, the increased editing efficiency is in a hepatocyte. In some embodiments, the increased editing efficiency is in a human hepatocyte. In some embodiments, the increased editing efficiency is in a primary human hepatocyte derived from an induced human pluripotent stem cell (iPSC). In some embodiments, the increased editing efficiency is in a hematopoietic stem cell (HSC). In some embodiments, the increased editing efficiency is in a primary cell. In some embodiments, the increased editing efficiency is in a human CD34+ HSC.

[0500] In some embodiments, the prime editing compositions provided herein are capable of incorporating one or more intended nucleotide edits without generating a significant proportion of indels. The term “indel(s)”, as used herein, refers to the insertion or deletion of a nucleotide base within a polynucleotide, for example, a double stranded target DNA, *e.g.*, a target gene. Such insertions or deletions can lead to frame shift mutations within a coding region of a gene. Indel frequency of editing can be calculated by methods known in the art. . In some embodiments, indel frequency can be calculated based on sequence alignment such as the CRISPResso 2 algorithm as described in Clement et al., Nat. Biotechnol. 37(3): 224-226 (2019), which is incorporated herein in its entirety. In some embodiments, the methods disclosed herein can have an indel frequency of less than 20%, less than 10%, less than 9%, less than 8%, less than 7%, less than 6%, less than 5%, less than 4%, less than 3%, less than 2%, less than 1.5%, or less than 1%. In some embodiments, any number of indels is determined after at least 1 hour, at least 2 hours, at least 6 hours, at least 12 hours, at least 24 hours, at least 36 hours, at least 48 hours, at least 3 days, at least 4 days, at least 5 days, at least 7 days, at least 10 days, or at least 14 days of exposing a double stranded target DNA, *e.g.*, a target gene.

[0501] In some embodiments, the prime editing compositions provided herein are capable of incorporating one or more intended nucleotide edits efficiently without generating a significant proportion of indels. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 1% in a target cell, *e.g.*, a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 0.5% in a target cell, . a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 0.1% in a target cell, *e.g.*, a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 1% in a target cell, *e.g.* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 0.5% in a target cell, *e.g.*, a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 0.1% in a target cell, *e.g.*, a human HSC.

[0502] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5% and an indel frequency of less than 1% in a target cell, *e.g.*, a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5% and an indel frequency of less than 0.5% in a target cell, *e.g.*, a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5% and an indel frequency of less than 0.1% in a target cell, *e.g.*, a human HSC.

[0503] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0504] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0505] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0506] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0507] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0508] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0509] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0510] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0511] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0512] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90% and an indel frequency of less than 1% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90% and an indel frequency of less than 0.5% in a target cell, *e.g.,* a human HSC. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90% and an indel frequency of less than 0.1% in a target cell, *e.g.,* a human HSC.

[0513] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95% and an indel frequency of less than 1% in a target cell, *e.g.*, a human cell. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95% and an indel frequency of less than 0.5% in a target cell, *e.g.*, a human cell. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95% and an indel frequency of less than 0.1% in a target cell, *e.g.*, a human cell.

[0514] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 10% in a population of target cells, e.g., a population of human cells, such as a human stem cell. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 1% and an indel frequency of less than 0.1% in a population of target cells.

[0515] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 5% and an indel frequency of less than 0.1% in a population of target cells.

[0516] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 7.5 % and an indel frequency of less than 0.1% in a population of target cells.

[0517] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 10% in a population of target cell. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 10 % and an indel frequency of less than 0.1% in a population of target cells.

[0518] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 15 % and an indel frequency of less than 0.1% in a population of target cells.

[0519] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 1% in a population of target cells, *e.g.*, a population of human stem cell. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 20 % and an indel frequency of less than 0.1% in a population of target cells.

[0520] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 30 % and an indel frequency of less than 0.1% in a population of target cells.

[0521] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 40 % and an indel frequency of less than 0.1% in a population of target cells.

[0522] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 50 % and an indel frequency of less than 0.1% in a population of target cells.

[0523] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 60 % and an indel frequency of less than 0.1% in a population of target cells.

[0524] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 70 % and an indel frequency of less than 0.1% in a population of target cells.

[0525] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 80 % and an indel frequency of less than 0.1% in a population of target cells.

[0526] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 90 % and an indel frequency of less than 0.1% in a population of target cells.

[0527] In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 10% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 7.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 2.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 1% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 0.5% in a population of target cells. In some embodiments, the prime editing methods disclosed herein have an editing efficiency of at least about 95 % and an indel frequency of less than 0.1% in a population of target cells.

[0528] In some embodiments, the target gene is in a target cell. Accordingly, in one aspect provided herein is a method of editing a target cell comprising a double stranded target DNA (e.g., a target gene) that encoded a polypeptide, wherein the double stranded target DNA comprises one or more mutations relative to the wild-type double stranded DNA (e.g., wild-type gene). In some embodiments, the methods of the present disclosure comprise introducing a prime editing composition comprising a PEgRNA, a prime editor polypeptide, a ngRNA, and/or a polynucleotide encoding the PEgRNA, the prime editor polypeptide, or the ngRNA into the target cell that has the target gene to edit the target gene, thereby generating an edited cell. In some embodiments, a target cell is a cell disclosed herein. In some embodiments, the target cell is a mammalian cell. In some embodiments, the target cell is a human cell.

[0529] In some embodiments, components of a prime editing composition described herein are provided to a target cell in vitro. In some embodiments, components of a prime editing composition described herein are provided to a target cell ex vivo. In some embodiments, components of a prime editing composition described herein are provided to a target cell in vivo.

[0530] In some embodiments, any number of indels is determined after at least 1 hour, at least 2 hours, at least 6 hours, at least 12 hours, at least 24 hours, at least 36 hours, at least 48 hours, at least 3 days, at least 4 days, at least 5 days, at least 7 days, at least 10 days, or at least 14 days of exposing a double stranded target DNA, *e.g.*, a target gene to a prime editing composition. In some embodiments, the editing efficiency is determined after 1 hour, 2 hours, 6 hours, 12 hours, 24 hours, 36 hours, 48 hours, 3 days, 4 days, 5 days, 7 days, 10 days, or 14 days of exposing a double stranded target DNA, *e.g.*, a target gene, to a prime editing composition.

[0531] In some embodiments, the prime editing composition described herein result in less than 50%, less than 40%, less than 30%, less than 20%, less than 19%, less than 18%, less than 17%, less than 16%, less than 15%, less than 14%, less than 13%, less than 12%, less than 11%, less than 10%, less than 9%, less than 8%, less than 7%, less than 6%, less than 5%, less than 4%, less than 3%, less than 2%, less than 1%, less than 0.9%, less than 0.8%, less than 0.7%, less than 0.6%, less than 0.5%, less than 0.4%, less than 0.3%, less than 0.2%, less than 0.1%, less than 0.09%, less than 0.08%, less than 0.07%, less than 0.06%, less than 0.05%, less than 0.04%, less than 0.03%, less than 0.02%, or less than 0.01% off-target editing in a chromosome that includes the double stranded target DNA, *e.g.*, a target gene. In some embodiments, off-target editing is determined after at least 1 hour, at least 2 hours, at least 6 hours, at least 12 hours, at least 24 hours, at least 36 hours, at least 48 hours, at least 3 days, at least 4 days, at least 5 days, at least 7 days, at least 10 days, or at least 14 days of exposing a double stranded target DNA, *e.g.*, a target gene (*e.g.*, a nucleic acid within the genome of a cell) to a prime editing composition.

[0532] In some embodiments, components of a prime editing composition described herein are provided to a target cell *in vitro*. In some embodiments, components of a prime editing composition described herein are provided to a target cell *ex vivo*. In some embodiments, components of a prime editing composition described herein are provided to a target cell *in vivo*.

[0533] In some embodiments, the prime editing compositions (*e.g.*, PEgRNAs and prime editors as described herein) and prime editing methods disclosed herein can be used to edit a double stranded target DNA, *e.g.*, a target gene. In some embodiments, the double stranded target DNA, *e.g.*, a target gene, comprises a mutation compared to a wild-type sequence of the same gene. In some embodiments, the mutation is associated with a genetic disease or disorder. In some embodiments, the mutation is in a coding region of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the mutation is in an exon of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the prime editing method comprises contacting a double stranded target DNA, *e.g.*, a target gene, with a prime editing composition comprising a prime editor, a PEgRNA, and/or a ngRNA. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene, with the prime editing composition results in incorporation of one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the incorporation is in a region of the double stranded target DNA, *e.g.*, a target gene, that corresponds to an editing target sequence in the target gene. In some embodiments, the one or more intended nucleotide edits comprises a single nucleotide substitution, an insertion, a deletion, or any combination thereof, compared to the endogenous sequence of the double stranded target DNA, *e.g.*, a target gene. In some embodiments, incorporation of the one or more intended nucleotide edits results in replacement of one or more mutations with a DNA sequence that encodes a corresponding wild-type protein. In some embodiments, incorporation of the one or more intended nucleotide edits results in replacement of the one or more mutations with the corresponding wild-type gene sequence. In some embodiments, incorporation of the one more intended nucleotide edits results in correction of a mutation in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, the double stranded target DNA, *e.g.*, a target gene, comprises an editing template sequence that contains the mutation. In some embodiments, contacting the double stranded target DNA, *e.g.*, a target gene, with the prime editing composition results in incorporation of one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene,, which corrects the mutation in the editing target sequence (or a double stranded region comprising the editing target sequence and the complementary sequence to the editing target sequence on a target strand) in the double stranded target DNA, *e.g.*, a target gene. In some embodiments, incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene, that comprises one or more mutations, restores wild-type expression and function of a protein encoded by the target gene. In some embodiments, expression and/or function of the protein encoded by the target gene may be measured when expressed in a target cell. In some embodiments, incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene, leads to a fold change in a level of the target gene expression and/or a fold change in a level of the functional protein encoded by the target gene. In some embodiments, a change in the level of the target gene expression level can comprise a fold change of, *e.g.*, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 15-fold, 20-fold, 25-fold, 30-fold, 40-fold, 50-fold, 60-fold, 70-fold, 80-fold, 90-fold, 100-fold or greater as compared to expression in a suitable control cell not introduced with a prime editing composition described herein. In some embodiments, incorporation of the one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene, that comprises one or more mutations, restores wild-type expression of the functional protein encoded by the target gene by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, o99% or more as compared to wild-type expression of the corresponding protein in a suitable control cell that comprises a wild-type target gene.

[0534] In some embodiments, an expression increase can be measured by a functional assay. In some embodiments, protein expression can be measured using a protein assay. In some embodiments, protein expression can be measured using antibody testing. In some embodiments, protein expression can be measured using ELISA, mass spectrometry, Western blot, sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE), high performance liquid chromatography (HPLC), electrophoresis, or any combination thereof. In some embodiments, a protein assay can comprise SDS-PAGE and densitometric analysis of a Coomassie Blue-stained gel.

[0535] In some embodiments, the target gene comprises one or more mutations associated with a genetic disease or disorder. Accordingly, in some embodiments, provided herein are methods for treatment of a subject diagnosed with a disease associated with or caused by one or more pathogenic mutations that can be corrected by prime editing.

[0536] In some embodiments, provided herein are methods for treating a genetic disease that comprise administering to a subject a therapeutically effective amount of a prime editing composition, or a pharmaceutical composition comprising a prime editing composition as described herein. In some embodiments, administration of the prime editing composition results in incorporation of one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene, in the subject. In some embodiments, administration of the prime editing composition results in correction of one or more pathogenic mutations, *e.g.,* point mutations, insertions, or deletions, associated with a disease in the subject. In some embodiments, the double stranded target DNA, *e.g.*, a target gene comprises an editing target sequence that contains the pathogenic mutation. In some embodiments, administration of the prime editing composition results in incorporation of one or more intended nucleotide edits in the double stranded target DNA, *e.g.*, a target gene that corrects the pathogenic mutation in the editing target sequence (or a double stranded region comprising the editing target sequence and the complementary sequence to the editing target sequence on a target strand) of the double stranded target DNA, *e.g.*, a target gene in the subject.

[0537] In some embodiments, the method provided herein comprises administering to a subject an effective amount of a prime editing composition, for example, a PEgRNA, a prime editor, and/or a ngRNA. In some embodiments, the method comprises administering to the subject an effective amount of a prime editing composition described herein, for example, polynucleotides, vectors, or constructs that encode prime editing composition components, or RNPs, LNPs, and/or polypeptides comprising prime editing composition components. Prime editing compositions can be administered to target the target gene having pathogenic mutation(s) in a subject, *e.g.*, a human subject, suffering from, having, susceptible to, or at risk for the disease. Identifying a subject in need of such treatment can be in the judgment of a subject or a health care professional and can be subjective (*e.g.* opinion) or objective (*e.g.* measurable by a test or diagnostic method).

[0538] In some embodiments, the method comprises directly administering prime editing compositions provided herein to a subject. The prime editing compositions described herein can be delivered with in any form as described herein, *e.g.*, as LNPs, RNPs, polynucleotide vectors such as viral vectors, or mRNAs. The prime editing compositions can be formulated with any pharmaceutically acceptable carrier described herein or known in the art for administering directly to a subject. Components of a prime editing composition or a pharmaceutical composition thereof may be administered to the subject simultaneously or sequentially. For example, in some embodiments, the method comprises administering a prime editing composition, or pharmaceutical composition thereof, comprising a complex that comprises a prime editor fusion protein and a PEgRNA and/or a ngRNA, to a subject. In some embodiments, the method comprises administering a polynucleotide or vector encoding a prime editor to a subject simultaneously with a PEgRNA and/or a ngRNA. In some embodiments, the method comprises administering a polynucleotide or vector encoding a prime editor to a subject before administration with a PEgRNA and/or a ngRNA.

[0539] Suitable routes of administrating the prime editing compositions to a subject include, without limitation: topical, subcutaneous, transdermal, intradermal, intralesional, intraarticular, intraperitoneal, intravesical, transmucosal, gingival, intradental, intracochlear, transtympanic, intraorgan, epidural, intrathecal, intramuscular, intravenous, intravascular, intraosseus, periocular, intratumoral, intracerebral, and intracerebroventricular administration. In some embodiments, the compositions described are administered intraperitoneally, intravenously, or by direct injection or direct infusion. In some embodiments, the compositions described are administered by direct injection or infusion or transfusion, transplantation (e.g., allogeneic hematopoietic stem cell transplantation (HSCT) using cells that have been contacted with a prime editing complex as described herein) to a subject. In some embodiments, the compositions described herein are administered to a subject by injection, by means of a catheter, by means of a suppository, or by means of an implant.

[0540] In some embodiments, the method comprises administering cells edited with a prime editing composition described herein to a subject. In some embodiments, the cells are allogeneic. In some embodiments, allogeneic cells are or have been contacted *ex vivo* with a prime editing composition or pharmaceutical composition thereof and are introduced into a human subject in need thereof. In some embodiments, the cells are autologous to the subject. In some embodiments, cells are removed from a subject and contacted *ex vivo* with a prime editing composition or pharmaceutical composition thereof and are re-introduced into the subject.

[0541] In some embodiments, cells are contacted *ex vivo* with one or more components of a prime editing composition. The cells may be contacted *ex vivo* with any approach described herein or known in the art. For example, in some embodiments, one or more target cells are contacted with one or more components of a prime editing composition *ex vivo* by electroporation. In some embodiments, one or more target cells are contacted with one or more components of a prime editing composition *ex vivo* by a LNP comprising the prime editing composition or components thereof. In some embodiments, one or more target cells are contacted with one or more components of a prime editing composition *ex vivo*, wherein one or more components of the prime editing composition is associated with a cell penetrating peptide. In some embodiments, the *ex vivo*-contacted cells are introduced into the subject, and the subject is administered *in vivo* with one or more components of a prime editing composition. For example, in some embodiments, cells are contacted *ex vivo* with a prime editor and introduced into a subject. In some embodiments, the subject is then administered with a PEgRNA and/or a ngRNA, or a polynucleotide encoding the PEgRNA and/or the ngRNA.

[0542] In some embodiments, cells contacted with the prime editing composition are determined for incorporation of the one or more intended nucleotide edits in the genome before re-introduction into the subject. In some embodiments, the cells are enriched for incorporation of the one or more intended nucleotide edits in the genome before re-introduction into the subject. In some embodiments, the edited cells are primary cells. In some embodiments, the edited cells are progenitor cells. In some embodiments, the edited cells are stem cells. In some embodiments, the edited cells are hepatocytes. In some embodiments, the edited cells are primary human cells. In some embodiments, the edited cells are human progenitor cells. In some embodiments, the edited cells are human stem cells. In some embodiments, the edited cells are human hepatocytes. In some embodiments, the cell is a neuron. In some embodiments, the cell is a neuron from basal ganglia. In some embodiments, the cell is a neuron from basal ganglia of a subject. In some embodiments, the cell is a neuron in the basal ganglia of a subject.

[0543] The prime editing composition or components thereof may be introduced into a cell by any delivery approaches as described herein, including LNP administration, RNP administration, electroporation, nucleofection, transfection, viral transduction, microinjection, cell membrane disruption and diffusion, or any other approach known in the art.

[0544] The cells edited with prime editing can be introduced into the subject by any route known in the art. In some embodiments, the edited cells are administered to a subject by direct infusion. In some embodiments, the edited cells are administered to a subject by intravenous infusion. In some embodiments, the edited cells are administered to a subject as implants.

[0545] In some embodiments, the target gene to be edited in a subject is a *HBB* gene. In some embodiments, the *HBB* gene comprises a mutation associated with sickle cell disease. In some embodiments, the *HBB* gene comprises a mutation that encodes a E6V amino acid substitution in the beta globin protein encoded by the *HBB* gene compared to a wild type beta globin protein. In some embodiments, provided herein is a prime editing composition comprising a prime editor and a PEgRNA, wherein the PEgRNA is capable of directing the prime editor to correct the mutation associated with sickle cell diseases in a *HBB* gene. In some embodiments, the PEgRNA comprises an editing template that comprises an intended nucleotide edit, and wherein incorporation of the intended nucleotide edit in the *HBB* gene corrects the mutation in the *HBB* gene associated with sickle cell disease. In some embodiments, the editing template comprises a wild type sequence of a wild type *HBB* gene. Accordingly, in some embodiments, provided herein are methods of correcting a mutation associated with sickle cell disease in a *HBB* gene. In some embodiments, the method comprises contacting the *HBB* gene with a PEgRNA and a prime editor, wherein the PEgRNA directs the prime editor to incorporate an intended nucleotide edit in the *HBB* gene, thereby correcting the mutation associated with sickle cell disease in the *HBB* gene. In some embodiments, the *HBB* gene is in a cell. Accordingly, in some embodiments, the method comprises introducing into the cell comprising the *HBB* gene with a PEgRNA and a prime editor, wherein the PEgRNA directs the prime editor to incorporate an intended nucleotide edit in the *HBB* gene, thereby correcting the mutation associated with sickle cell disease in the *HBB* gene. In some embodiments, the method comprises introducing into the cell comprising the *HBB* gene with a PEgRNA and a polynucleotide encoding the prime editor, wherein upon expression of the prime editor, the PEgRNA directs the prime editor to incorporate an intended nucleotide edit in the *HBB* gene, thereby correcting the mutation associated with sickle cell disease in the *HBB* gene. In some embodiments, the cell is a blood cell. In some embodiments, the *HBB* gene is a hematopoietic stem cell (HSC). In some embodiments, the cell is *in vivo*. In some embodiments, the cell is *ex vivo*. In some embodiments, the PEgRNA and the prime editor are introduced into the cell simultaneously. In some embodiments, the PEgRNA and the polynucleotide encoding the prime editor are introduced into the cell simultaneously. In some embodiments, the PEgRNA and the prime editor are introduced into the cell sequentially, for example, the PEgRNA may be introduced prior to or after introduction of the prime editor. In some embodiments, the PEgRNA and the polynucleotide encoding the prime editor are introduced into the cell sequentially, for example, the PEgRNA may be introduced prior to or after introduction of the polynucleotide encoding the prime editor.

[0546] Accordingly, in some embodiments, provided herein is a method of treating sickle cell disease, wherein the method comprises administering to a subject in need thereof a PEgRNA and a prime editor or a polynucleotide encoding the prime editor, wherein the PEgRNA directs the prime editor to incorporate the intended nucleotide edit in a *HBB* gene in the subject, thereby correcting a mutation in the *HBB* gene and treating sickle cell disease. In some embodiments, the method of treating sickle cell disease comprises introducing a PEgRNA and a prime editor or a polynucleotide encoding the prime editor to a cell or a population of cells to correct a mutation associated with sickle cell disease in a *HBB*, and subsequently administering the edited cell or the edited population of cells to a subject in need thereof. In some embodiments, the cell or the population of cells are obtained from the subject in need thereof prior to editing. In some embodiments, the cell or the population of cells are obtained from a donor prior to editing. In some embodiments, the cell or the population of cells are hematopoietic stem cells. In some embodiments, the PEgRNA and the prime editor are administered simultaneously. In some embodiments, the PEgRNA and the polynucleotide encoding the prime editor are administered simultaneously. In some embodiments, the PEgRNA and the prime editor are administered sequentially, for example, the PEgRNA may be administered prior to or after administration of the prime editor. In some embodiments, the PEgRNA and the polynucleotide encoding the prime editor are administered sequentially, for example, the PEgRNA may be administered prior to or after administration of the polynucleotide encoding the prime editor.

[0547] The pharmaceutical compositions, prime editing compositions, and cells, as described herein, can be administered in effective amounts. In some embodiments, the effective amount depends upon the mode of administration. In some embodiments, the effective amount depends upon the stage of the condition, the age and physical condition of the subject, the nature of concurrent therapy, if any, and like factors well-known to the medical practitioner.

[0548] The specific dose administered can be a uniform dose for each subject. Alternatively, a subject's dose can be tailored to the approximate body weight of the subject. Other factors in determining the appropriate dosage can include the disease or condition to be treated or prevented, the severity of the disease, the route of administration, and the age, sex and medical condition of the patient.

[0549] In embodiments wherein components of a prime editing composition are administered sequentially, the time between sequential administration can be at least 1 hour, at least 2 hours, at least 6 hours, at least 12 hours, at least 24 hours, at least 36 hours, at least 48 hours, at least 3 days, at least 4 days, at least 5 days, at least 7 days, at least 10 days, or at least 14 days.

Delivery

[0550] Prime editing compositions described herein can be delivered to a cellular environment with any approach known in the art. Components of a prime editing composition can be delivered to a cell by the same mode or different modes. For example, in some embodiments, a prime editor or components thereof (e.g., a DNA binding domain or a DNA polymerase domain) can be delivered as a polypeptide or a polynucleotide (DNA or RNA) encoding the polypeptide or as a ribonucleoprotein (RNP) complex. In some embodiments, a PEgRNA can be delivered directly as an RNA or as a DNA encoding the PEgRNA or as an RNA complexed to the PE protein as an RNP complex. In some embodiments, components of a prime editing composition can be delivered as a combination of DNA and RNA. In some embodiments, components of a prime editor composition can be delivered as a combination of polynucleotide e.g., DNA, or RNA, and protein.

[0551] In some embodiments, a prime editing composition component is encoded by a polynucleotide, a vector, or a construct. In some embodiments, a prime editor polypeptide, a PEgRNA and/or a ngRNA is encoded by a polynucleotide. In some embodiments, the polynucleotide encodes a prime editor fusion protein comprising a DNA binding domain and a DNA polymerase domain. In some embodiments, the polynucleotide encodes a DNA polymerase domain of a prime editor. In some embodiments, the polynucleotide encodes a DNA binding domain of a prime editor. In some embodiments, the polynucleotide encodes a portion of a prime editor protein, for example, a N-terminal portion of a prime editor fusion protein connected to an intein-N. In some embodiments, the polynucleotide encodes a portion of a prime editor protein, for example, a C-terminal portion of a prime editor fusion protein connected to an intein-C. In some embodiments, the polynucleotide encodes a PEgRNA and/or a ngRNA. In some embodiments, the polypeptide encodes two or more components of a prime editing composition, for example, a prime editor fusion protein and a PEgRNA.

[0552] In some embodiments, the polynucleotide encoding one or more prime editing composition components is delivered to a target cell is integrated into the genome of the cell for long-term expression, for example, by a retroviral vector. In some embodiments, the polynucleotide delivered to a target cell is expressed transiently. For example, the polynucleotide may be delivered in the form of a mRNA, or a non-integrating vector (non-integrating virus, plasmids, minicircle DNAs) for episomal expression.

[0553] In some embodiments, a polynucleotide encoding one or more prime editing system components can be operably linked to a regulatory element, *e.g.*, a transcriptional control element, such as a promoter. In some embodiments, the polynucleotide is operably linked to multiple control elements. Depending on the expression system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. may be used in the expression vector (*e.g.*, U6 promoter, H1 promoter).

[0554] In some embodiments, the polynucleotide encoding one or more prime editing composition components is a part of, or is encoded by, a vector (e.g., a plasmid vector or a viral vector). In some embodiments, the vector is a viral vector. In some embodiments, the vector is a non-viral vector. In some embodiments, delivery is in vivo, in vitro, ex vivo, or in situ.

[0555] Non-viral vector delivery systems can 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. In some embodiments, the polynucleotide is provided as an RNA, *e.g.*, a mRNA or a transcript. Any RNA of the prime editing systems, for example a guide RNA or a prime editor-encoding mRNA, can be delivered in the form of RNA. In some embodiments, one or more components of the prime editing system that are RNAs is produced by direct chemical synthesis or may be transcribed *in vitro* from a DNA. In some embodiments, an mRNA that encodes a prime editor polypeptide is generated using *in vitro* transcription. Guide polynucleotides (*e.g.*, PEgRNA or ngRNA) can also be transcribed using *in vitro* transcription from a cassette containing a T7 promoter, followed by the sequence "GG", and guide polynucleotide sequence. In some embodiments, the prime editor encoding mRNA, PEgRNA, and/or ngRNA are synthesized in vitro using an RNA polymerase enzyme (*e.g.*, T7 polymerase, T3 polymerase, SP6 polymerase, etc.). Once synthesized, the RNA can directly contact a double stranded target DNA, *e.g.*, a target gene, or can be introduced into a cell using any suitable technique for introducing nucleic acids into cells (*e.g.*, microinjection, electroporation, transfection). In some embodiments, the prime editor-coding sequences, the PEgRNAs, and/or the ngRNAs are modified to include one or more modified nucleoside *e.g.,* using pseudo-U or 5-Methyl-C.

[0556] Methods of non-viral delivery of nucleic acids can include lipofection, nucleofection, electroporation, microinjection, biolistics, virosomes, liposomes, immunoliposomes, cell penetrating peptides, polycation or lipid:nucleic acid conjugates, naked DNA, artificial virions, cell membrane disruption by a microfluidics device, and agent-enhanced uptake of DNA. Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides can be used. 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, can be used.

[0557] Viral vector delivery systems can include DNA and RNA viruses, which can have either episomal or integrated genomes after delivery to the cell. RNA or DNA viral based systems can be used to target specific cells and trafficking the viral payload to an organelle of the cell. Viral vectors can be administered directly (*in vivo*) or they can be used to treat cells in vitro, and the modified cells can optionally be administered (*ex vivo*).

[0558] In some embodiments, the viral vector is a retroviral, lentiviral, adenoviral, adeno-associated viral or herpes simplex viral vector. Retroviral vectors can include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations thereof. In some embodiments, the retroviral vector is a lentiviral vector. In some embodiments, the retroviral vector is a gamma retroviral vector. In some embodiments, the viral vector is an adenoviral vector. In some embodiments, the viral vector is an adeno-associated virus ("AAV") vector. In some embodiments, the AAV is a recombinant AAV (rAAV).

[0559] In some embodiments, polynucleotides encoding one or more prime editing composition components are packaged in a virus particle. Packaging cells can be used to form virus particles that can infect a target cell. Such cells can include 293 cells, (*e.g.*, for packaging adenovirus), and ψ2 cells or PA317 cells (*e.g.*, for packaging retrovirus). Viral vectors can be generated by producing a cell line that packages a nucleic acid vector into a viral particle. The vectors can contain the minimal viral sequences required for packaging and subsequent integration into a host. The vectors can contain other viral sequences being replaced by an expression cassette for the polynucleotide(s) to be expressed. The missing viral functions can be supplied in trans by the packaging cell line. For example, AAV vectors can comprise ITR sequences from the AAV genome which are required for packaging and integration into the host genome.

[0560] In some embodiments, dual AAV vectors are generated by splitting a large transgene expression cassette in two separate halves (5' and 3' ends that encode N-terminal portion and C-terminal portion of, *e.g.*, a prime editor polypeptide), where each half of the cassette is no more than 5kb in length, optionally no more than 4.7 kb in length, and is packaged in a single AAV vector. In some embodiments, the full-length transgene expression cassette is reassembled upon co-infection of the same cell by both dual AAV vectors. In some embodiments, a portion or fragment of a prime editor polypeptide, *e.g.,* a Cas9 nickase, is fused to an intein. The portion or fragment of the polypeptide can be fused to the N-terminus or the C-terminus of the intein. In some embodiments, a N-terminal portion of the polypeptide is fused to an intein-N, and a C-terminal portion of the polypeptide is separately fused to an intein-C. In some embodiments, a portion or fragment of a prime editor fusion protein is fused to an intein and fused to an AAV capsid protein. The intein, nuclease and capsid protein can be fused together in any arrangement (*e.g.*, nuclease-intein-capsid, intein-nuclease-capsid, capsid-intein-nuclease, etc.). In some embodiments, a polynucleotide encoding a prime editor fusion protein is split in two separate halves, each encoding a portion of the prime editor fusion protein and separately fused to an intein. In some embodiments, each of the two halves of the polynucleotide is packaged in an individual AAV vector of a dual AAV vector system. In some embodiments, each of the two halves of the polynucleotide is no more than 5kb in length, optionally no more than 4.7 kb in length. In some embodiments, the full-length prime editor fusion protein is reassembled upon co-infection of the same cell by both dual AAV vectors, expression of both halves of the prime editor fusion protein, and self-excision of the inteins. In some embodiments, the in vivo use of dual AAV vectors results in the expression of full-length full-length prime editor fusion proteins. In some embodiments, the use of the dual AAV vector platform allows viable delivery of transgenes of greater than about 4.5, 4.6, 4.7, 4.8, 4.9, or 5.0 kb in size.A target cell can be transiently or non-transiently transfected with one or more vectors described herein. A cell can be transfected as it naturally occurs in a subject. A cell can be taken or derived from a subject and transfected. A cell can be derived from cells taken from a subject, such as a cell line. In some embodiments, a cell transfected with one or more vectors described herein can be used to establish a new cell line comprising one or more vector-derived sequences. In some embodiments, a cell transiently transfected with the compositions of the disclosure (such as by transient transfection of one or more vectors, or transfection with RNA), and modified through the activity of a prime editor, can be used to establish a new cell line comprising cells containing the modification but lacking any other exogenous sequence. Any suitable vector compatible with the host cell can be used with the methods of the disclosure. Non-limiting examples of vectors include pXT1, pSG5, pSVK3, pBPV, pMSG, and pSVLSV40.

[0561] In some embodiments, a prime editor protein can be provided to cells as a polypeptide. In some embodiments, the prime editor protein is fused to a polypeptide domain that increases solubility of the protein. In some embodiments, the prime editor protein is formulated to improve solubility of the protein.

[0562] In some embodiment, a prime editor polypeptide is fused to a polypeptide permeant domain to promote uptake by the cell. In some embodiments, the permeant domain is a including peptide, a peptidomimetic, or a non-peptide carrier. For example, a permeant peptide may be derived from the third alpha helix of Drosophila melanogaster transcription factor Antennapaedia, referred to as penetratin, which comprises the amino acid sequence RQIKIWFQNRRMKWKK. As another example, the permeant peptide can comprise the HIV-1 tat basic region amino acid sequence, which may include, for example, amino acids 49-57 of naturally-occurring tat protein. Other permeant domains can include poly-arginine motifs, for example, the region of amino acids 34-56 of HIV-1 rev protein, nona-arginine, and octa-arginine. The nona-arginine (R9) sequence can be used. The site at which the fusion can be made may be selected in order to optimize the biological activity, secretion or binding characteristics of the polypeptide.

[0563] In some embodiments, a prime editor polypeptide is produced *in vitro* or by host cells, and it may be further processed by unfolding, *e.g.*, heat denaturation, DTT reduction, etc. and may be further refolded. In some embodiments, a prime editor polypeptide is prepared by in vitro synthesis. Various commercial synthetic apparatuses can be used. By using synthesizers, naturally occurring amino acids can be substituted with unnatural amino acids. In some embodiments, a prime editor polypeptide is isolated and purified in accordance with recombinant synthesis methods, for example, by expression in a host cell and the lysate purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, or other purification technique.

[0564] In some embodiments, a prime editing composition, for example, prime editor polypeptide components and PEgRNA/ngRNA are introduced to a target cell by nanoparticles. In some embodiments, the prime editor polypeptide components and the PEgRNA and/or ngRNA form a complex in the nanoparticle. Any suitable nanoparticle design can be used to deliver genome editing system components or nucleic acids encoding such components. In some embodiments, the nanoparticle is inorganic. In some embodiments, the nanoparticle is organic. In some embodiments, a prime editing composition is delivered to a target cell, *e.g.*, a hepatocyte, in an organic nanoparticle, *e.g.*, a lipid nanoparticle (LNP) or polymer nanoparticle.

[0565] In some embodiments, LNPs are formulated from cationic, anionic, neutral lipids, or combinations thereof. In some embodiments, neutral lipids, such as the fusogenic phospholipid DOPE or the membrane component cholesterol, are included to enhance transfection activity and nanoparticle stability. In some embodiments, LNPs are formulated with hydrophobic lipids, hydrophilic lipids, or combinations thereof. Lipids may be formulated in a wide range of molar ratios to produce an LNP. Any lipid or combination of lipids that are known in the art can be used to produce an LNP. Exemplary lipids used to produce LNPs are provided in **Table 4** below.

[0566] In some embodiments, components of a prime editing composition form a complex prior to delivery to a target cell. For example, a prime editor fusion protein, a PEgRNA, and/or a ngRNA can form a complex prior to delivery to the target cell. In some embodiments, a prime editing polypeptide (*e.g*,. a prime editor fusion protein) and a guide polynucleotide (*e.g.,* a PEgRNA or ngRNA) form a ribonucleoprotein (RNP) for delivery to a target cell. In some embodiments, the RNP comprises a prime editor fusion protein in complex with a PEgRNA. RNPs may be delivered to cells using known methods, such as electroporation, nucleofection, or cationic lipid-mediated methods, or any other approaches known in the art. In some embodiments, delivery of a prime editing composition or complex to the target cell does not require the delivery of foreign DNA into the cell. In some embodiments, the RNP comprising the prime editing complex is degraded over time in the target cell. Exemplary lipids for use in nanoparticle formulations and/or gene transfer are shown in **Table 4** below.

[0567] Table 4: Exemplary lipids for nanoparticle formulation or gene transfer

Lipid	**Abbreviation**	**Feature**
1,2-Dioleoyl-sn-glycero-3-phosphatidylcholine	DOPC	Helper
1,2-Dioleoyl-sn-glycero-3-phosphatidylethanolamine	DOPE	Helper
Cholesterol		Helper
N41-(2,3-Dioleyloxy)prophyliN,N,N-trimethylammonium chloride	DOTMA	Cationic
1,2-Dioleoyloxy-3-trimethylammonium-propane Dioctadecylamidoglycylspermine	DOGS	Cationic
N-(3-Aminopropy1)-N,N-dimethy1-2,3-bis(dodecyloxy)- 1-propanaminium bromide	GAP-DLRIE	Cationic
Cetyltrimethylammonium bromide	CTAB	Cationic
6-Lauroxyhexyl omithinate	LHON	Cationic
1-(2,3-Dioleoyloxypropy1)-2,4,6-trimethylpyridinium	2Oc	Cationic
2,3-Dioleyloxy-N-P(spenninecarboxamido-ethy1J-N,Ndimethyl-l-propanatninium trifluoroacetate	DOSPA	Cationic
1,2-Dioley1-3-trimethylamtnonium-propane	DOPA	Cationic
N-(2-Hydroxyethyl)-N,N-dimethy1-2,3-bis(tetradecyloxy)-1-propanaminium bromide	MDRIE	Cationic
Dimyristooxypropyl dimethyl hydroxyethyl ammonium bromide	DMRI	Cationic
3β-[N-(N’, N’-Dimethylaminoethane)-carbamoyl]cholesterol	DC-Chol	Cationic
Bis-guanidium-tren-cholesterol	BGTC	Cationic
1,3-Diodeoxy-2-(6-carboxy-spermy1)-propylamide	DOSPER	Cationic
Dimethyloctadecylammonium bromide	DDAB	Cationic
Dioctadecylamidoglicylspermidin	DSL	Cationic
rac-[(2,3-Dioctadecyloxypropyl)(2-hydroxyethyl)]-dimethylammonium chloride	CLIP-1	Cationic
rac-[2(2,3-Dihexadecyloxypropyloxymethyloxy) ethyl]trimethylammoniun bromide	CLIP-6	Cationic
Ethyldimyristoylphosphatidylcholine	EDMPC	Cationic
1,2-Distearyloxy-N,N-dimethyl-3-aminopropane	DSDMA	Cationic
1,2-Dimyristoyl-trimethylammonium propane	DMTAP	Cationic
O,O'-Dimyristyl-N-lysyl aspartate	DMKE	Cationic
1,2-Distearoyl-sn-glycero-3-ethylpho sphocholine	DSEPC	Cationic
N-Palmitoyl D-erythro-sphingosyl carbamoyl-spenmine	CCS	Cationic
N-t-Butyl-N0-tetradecyl-3-tetradecylaminopropionamidine	diC14-amidine	Cationic
Octadecenolyoxy[ethyl-2-heptadecenyl-3 hydroxyethyl] imidazolinium chloride	DOTIM	Cationic
N1 -Cholesteryloxycarbonyl-3,7-diazanonane-1,9-diamine	CDAN	Cationic
2-(3-Bis(3-amino-propy1)-amino]propylamino)-Nditetradecylcarbamoylme-ethyl-acetamide	RPR209120	Cationic

Lipid	Abbreviation	Feature
1,2-dilinoleyloxy-3-dimethylaminopropane	DLinDMA	Cationic
2,2-dilinoley1-4-dimethylaminoethyl-[1,3]-dioxolane	DLin-KC2-DMA	Cationic
dilinoleyl-methyl-4-dimethylaminobutyrate	DLin-MC3-DMA	Cationic

[0568] Exemplary polymers for use in nanoparticle formulations and/or gene transfer are shown in **Table 5** below.

[0569] Table 5: Exemplary lipids for nanoparticle formulation or gene transfer

Polymer	Abbreviation
Poly(ethylene)glycol	PEG
Polyethylenimine	PEI
Dithiobis (succinimidylpropionate)	DSP
Dimethyl-3,3'-dithiobispropionimidate	DTBP
Poly(ethylene imine)biscarbamate	PEIC
Poly(L-lysine)	PLL
Histidine modified PLL	
Poly(N-vinylpyrrolidone)	PVP
Poly(propylenimine)	PPI
Poly(amidoamine)	PAMAM
Poly(amidoethylenimine)	SS_PAEI
Triethylenetetramine	TETA
Poly(β-aminoester)	
Poly(4-hydroxy-L-proline ester)	PHP
Poly(allylamine)	
Poly(α-[4-aminobutyl]-L-glycolic acid)	PAGA
Poly(D,L-lactic-co-glycolic acid)	PLGA
Poly(N-ethyl-4-vinylpyridinium bromide)	
Poly(phosphazene)s	PPZ
Poly(phosphoester)s	PPE
Poly(phosphoramidate)s	PPA
Poly(N-2-hydroxypropylmethacrylamide)	pHPMA
Poly (2-(dimethylamino)ethyl methacrylate)	pDMAEMA
Poly(2-aminoethyl propylene phosphate)	PPE-EA
Chitosan	
Galactosylated chitosan	
N-dodacylated chitosam	
Histone	
Collagen	
Dextran-spermine	D-SPM

[0570] Exemplary delivery methods for polynucleotides encoding prime editing composition components are shown in **Table 6** below.

[0571] Table 6: Exemplary polynucleotide delivery methods

Delivery	Vector/Mode	Delivery into Non-Dividing Cells	Duration of Expression	Genome Integration	Type of Molecule Delivered
Physical	(*e.g.*, electroporation, particle gun,	YES	Transient	NO	Nucleic Acids and Proteins

Delivery	**Vector/Mode**	**Delivery into Non-Dividing Cells**	**Duration of Expression**	**Genome Integration**	**Type of Molecule Delivered**
	Calcium phosphate transfection)				
Viral	Retrovirus	NO	Stable	YES	RNA
	Lentivirus	YES	Stable	YES/NO with modification	RNA
	Adenovirus	YES	Transient	NO	DNA
	Adeno-Associated Virus (AAV)	YES	Stable	NO	DNA
	Vaccinia Virus	YES	Very Transient	NO	DNA
	Herpes Simplex Virus	YES	Stable	NO	DNA
Non-Viral	Cationic	YES	Transient	Depends on what is delivered	Nucleic acids and Proteins
	Polymeric Nanoparticles	YES	Transient	NO	Nucleic Acids
Biological	Attenuated Bacteria	YES	Transient	NO	Nucleic Acids
Non-Viral Delivery Vehicles	Engineered Bacteriophages	YES	Transient	NO	Nucleic Acids
	Mammalian Virus-like Particles	YES	Transient	NO	Nucleic Acids
	Biological liposomes: Erythrocyte Ghosts and Exosomes	YES	Transient	NO	Nucleic Acids

[0572] The prime editing compositions of the disclosure, whether introduced as polynucleotides or polypeptides, can be provided to the cells for about 30 minutes to about 24 hours, *e.g.*, 1 hour, 1.5 hours, 2 hours, 2.5 hours, 3 hours, 3.5 hours 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 12 hours, 16 hours, 18 hours, 20 hours, or any other period from about 30 minutes to about 24 hours, which can be repeated with a frequency of about every day to about every 4 days, *e.g.*, every 1.5 days, every 2 days, every 3 days, or any other frequency from about every day to about every four days. The compositions may be provided to the subject cells one or more times, *e.g.*, one time, twice, three times, or more than three times, and the cells allowed to incubate with the agent(s) for some amount of time following each contacting event *e.g.*, 16-24 hours. In cases in which two or more different prime editing system components, *e.g.*, two different polynucleotide constructs are provided to the cell (*e.g.*, different components of the same prime editing system, or two different guide nucleic acids that are complementary to different sequences within the same or different double stranded target DNA, *e.g.*, a target genes), the compositions may be delivered simultaneously (*e.g.*, as two polypeptides and/or nucleic acids). Alternatively, they may be provided sequentially, *e.g.*, one composition being provided first, followed by a second composition.

[0573] The prime editing compositions and pharmaceutical compositions of the disclosure, whether introduced as polynucleotides or polypeptides, can be administered to subjects in need thereof for about 30 minutes to about 24 hours, *e.g.*, 1 hour, 1.5 hours, 2 hours, 2.5 hours, 3 hours, 3.5 hours 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 12 hours, 16 hours, 18 hours, 20 hours, or any other period from about 30 minutes to about 24 hours, which can be repeated with a frequency of about every day to about every 4 days, *e.g.*, every 1.5 days, every 2 days, every 3 days, or any other frequency from about every day to about every four days. The compositions may be provided to the subject one or more times, *e.g.*, one time, twice, three times, or more than three times. In cases in which two or more different prime editing system components, *e.g.,* two different polynucleotide constructs are administered to the subject (*e.g.*, different components of the same prime editing system, or two different guide nucleic acids that are complementary to different sequences within the same or different double stranded target DNA, *e.g.*, a target genes), the compositions may be administered simultaneously (*e.g.*, as two polypeptides and/or nucleic acids). Alternatively, they may be provided sequentially, *e.g.*, one composition being provided first, followed by a second composition.

Table 14: Exemplary Cas9 amino acid sequences.

Sequence Description	SEQ ID NO.	Sequence
wtSpCas9	2	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
Sp Cas9 nickase H840A	6	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
met- Cas9 nickase H840A	7	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
saCas9	596	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG
SaCas9 nickase	597	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEEASKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG
met- SaCas9 nickase	598	KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEEASKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG
spCas9 NG	599	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGV

		EDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAFKYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
spCas9 NG nickase	600	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAFKYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
met- spCas9 NG nickase	601	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAFKYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
spCas9 VRQR	602	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
spCas9 VRQR nickase	603	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
met- spCas9 VRQR	604	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
sluCas9	605	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLERVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDDVGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFHQLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKYAYSADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRITKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDKENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEFILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIGKYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIESKQLDIQVDSEDNYSEMFIIPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN

sluCas9 nickase	606	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLERVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDDVGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFHQLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKYAYSADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRITKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDKENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEFILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIGKYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIESKQLDIQVDSEDNYSEMFIIPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN
met- sluCas9 nickase	607	NQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLERVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDDVGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFHQLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKYAYSADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRITKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDKENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEFILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIGKYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSEASKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIESKQLDIQVDSEDNYSEMFIIPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN
SpRY	608	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTRLGAPRAFKYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
SpRY nickase	609	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTRLGAPRAFKYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
met- SpRY nickase	610	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESIRPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTRLGAPRAFKYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
SpG	611	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD
SpG nickase	612	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD

met- SpG nickase	613	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD

Table 15: Exemplary PE construct, PE fusion protein and component amino acid and nucleotide sequences

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2)	Polypeptide	25	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2) without N terminus methionine	Polypeptide	624	KRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2)	DNA	26	ATGAAACGTACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			GGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCCTCTGGCGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2)	RNA	27	AUGAAACGUACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAA

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			AGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCCUCUGGCGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2)	DNA	32	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCT

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			ATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCCTCTGGCGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1 (PE2)	RNA	33	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCCUCUGGCGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding	DNA	243	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC2-SGGS-SV40BPNLS1			AGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGAGGCAGCAGCGGCTCCGAGACCCCCGGCACCTCCGAGAGCGCCACCCCCGAGTCCAGCGGCGGCAGCTCCGGCGGCAGCTCCACACTGAATATCGAGGACGAGTACCGCCTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCCACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGAGACAGGCCCCTCTGATCATCCCCCTGAAGGCCACCTCCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCCCACATCCAGCGGCTGCTGGATCAGGGCATCCTGGTGCCCTGTCAGAGCCCCTGGAACACCCCCCTGCTGCCAGTGAAGAAGCCCGGCACCAACGACTATCGGCCTGTGCAGGACCTGCGGGAGGTGAACAAACGGGTGGAGGACATCCACCCCACCGTGCCTAACCCATACAACCTGCTGTCCGGCCTGCCCCCAAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGCGGCTGCACCCCACCAGCCAGCCCCTGTTCGCCTTCGAGTGGAGGGACCCCGAGATGGGCATCTCCGGCCAGCTGACCTGGACCAGGCTGCCCCAGGGCTTCAAGAACAGCCCCACCCTGTTCAACGAGGCCCTGCACCGCGACCTGGCCGATTTTAGAATCCAGCACCCTGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTGGACTGCCAGCAGGGCACCAGGGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGCGGTGGCTGACAGAGGCCAGAAAGGAGACCGTGATGGGCCAGCCCACACCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCCGGCTGTTCATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCCCTGACCAAGCCTGGGACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCTGCCCTGGGACTGCCAGACCTGACCAAGCCCTTCGAGCTGTTCGTGGACGAGAAGCAGGGCTACGCCAAGGGCGTGCTGACACAGAAGCTGGGCCCATGGAGGAGACCCGTGGCCTACCTGTCCAAGAAGCTGGACCCAGTGGCCGCCGGCTGGCCACCCTGCCTGAGGATGGTGGCCGCCATCGCCGTGCTGACCAAGGATGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGACAGGTGGCTGAGCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCCCTGCCCGAGGAGGGCCTGCAGCACAATTGCCTGGACATCCTGGCCGAGGCCCACGGAACCCGCCCTGACCTGACCGACCAGCCTCTGCCCGACGCCGACCACACCTGGTATACCGACGGAAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGTGACAACCGAGACCGAGGTGATCTGGGCCAAGGCTCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACTCCCGGTACGCCTTCGCCACCGCCCACATCCACGGCGAAATCTACAGGCGGAGGGGCTGGCTGACCAGCGAGGGCAAGGAGATCAAGAACAAGGACGAGATCCTGGCCCTGCTGAAGGCCCTGTTCCTGCCCAAGAGGCTGTCTATCATCCACTGCCCCGGCCATCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGATGGCCGACCAGGCCGCCAGGAAAGCCGCCATCACCGAGACACCCGATACCTCCACCCTGCTGATCGAGAACAGCAGCCCCTCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC2-SGGS-SV40BPNLS1	RNA	244	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			AAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3-SGGS-SV40BPNLS1	DNA	233	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGCACCCTGAACATCGAGGACG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			AGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3-SGGS-SV40BPNLS1	RNA	234	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC4-SGGS-SV40BPNLS1	DNA	255	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACAGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGTCCGCCACCCCCGAGAGCAGCGGCGGCTCAAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGACTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCTACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGAATGGGCCTGGCCGTGAGACAGGCCCCACTGATCATCCCACTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCTATGTCACAGGAGGCCAGACTGGGCATCAAGCCACACATCCAGAGACTGCTGGACCAGGGCATCCTGGTGCCCTGCCAGAGCCCATGGAACACCCCCCTGCTGCCCGTCAAGAAGCCCGGCACCAACGACTACAGGCCCGTGCAGGACCTGCGGGAGGTGAACAAGCGCGTGGAGGACATCCACCCTACCGTGCCCAACCCCTACAACCTGCTGTCCGGCCTGCCACCCAGCCATCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCCCAGCCTCTGTTCGCCTTCGAGTGGAGAGACCCCGAGATGGGCATCTCCGGCCAGCTGACTTGGACAAGACTGCCCCAGGGCTTCAAGAATTCTCCAACCCTGTTCAACGAGGCCCTGCACCGGGACCTGGCCGACTTCAGGATCCAGCACCCAGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTCGACTGCCAGCAGGGCACCCGGGCCCTGCTGCAGACTCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGAGGTGGCTGACCGAGGCCAGGAAGGAGACCGTGATGGGCCAGCCAACCCCTAAGACCCCCAGACAGCTGAGGGAGTTCCTGGGCAAGGCCGGCTTCTGCCGGCTGTTCATCCCCGGCTTCGCCGAGATGGCCGCCCCCCTGTACCCCCTGACCAAGCCTGGCACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGATCTGACCAAGCCATTCGAGCTGTTCGTGGACGAGAAACAGGGCTACGCCAAGGGCGTGCTGACCCAGAAGCTGGGCCCCTGGAGGAGACCTGTGGCCTACCTGAGCAAAAAGCTGGACCCAGTGGCCGCCGGGTGGCCCCCCTGCCTGAGAATGGTGGCCGCCATCGCCGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGACAGCCTCTGGTGATCCTGGCCCCCCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGATAGGTGGCTGAGTAATGCCCGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCCGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCACTGCCCGAGGAGGGCCTGCAGCATAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGATCAGCCTCTGCCCGACGCCGATCACACCTGGTACACCGATGGCAGCAGCCTGCTGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAGGCCCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACAGCCGGTACGCCTTCGCCACCGCTCACATCCACGGCGAGATTTACAGGAGAAGAGGCTGGCTGACCAGCGAAGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGTCTATCATCCACTGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGATGGCCGACCAGGCCGCCCGGAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACTCCAGCCCTTCCGGCGGCTCCAAGAGGACTGCCGACGGCTCCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC4-SGGS-SV40BPNLS1	RNA	256	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCG AGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUC CUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUC GGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUC GAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAA UCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGC CAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAG AAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAA UGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGG GGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAAC UGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACC CUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCU GGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUA CCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAA AGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGU GCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAG UGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCU GUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUG GCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACAC CACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACAGCGGCGGCAGCAGCGGCGG CAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUC CCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAU GUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUG CAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGA GACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCG GGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGG CUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCC CAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGC CUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAG GAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCU GGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCG CCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCA GCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUG GCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGG CCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCC CGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCUUCCGGCGGCUCCAAGAGGACUGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M	Polypeptide	625	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLA LAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITK APLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKS EETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTL FEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNS RERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKH VAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRK VLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLAS HYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGG SSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWY TVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPP DRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M	DNA	30	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCG GAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAG CTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGG ACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGAC CTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTC GGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGT ACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCC
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M	RNA	31	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGA

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			UCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCC
Codon optimized polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC2	DNA	253	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGAGGCAGCAGCGGCTCCGAGACCCCCGGCACCTCCGAGAGCGCCACCCCCGAGTCCAGCGGCGGCAGCTCCGGCGGCAGCTCCACACTGAATATCGAGGACGAGTACCGCCTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCCACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGAGACAGGCCCCTCTGATCATCCCCCTGAAGGCCACCTCCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCCCACATCCAGCGGCTGCTGGATCAGGGCATCCTGGTGCCCTGTCAGAGCCCCTGGAACACCCCCCTGCTGCCAGTGAAGAAGCCCGGCACCAACGACTATCGGCCTGTGCAGGACCTGCGGGAGGTGAACAAACGGGTGGAGGACATCCACCCCACCGTGCCTAACCCATACAACCTGCTGTCCGGCCTGCCCCCAAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGCGGCTGCACCCCACCAGCCAGCCCCTGTTCGCCTTCGAGTGGAGGGACCCCGAGATGGGCATCTCCGGCCAGCTGACCTGGACCAGGCTGCCCCAGGGCTTCAAGAACAGCCCCACCCTGTTCAACGAGGCCCTGCACCGCGACCTGGCCGATTTTAGAATCCAGCACCCTGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTGGACTGCCAGCAGGGCACCAGGGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGCGGTGGCTGACAGAGGCCAGAAAGGAGACCGTGATGGGCCAGCCCACACCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			GCTTTTGCCGGCTGTTCATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCCCTGACCAAGCCTGGGACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCTGCCCTGGGACTGCCAGACCTGACCAAGCCCTTCGAGCTGTTCGTGGACGAGAAGCAGGGCTACGCCAAGGGCGTGCTGACACAGAAGCTGGGCCCATGGAGGAGACCCGTGGCCTACCTGTCCAAGAAGCTGGACCCAGTGGCCGCCGGCTGGCCACCCTGCCTGAGGATGGTGGCCGCCATCGCCGTGCTGACCAAGGATGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGACAGGTGGCTGAGCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCCCTGCCCGAGGAGGGCCTGCAGCACAATTGCCTGGACATCCTGGCCGAGGCCCACGGAACCCGCCCTGACCTGACCGACCAGCCTCTGCCCGACGCCGACCACACCTGGTATACCGACGGAAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGTGACAACCGAGACCGAGGTGATCTGGGCCAAGGCTCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACTCCCGGTACGCCTTCGCCACCGCCACATCCACGGCGAAATCTACAGGCGGAGGGGCTGGCTGACCAGCGAGGGCAAGGAGATCAAGAACAAGGACGAGATCCTGGCCCTGCTGAAGGCCCTGTTCCTGCCCAAGAGGCTGTCTATCATCCACTGCCCCGGCCATCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGATGGCCGACCAGGCCGCCAGGAAAGCCGCCATCACCGAGACACCCGATACCTCCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC2	RNA	254	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding Cas9H840A-	DNA	241	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGAC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3			CTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3	RNA	242	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACU

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			GGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC4	DNA	265	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACAGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGTCCGCCACCCCCGAGAGCAGCGGCGGCTCAAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGACTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCTACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGAATGGGCCTGGCCGTGAGACAGGCCCCACTGATCATCCCACTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCTATGTCACAGGAGGCCAGACTGGGCATCAAGCCACACATCCAGAGACTGCTGGACCAGGGCATCCTGGTGCCCTGCCAGAGCCCATGGAACACCCCCCTGCTGCCCGTCAAGAAGCCCGGCACCAACGACTACAGGCCCGTGCAGGACCTGCGGGAGGTGAACAAGCGCGTGGAGGACATCCACCCTACCGTGCCCAACCCCTACAACCTGCTGTCCGGCCTGCCACCCAGCCATCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCCCAGCCTC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			TGTTCGCCTTCGAGTGGAGAGACCCCGAGATGGGCATCTCCGGCCAGCTGACTTGGACAAGACTGCCCCAGGGCTTCAAGAATTCTCCAACCCTGTTCAACGAGGCCCTGCACCGGGACCTGGCCGACTTCAGGATCCAGCACCCAGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTCGACTGCCAGCAGGGCACCCGGGCCCTGCTGCAGACTCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGAGGTGGCTGACCGAGGCCAGGAAGGAGACCGTGATGGGCCAGCCAACCCCTAAGACCCCCAGACAGCTGAGGGAGTTCCTGGGCAAGGCCGGCTTCTGCCGGCTGTTCATCCCCGGCTTCGCCGAGATGGCCGCCCCCCTGTACCCCCTGACCAAGCCTGGCACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGATCTGACCAAGCCATTCGAGCTGTTCGTGGACGAGAAACAGGGCTACGCCAAGGGCGTGCTGACCCAGAAGCTGGGCCCCTGGAGGAGACCTGTGGCCTACCTGAGCAAAAAGCTGGACCCAGTGGCCGCCGGGTGGCCCCCCTGCCTGAGAATGGTGGCCGCCATCGCCGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGACAGCCTCTGGTGATCCTGGCCCCCCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGATAGGTGGCTGAGTAATGCCCGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCCGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCACTGCCCGAGGAGGGCCTGCAGCATAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGATCAGCCTCTGCCCGACGCCGATCACACCTGGTACACCGATGGCAGCAGCCTGCTGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAGGCCCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACAGCCGGTACGCCTTCGCCACCGCTCACATCCACGGCGAGATTTACAGGAGAAGAGGCTGGCTGACCAGCGAAGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGTCTATCATCCACTGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGATGGCCGACCAGGCCGCCCGGAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACTCCAGCCCT
Codon optimized polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC4	RNA	266	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACAGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCU

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M-SGGS-SV40BPNLS1	Polypeptide	626	SGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC2-SGGS-SV40BPNLS1	DNA	249	TCCGGCGGCAGCAGCGGAGGCAGCAGCGGCTCCGAGACCCCCGGCACCTCCGAGAGCGCCACCCCCGAGTCCAGCGGCGGCAGCTCCGGCGGCAGCTCCACACTGAATATCGAGGACGAGTACCGCCTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCCACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGAGACAGGCCCCTCTGATCATCCCCCTGAAGGCCACCTCCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCCCACATCCAGCGGCTGCTGGATCAGGGCATCCTGGTGCCCTGTCAGAGCCCCTGGAACACCCCCCTGCTGCCAGTGAAGAAGCCCGGCACCAACGACTATCGGCCTGTGCAGGACCTGCGGGAGGTGAACAAACGGGTGGAGGACATCCACCCCACCGTGCCTAACCCATACAACCTGCTGTCCGGCCTGCCCCCAAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGCGGCTGCACCCCACCAGCCAGCCCCTGTTCGCCTTCGAGTGGAGGGACCCCGAGATGGGCATCTCCGGCCAGCTGACCTGGACCAGGCTGCCCCAGGGCTTCAAGAACAGCCCCACCCTGTTCAACGAGGCCCTGCACCGCGACCTGGCCGATTTTAGAATCCAGCACCCTGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTGGACTGCCAGCAGGGCACCAGGGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGCGGTGGCTGACAGAGGCCAGAAAGGAGACCGTGATGGGCCAGCCCACACCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCCGGCTGTTCATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCCCTGACCAAGCCTGGGACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCTGCCCTGGGACTGCCAGACCTGACCAAGCCCTTCGAGCTGTTCGTGGACGAGAAGCAGGGCTACGCCAAGGGCGTGCTGACACAGAAGCTGGGCCCATGGAGGAGACCCGTGGCCTACCTGTCCAAGAAGCTGGACCCAGTGGCCGCCGGCTGGCCACCCTGCCTGAGGATGGTGGCCGCCATCGCCGTGCTGACCAAGGATGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGACAGGTGGCTGAGCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCCCTGCCCGAGGAGGGCCTGCAGCACAATTGCCTGGACATCCTGGCCGAGGCCCACGGAACCCGCCCTGACCTGACCGACCAGCCTCTGCCCGACGCCGACCACACCTGGTATACCGACGGAAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGTGACAACCGAGACCGAGGTGATCTGGGCCAAGGCTCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACTCCCGGTACGCCTTCGCCACCGCCCACATCCACGGCGAAATCTACAGGCGGAGGGGCTGGCTGACCAGCGAGGGCAAGGAGATCAAGAACAAGGACGAGATCCTGGCCCTGCTGAAGGCCCTGTTCCTGCCCAAGAGGCTGTCTATCATCCACTGCCCCGGCCATCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGATGGCCGACCAGGCCGCCAGGAAAGCCGCCATCACCGAGACACCCGATACCTCCACCCTGCTGATCGAGAACAGCAGCCCCTCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M C2-SGGS-SV40BPNLS1	RNA	250	UCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3-SGGS-SV40BPNLS1	DNA	237	TCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3-SGGS-SV40BPNLS1	RNA	238	UCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M C4-SGGS-SV40BPNLS1	DNA	261	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGTCCGCCACCCCCGAGAGCAGCGGCGGCTCAAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGACTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCTACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGAATGGGCCTGGCCGTGAGACAGGCCCCACTGATCATCCCACTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCTATGTCACAGGAGGCCAGACTGGGCATCAAGCCACACATCCAGAGACTGCTGGACCAGGGCATCCTGGTGCCCTGCCAGAGCCCATGGAACACCCCCCTGCTGCCCGTCAAGAAGCCCGGCACCAACGACTACAGGCCCGTGCAGGACCTGCGGGAGGTGAACAAGCGCGTGGAGGACATCCACCCTACCGTGCCCAACCCCTACAACCTGCTGTCCGGCCTGCCACCCAGCCATCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCCCAGCCTCTGTTCGCCTTCGAGTGGAGAGACCCCGAGATGGGCATCTCCGGCCAGCTGACTTGGACAAGACTGCCCCAGGGCTTCAAGAATTCTCCAACCCTGTTCAACGAGGCCCTGCACCGGGACCTGGCCGACTTCAGGATCCAGCACCCAGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTCGACTGCCAGCAGGGCACCCGGGCCCTGCTGCAGACTCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGAGGTGGCTGACCGAGGCCAGGAAGGAGACCGTGATGGGCCAGCCAACCCCTAAGACCCCCAGACAGCTGAGGGAGTTCCTGGGCAAGGCCGGCTTCTGCCGGCTGTTCATCCCCGGCTTCGCCGAGATGGCCGCCCCCCTGTACCCCCTGACCAAGCCTGGCACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGATCTGACCAAGCCATTCGAGCTGTTCGTGGACGAGAAACAGGGCTACGCCAAGGGCGTGCTGACCCAGAAGCTGGGCCCCTGGAGGAGACCTGTGGCCTACCTGAGCAAAAAGCTGGACCCAGTGGCCGCCGGGTGGCCCCCCTGCCTGAGAATGGTGGCCGCCATCGCCGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGACAGCCTCTGGTGATCCTGGCCCCCCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGATAGGTGGCTGAGTAATGCCCGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCCGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCACTGCCCGAGGAGGGCCTGCAGCATAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGATCAGCCTCTGCCCGACGCCGATCACACCTGGTACACCGATGGCAGCAGCCTGCTGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAGGCCCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACAGCCGGTACGCCTTCGCCACCGCTCACATCCACGGCGAGATTTACAGGAGAAGAGGCTGGCTGACCAGCGAAGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGTCTATCATCCACTGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGATGGCCGACCAGGCCGCCCGGAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACTCCAGCCCTTCCGGCGGCTCCAAGAGGACTGCCGACGGCTCCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding [(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC4-SGGS-SV40BPNLS1	RNA	262	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCUUCCGGCGGCUCCAAGAGGACUGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
(SGGS)2-XTEN-(SGGS)2S	Polypeptide	289	SGGSSGGSSGSETPGTSESATPESSGGSSGGSS
Codon optimized polynucleotide	DNA	247	TCCGGCGGCAGCAGCGGAGGCAGCAGCGGCTCCGAGACCCCCGGCACCTCCGAGAGCGCCACCCCCGAGTCCAGCGGCGGCAGCTCCGGCGGCAGCTCC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
encoding (SGGS)2-XTEN-(SGGS)2S (linker C2)			
Codon optimized polynucleotide encoding (SGGS)2-XTEN-(SGGS)2S (linker C2)	RNA	248	UCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCC
Codon optimized polynucleotide encoding (SGGS)2-XTEN-(SGGS)2S (linker C3)	DNA	235	TCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGC
Codon optimized polynucleotide encoding (SGGS)2-XTEN-(SGGS)2S (linker C3)	RNA	236	UCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGC
Codon optimized polynucleotide encoding (SGGS)2-XTEN-(SGGS)2S (linker C4)	DNA	259	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGTCCGCCACCCCCGAGAGCAGCGGCGGCTCAAGCGGCGGCAGCAGC
Codon optimized polynucleotide encoding (SGGS)2-XTEN-(SGGS)2S (linker C4)	RNA	260	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGC
SGGS-SV40BPNLS1	Polypeptide	24	SGGSKRTADGSEFEPKKKRKV
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C2)	DNA	251	TCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C2)	RNA	252	UCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding SGGS-	DNA	239	AGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C3)			
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C3)	RNA	240	AGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C4)	DNA	263	TCCGGCGGCTCCAAGAGGACTGCCGACGGCTCCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C4)	RNA	264	UCCGGCGGCUCCAAGAGGACUGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9 H840A without N terminus methionine	Polypeptide	7	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
Polynucleotide encoding Cas9 H840A without N terminus methionine	DNA	627	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCA

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			AGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGAC
Polynucleotide encoding Cas9 H840A without N terminus methionine	RNA	628	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGAC
Polynucleotide encoding Cas9 H840A without N terminus methionine	DNA	629	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			GGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGAC
Polynucleotide encoding Cas9 H840A without N terminus methionine	RNA	630	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGAC
MMLVRT5M, without N terminus methionine	Polypeptide	5	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding MMLVRT5M(without N terminus methionine	DNA	28	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGA

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			AGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCC
Polynucletide encoding MMLVRT5Mwithout N terminus methionine	RNA	29	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCC
Codon optimized polynucleotide without N terminus methionine (MMLVRT5M C2)	DNA	245	ACACTGAATATCGAGGACGAGTACCGCCTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCCACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGAGACAGGCCCCTCTGATCATCCCCCTGAAGGCCACCTCCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCCCACATCCAGCGGCTGCTGGATCAGGGCATCCTGGTGCCCTGTCAGAGCCCCTGGAACACCCCCCTGCTGCCAGTGAAGAAGCCCGGCACCAACGACTATCGGCCTGTGCAGGACCTGCGGGAGGTGAACAAACGGGTGGAGGACATCCACCCCACCGTGCCTAACCCATACAACCTGCTGTCCGGCCTGCCCCCAAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGCGGCTGCACCCCACCAGCCAGCCCCTGTTCGCCTTCGAGTGGAGGGACCCCGAGATGGGCATCTCCGGCCAGCTGACCTGGACCAGGCTGCCCCAGGGCTTCAAGAACAGCCCCACCCTGTTCAACGAGGCCCTGCACCGCGACCTGGCCGATTTTAGAATCCAGCACCCTGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTGGACTGCCAGCAGGGCACCAGGGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGCGGTGGCTGACAGAGGCCAGAAAGGAGACCGTGATGGGCCAGCCCACACCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCCGGCTGTTCATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCCCTGACCAAGCCTGGGACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCTGCCCTGGGACTGCCAGACCTGACCAAGCCCTTCGAGCTGTTCGTGGACGAGAAGCAGGGCTACGCCAAGGGCGTGCTGACACAGAAGCTGGGCCCATGGAGGAGACCCGTGGCCTACCTGTCCAAGAAGCTGGACCCAGTGGCCGCCGGCTGGCCACCCTGCCTGAGGATGGTGGCCGCCATCGCCGTGCTGACCAAGGATGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGACAGGTGGCTGAGCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCCCTGCCCGAGGAGGGCCTGCAGCACAATTGCCTGGACATCCTGGCCGAGGCCCACGGAACCCGCCCTGACCTGACCGACCAGCCTCTGCCCGACGCCGACCACACCTGGTATACCGACGGAAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGTGACAACCGAGACCGAGGTGATCTGGGCCAAGGCTCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACTCCCGGTACGCCTTCGCCACCGCCCACATCCACGGCGAAATCTACAGGCGGAGGGGCTGGCTGACCAGCGAGGGCAAGGAGATCAAGAACAAGGACGAGATCCTGGCCCTGCTGAAGGCCCTGTTCCTGCCCAAGAGGCTGTCTATCATCCACTGCCCCGGCCATCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGATGGCCGACCAGGCCGCCAGGAAAGCCGCCATCACCGAGACACCCGATACCTCCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M without N terminus methionine (MMLVRT5M C2)	RNA	246	ACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M without N terminus	DNA	83	ACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCA

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
methionine (MMLVRT5M C3)			GAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5Mwithout N terminus methionine (MMLVRT5M C3)	RNA	84	ACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M without N terminus methionine (MMLVRT5M C4)	DNA	257	ACCCTGAACATCGAGGACGAGTACAGACTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCTACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGAATGGGCCTGGCCGTGAGACAGGCCCCACTGATCATCCCACTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCTATGTCACAGGAGGCCAGACTGGGCATCAAGCCACACATCCAGAGACTGCTGGACCAGGGCATCCTGGTGCCCTGCCAGAGCCCATGGAACACCCCCCTGCTGCCCGTCAAGAAGCCCGGCACCAACGACTACAGGCCCGTGCAGGACCTGCGGGAGGTGAACAAGCGCGTGGAGGACATCCACCCTACCGTGCCCAACCCCTACAACCTGCTGTCCGGCCTGCCACCCAGCCATCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCCCAGCCTCTGTTCGCCTTCGAGTGGAGAGACCCCGAGATGGGCATCTCCGGCCAGCTGACTTGGACAAGACTGCCCCAGGGCTTCAAGAATTCTCCAACCCTGTTCAACGAGGCCCTGCACCGGGACCTGGCCGACTTCAGGATCCAGCACCCAGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTCGACTGCCAGCAGGGCACCCGGGCCCTGCTGCAGACTCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGAGGTGGCTGACCGAGGCCAGGAAGGAGACCGTGATGGGCCAGCCAACCCCTAAGACCCCCAGACAGCTGAGGGAGTTCCTGGGCAAGGCCGGCTTCTGCCGGCTGTTCATCCCCGGCTTCGCCGAGATGGCCGCCCCCCTGTACCCCCTGACCAAGCCTGGCACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGATCTGACCAAGCCATTCGAGCTGTTCGTGGACGAGAAACAGGGCTACGCCAAGGGCGTGCTGACCCAGAAGCTGGGCCCCTGGAGGAGACCTGTGGCCTACCTGAGCAAAAAGCTGGACCCAGTGGCCGCCGGGTGGCCCCCCTGCCTGAGAATGGTGGCCGCCATCGCCGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGACAGCCTCTGGTGATCCTGGCCCCCCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGATAGGTGGCTGAGTAATGCCCGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCCGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCACTGCCCGAGGAGGGCCTGCAGCATAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGATCAGCCTCTGCCCGACGCCGATCACACCTGGTACACCGATGGCAGCAGCCTGCTGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAGGCCCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACAGCCGGTACGCCTTCGCCACCGCTCACATCCACGGCGAGATTTACAGGAGAAGAGGCTGGCTGACCAGCGAAGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGTCTATCATCCACTGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGATGGCCGACCAGGCCGCCCGGAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACTCCAGCCCT
Codon optimized polynucleotide encoding MMLVRT5M without N terminus methionine (MMLVRT5M C4)	RNA	258	ACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCU

Table 16: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M-SGGS-SV40BPNLS1	Polypeptide	77	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKA DLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGAS AQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRY TGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDM YVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAY LNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSK KLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFK YFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPC QSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRA SAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIA VLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVY TDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M-SGGS-SV40BPNLS1 without N-terminal methionine	Polypeptide	620	KRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKAD LRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASM IKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTG WGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYV DQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLN AVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKL KSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYF DTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASA KKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVL TKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTD SRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1	DNA	79	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGG TGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGAT CTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACC ACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCT GGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGA AACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCT GGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAG CTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAA CAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACC TTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCA ACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATC GTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATT ATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAG CGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCT TTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAA GCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTG CAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGAC CAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGC GAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAA GCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTA CAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGA CAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAG CGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACC ATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAA CTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGA GCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCG CCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGG CGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACC

Sequence description	Type	SEQ ID No	SEQUENCE
			TGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1	RNA	80	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)8-MMLVRT5M	Polypeptide	78	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-(SGGS)8-MMLVRT5M C3	DNA	81	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding	RNA	82	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGA

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)8-MMLVRT5MC3			AGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC
5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1(TAA)-3'UTR	DNA	274	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACCATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACG

Sequence description	Type	SEQ ID No	SEQUENCE
			AGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAAGCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG
5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1(TAA)-3'UTR	RNA	592	AGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACCAUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCC

Sequence description	Type	SEQ ID No	SEQUENCE
			UCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAGCGGCCGCUUAAUUAAGCUGCCUUCUGCGGGGCUUGCCUUCUGGCCAAGCCCUUCUUCUCUCCCUUGCACCUGUACCUCUUGGUCUUUGAAUAAAGCCUGAGUAGGAAG
5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1-(TAATAGTGA) 3'UTR	DNA	275	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACCATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAATAGTGAGCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG

Sequence description	Type	SEQ ID No	SEQUENCE
5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1-(TAATAGTGA) 3'UTR	RNA	593	AGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACCAUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAUAGUGAGCGGCCGCUUAAUUAAGCUGCCUUCUGCGGGGCUUGCCUUCUGGCCAAGCCCUUCUUCUCUCCCUUGCACCUGUACCUCUUGGUCUUUGAAUAAAGCCUGAGUAGGAAG
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1 (TAA)	DNA	276	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTC*GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATC*

Sequence description	Type	SEQ ID No	SEQUENCE
			*GTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGAC*TCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC*AGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAA*
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1 (TAA)	RNA	277	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUG

Sequence description	Type	SEQ ID No	SEQUENCE
			UCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGU GCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAA GCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUG GCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAG UCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCA GCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCU UUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAG CCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGC CCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGA AGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCC GUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGA GGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCC UGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGA CCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCG CCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGG CCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAG CCCAAGAAGAAGAGGAAAGUCUAA
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1 (TAATAGTGA)	DNA	278	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTC*GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGG* *TGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGAT* *CTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACC* *ACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCT* *GGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGA* *AACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCT* *GGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAG* *CTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAA* *CAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACC* *TTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCA* *ACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATC* *GTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATT* *ATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAG* *CGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCT* *TTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAA* *GCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTG* *CAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGAC* *CAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGC* *GAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAA* *GCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTA* *CAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGA* *CAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAG* *CGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACC* *ATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAA* *CTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGA* *GCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCG* *CCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGA*CTCCGGCGGCTCCTCCGG CGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACC TGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAG CCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACC CAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGG CATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCC GCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTG ACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCA CCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCC AGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTG ATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTG CCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAA GGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATA CGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGC

Sequence description	Type	SEQ ID No	SEQUENCE
			CACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC*AGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAATAGTGA*
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1 (TAATAGTGA)	RNA	279	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAUAGUGA
NLS-N	Polypeptide	9	MKRTADGSEFESPKKKRKV
Polynucleotide encoding NLS-N	DNA	631	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTC

Sequence description	Type	SEQ ID No	SEQUENCE
Polynucleotide encoding NLS-N	RNA	632	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUC
Cas9 H840A without N terminus methionine	Polypeptide	7	
Polynucleotide encoding Cas9 H840A without N terminus methionine	DNA	627	
Polynucleotide encoding Cas9 H840A without N terminus methionine	RNA	628	
(SGGS)8 linker	Polypeptide	302	
Polynucleotide encoding (SGGS)8 linker	DNA	633	TCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCT
Polynucleotide encoding (SGGS)8 linker	RNA	634	UCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCU
MMLVRT5M (H8Y), D200N,T306K,W313 F,T330P,L603W without N terminus methionine	Polypeptide	5	
Codon optimized polynucleotide encoding MMLVRT5Mwithout N terminus methionine (MMLVRT5M_C3)	DNA	83	
Codon optimized polynucleotide encoding MMLVRT5M without N terminus methionine (MMLVRT5M_C3)	RNA	84	
C-linker	Polypeptide	288	

Sequence description	Type	SEQ ID No	SEQUENCE
Polynucleotide encoding C-linker	DNA	635	AGCGGCGGCTCC
Polynucleotide encoding C-linker	RNA	636	AGCGGCGGCUCC
NLS-C	Polypeptide	11	
Polynucleotide encoding NLS-C	DNA	637	AAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding NLS-C	RNA	638	AAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
SGGS-SV40BPNLS1	Polypeptide	24	
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C3)	DNA	239	
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C3)	RNA	240	
T7 promoter	DNA	267	TAATACGACTCACTATA
5'UTR	DNA	268	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACC
stop codon 1	DNA	269	TAA
stop codon 2	DNA	270	TAG
stop codon 3	DNA	271	TGA
stop codon 4	DNA	272	TAATAGTGA
3' UTR	DNA	273	GCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG

Table 17: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M(G504X) -SGGS-SV40BPNLS1	Polypeptide	85	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGSGGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M(G504X) -SGGS-SV40BPNLS1 without N terminal methionine	Polypeptide	622	KRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGSGGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1	DNA	87	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTA

Sequence description	Type	SEQ ID No	SEQUENCE
			CCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1	RNA	88	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)	Polypeptide	86	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)	DNA	89	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)	RNA	90	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGG

Sequence description	Type	SEQ ID No	SEQUENCE
			AAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC
T7promoter-5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1 -3'UTR (TAA)	DNA	280	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACCATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAAGCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG
T7promoter-5'UTR-SV40BPNLS-Cas9H840A-	RNA	594	AGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACCAUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAU

Sequence description	Type	SEQ ID No	SEQUENCE
(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1 -3'UTR (TAA)			CGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAGCGGCCGCUUAAUUAAGCUGCCUUCUGCGGGGCUUGCCUUCUGGCCAAGCCCUUCUUCUCUCCCUUGCACCUGUACCUCUUGGUCUUUGAAUAAAGCCUGAGUAGGAAG
T7promoter-5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1 -3'UTR (TAATAGTGA)	DNA	281	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACCATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTC

Sequence description	Type	SEQ ID No	SEQUENCE
			TGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAATAGTGAGCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG
T7promoter-5'UTR-SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1 -3'UTR (TAATAGTGA)	RNA	595	AGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACCAUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAUAGUGAGCGGCCGCUUAAUUAAGCUGCCUUCUGCGGGGCUUGCCUUCUGGCCAAGCCCUUCUUCUCUCCCUUGCACCUGUACCUCUUGGUCUUUGAAUAAAGCCUGAGUAGGAAG
SV40BPNLS-Cas9H840A-(SGGS)8-	DNA	282	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGA

Sequence description	Type	SEQ ID No	SEQUENCE
MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1-TAA			AACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAA
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1-TAA	RNA	283	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCA

Sequence description	Type	SEQ ID No	SEQUENCE
			GAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1-TAATAGTGA	DNA	284	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACTAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTCTAATAGTGA
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3(G504X)-SGGS-SV40BPNLS1-TAATAGTGA	RNA	285	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUG

Sequence description	Type	SEQ ID No	SEQUENCE
			CCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACUAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAAUAGUGA
NLS-N	Polypeptide	9	MKRTADGSEFESPKKKRKV
Polynucleotide encoding NLS-N	DNA	631	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTC
Polynucleotide encoding NLS-N	RNA	632	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUC
Cas9 H840A without N terminus methionine	Polypeptide	7	
Polynucleotide encoding Cas9 H840A without N terminus methionine	DNA	629	
Polynucleotide encoding Cas9 H840A without N terminus methionine	RNA	630	

Sequence description	Type	SEQ ID No	SEQUENCE
(SGGS)8 linker	Polypeptide	302	
Polynucleotide encoding (SGGS)8 linker	DNA	633	TCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCT
Polynucleotide encoding (SGGS)8 linker	RNA	634	UCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCU
MMLV-RT G504X	Polypeptide	36	
Codon optimized polynucleotide encoding MMLV-RT G504X	DNA	91	
Codon optimized polynucleotide encoding MMLV-RT [illegible]X	RNA	92	
C-linker	Polypeptide	288	
Polynucleotide encoding C-linker	DNA	635	AGCGGCGGCTCC
Polynucleotide encoding C-linker	RNA	636	AGCGGCGGCUCC
NLS-C	Polypeptide	11	
Polynucleotide encoding NLS-C	DNA	637	AAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding NLS-C	RNA	638	AAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
SGGS-SV40BPNLS1	Polypeptide	24	
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1	DNA	239	

Sequence description	Type	SEQ ID No	SEQUENCE
(optimized SGGS-SV40BPNLS1 C3)			
Codon optimized polynucleotide encoding SGGS-SV40BPNLS1 (optimized SGGS-SV40BPNLS1 C3)	RNA	240	
T7 promoter	DNA	267	TAATACGACTCACTATA
5'UTR	DNA	268	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACC
stop codon 1	DNA	269	TAA
stop codon 2	DNA	270	TAG
stop codon 3	DNA	271	TGA
stop codon 4	DNA	272	TAATAGTGA
	DNA	273	GCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG

Table 18: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X-GS-SV40BPNLS1	Polypeptide	34	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X-GS-SV40BPNLS1	Polypeptide	647	

Sequence description	Type	SEQ ID No	SEQUENCE
without N terminal methionine			
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X-GS-SV40BPNLS1	DNA	37	ATGAAACGTACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X-GS-SV40BPNLS1	RNA	38	AUGAAACGUACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUG

Sequence description	Type	SEQ ID No	SEQUENCE
			UGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X	Polypeptide	35	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X	DNA	39	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGG

Sequence description	Type	SEQ ID No	SEQUENCE
			CTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGA
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MG504X	RNA	40	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGA

Table 19: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N-SSGS-SV40BPNLS1	Polypeptide	43	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQK

Sequence description	Type	SEQ ID No	SEQUENCE
			QLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTNGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N-SSGS-SV40BPNLS1	DNA	46	ATGAAACGTACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGAATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCCTCTGGCGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N-SSGS-SV40BPNLS1	RNA	47	AUGAAACGUACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACG

Sequence description	Type	SEQ ID No	SEQUENCE
			AGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGAAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCCUCUGGCGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N	Polypeptide	44	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTNGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N	DNA	48	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCT

Sequence description	Type	SEQ ID No	SEQUENCE
			GATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGAATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCC
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MD524N	RNA	49	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGAAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCC

Table 20: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5ML478X-GS-SV40NLS1	Polypeptide	52	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5ML478X-GS-SV40NLS1	DNA	55	ATGAAACGTACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-	RNA	56	AUGAAACGUACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAA

Sequence description	Type	SEQ ID No	SEQUENCE
(SGGS)2S]-MMLVRT5ML478X-GS-SV40NLS1			CUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
	Polypeptide	53	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVAL
Polynucleotide encoding	DNA	57	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGAC

Sequence description	Type	SEQ ID No	SEQUENCE
			GCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTG
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5ML478X	RNA	58	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUG

Table 21: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)-GS-SV40BPNLS1	Polypeptide	61	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKF RGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYV TEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQV SGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQK QLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAET GGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVIKAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)-GS-SV40BPNLS1	DNA	64	ATGAAACGTACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACAC CGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGG ACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCG ACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCG TGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGAT GCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCT GAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTA CAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATT TTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGG GCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGA GCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATC TGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCG GCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCA GAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCC AGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCG GGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCG TGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTG GCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCT ACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGA ACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAG GTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAA GAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAG AGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGAC GAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCC TTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGC GAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCG GAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCC AGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACAC TGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCA CAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCA AATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGG TTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAA GCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGG GACAGCCACTAGTCATTAAGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCC CACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAGGCTCAAAAAGAACCGCCGACGGCAGCGAATTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)-GS-SV40BPNLS1	RNA	65	AUGAAACGUACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAA CACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCA AGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACC GACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCA UCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAA CUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAAC ACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGA CGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAG CUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAU

Sequence description	Type	SEQ ID No	SEQUENCE
			CACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUAAGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)	Polypeptide	62	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVIKAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)	DNA	66	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATC

Sequence description	Type	SEQ ID No	SEQUENCE
			GAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCTGGAGGATCTAGCGGAGGATCCTCTGGCAGCGAGACACCAGGAACAAGCGAGTCAGCAACACCAGAGAGCAGTGGCGGCAGCAGCGGCGGCAGCAGCACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTAAGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGA
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(G504X_L435K)	RNA	67	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUAAGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGA

Table 22: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MM428X-GS-SV40BPNLS1	Polypeptide	70	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M(P365X_Y133R_Y271R)-GS-SV40BPNLS1	Polypeptide	71	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPRNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGRLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MP365X-GS-SV40BPNLS1	Polypeptide	72	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MK378X-GS-SV40BPNLS1	Polypeptide	73	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MT328X-GS-SV40BPNLS1	Polypeptide	74	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTGSKRTADGSEFEPKKKRKV

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M R278X-GS-SV40BPNLS1	Polypeptide	75	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRGSKRTADGSEFEPKKKRKV
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5M (G504X_L435K_22aa Ntermdel)-GS-SV40BPNLS1	Polypeptide	76	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVIKAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGGSKRTADGSEFEPKKKRKV

Table 23: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
cmycBPNLSNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3-S-BPNLS-NLS	Polypeptide	93	MPAAKRVKLDGGKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSKRTADSQHSTPPKTKRKVEFEPKKKRKV
Polynucleotide encoding cmycBPNLSNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3-S-BPNLS-NLS	DNA	94	ATGCCCGCGGCCAAGAGAGTGAAGCTGGACGGCGGCAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGA

Sequence description	Type	SEQ ID No	SEQUENCE
			TCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCAAGAGAACCGCCGACTCTCAGCACAGCACCCCCCCCAAGACCAAACGGAAGGTGGAGTTCGAGCCCAAGAAGAAGAGGAAAGTG
Polynucleotide encoding cmycBPNLSNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3-S-BPNLS-NLS	RNA	95	AUGCCCGCGGCCAAGAGAGUGAAGCUGGACGGCGGCAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCC

Sequence description	Type	SEQ ID No	SEQUENCE
			CAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCAAGAGAACCGCCGACUCUCAGCACAGCACCCCCCCCAAGACCAAACGGAAGGUGGAGUUCGAGCCCAAGAAGAAGAGGAAAGUG

Table 24: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
CmycNLS-BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3(G504X)-BPNLS-NLS	Polypeptide	96	MPAAKRVKLDGGKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGKRTADSQHSTPPKTKRKVEFEPKKKRKV
Polynucleotide encoding CmycNLS-BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3(G504X)-BPNLS-NLS	DNA	97	ATGCCCGCGGCCAAGAGAGTGAAGCTGGACGGCGGCAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCTCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCTCTGGCGGATCTAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACAT

Sequence description	Type	SEQ ID No	SEQUENCE
			CCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCAAGAGAACCGCCGACTCTCAGCACAGCACCCCCCCAAGACCAAACGGAAGGTGGAGTTCGAGCCCAAGAAGAAGAGGAAAGTG
Polynucleotide encoding CmycNLS-BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M C3(G504X)-BPNLS-NLS	RNA	98	AUGCCCGCGGCCAAGAGAGUGAAGCUGGACGGCGGCAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCUCCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCGGCGGAAGCUCUGGCGGAUCUAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCAAGAGAACCGCCGACUCUCAGCACAGCACCCCCCCAAGACCAAACGGAAGGUGGAGUUCGAGCCCAAGAAGAAGAGGAAAGUG

Table 25: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3(G504X).	Polypeptide	99	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3(G504X).	DNA	100	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3(G504X).	RNA	101	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGA

Sequence description	Type	SEQ ID No	SEQUENCE
			AAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCCCCAAGAAGAAGAGGAAAGUC
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3(G504X).	DNA	102	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCTCCGGCGGCAGCAGCGGCGGCAGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCG

Sequence description	Type	SEQ ID No	SEQUENCE
			TGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-[(SGGS)2-XTEN-(SGGS)2S]-MMLVRT5MC3(G504X).	RNA	103	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 26: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3-SGGS-SV40BPNLS1	Polypeptide	104	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV

Sequence description	Type	SEQ ID No	SEQUENCE
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3-SGGS-SV40BPNLS1	DNA	106	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3-SGGS-SV40BPNLS1	RNA	107	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUG

Sequence description	Type	SEQ ID No	SEQUENCE
			UGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3	Polypeptide	105	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3	DNA	108	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCAC

Sequence description	Type	SEQ ID No	SEQUENCE
			CCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)4-SGGS-MMLVRT5M C3	RNA	109	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 27: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)-GGS-SV40BPNLS1	Polypeptide	110	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)-GGS-SV40BPNLS1	DNA	112	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)-GGS-SV40BPNLS1	RNA	113	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGA

Sequence description	Type	SEQ ID No	SEQUENCE
			AAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)	Polypeptide	111	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)	DNA	114	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCT

Sequence description	Type	SEQ ID No	SEQUENCE
			GATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-SGGS(EAAAK)4SGGS-MMLVRT5M C3(G504X)	RNA	115	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 28: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3-SGGS-SV40BPNLS1	Polypeptide	116	MKRTADGSEFESPKKKRKVDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEPKKKRKV
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3-SGGS-SV40BPNLS1	DNA	118	ATGAAACGGACAGCCGACGGAAGCGAGTTCGAGTCACCAAAGAAGAAGCGGAAAGTCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTGAGGCCGCTGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCTGCAGCCAAGGAGGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCCAGCGGCGGCTCCAAACGCACCGCCGACGGGAGCGAGTTCGAGCCCAAGAAGAAGAGGAAAGTC
Polynucleotide encoding SV40BPNLS-Cas9H840A-SGGS-(EAAAK)8-SGGS-	RNA	119	AUGAAACGGACAGCCGACGGAAGCGAGUUCGAGUCACCAAAGAAGAAGCGGAAAGUCGACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAA

Sequence description	Type	SEQ ID No	SEQUENCE
MMLVRT5M C3-SGGS-SV40BPNLS1			CUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUGAGGCCGCUGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCUGCAGCCAAGGAGGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUC
Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3	Polypeptide	117	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3	DNA	120	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGAC

Sequence description	Type	SEQ ID No	SEQUENCE
			CGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTGAGGCCGCTGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCTGCAGCCAAGGAGGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3	RNA	121	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUGAGGCCGCUGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCUGCAGCCAAGGAGGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGA

Sequence description	Type	SEQ ID No	SEQUENCE
			AGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 29: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5MC3(G504X)	Polypeptide	122	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5MC3(G504X)	DNA	123	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTGAGGCCGCTGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCTGCAGCCAAGGAGGCCGCTGCCAAGGAGGCCGCTGCTAAAAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGT

Sequence description	Type	SEQ ID No	SEQUENCE
			GCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)8-SGGS-MMLVRT5M C3(G504X)	RNA	124	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUGAGGCCGCUGCCAAAGAGGCCGCCGCCAAGGAAGCCGCCGCCAAGGAAGCCGCCGCCAAGGAGGCCGCCGCCAAGGAAGCUGCAGCCAAGGAGGCCGCUGCCAAGGAGGCCGCUGCUAAAAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 30: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3	Polypeptide	125	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAI

Sequence description	Type	SEQ ID No	SEQUENCE
			KKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3	DNA	126	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3	RNA	127	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU

Sequence description	Type	SEQ ID No	SEQUENCE
			CAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 31: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3-SGGS(G504X)	Polypeptide	128	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3-SGGS(G504X)	DNA	129	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAA

Sequence description	Type	SEQ ID No	SEQUENCE
			CGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)2-SGGS-MMLVRT5M C3-SGGS(G504X)	RNA	130	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAU

Sequence description	Type	SEQ ID No	SEQUENCE
			GGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGA CACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 32: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3	Polypeptide	131	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGAS QEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVD LLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAI KKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSEL DKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNI VKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEF SKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQT LGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRR GWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3	DNA	132	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGA AACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCA CGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCT GATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATC TGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCC CAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAA GCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAG CTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATC CCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAA CGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGAC CGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTG GAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGA CAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGC CGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGG ATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGAC GCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAG AAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCC GGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGA GTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATC GAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCT GATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCA AATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCT GGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCT GGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCTAAAGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGAGCGGCGGATCTACCCTGAACATCGAGGACGA GTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAA GCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAA GTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCG CGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGG CCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAG AAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACC AGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACC TGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAG GTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACC AGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCG GGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGAC

Sequence description	Type	SEQ ID No	SEQUENCE
			GAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3	RNA	133	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCUAAAGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 33: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3(G504X)	Polypeptide	134	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEF

Sequence description	Type	SEQ ID No	SEQUENCE
			SKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMS QEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQT LGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDA GKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3(G504X)	DNA	135	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGA AACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCA CGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCT GATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATC TGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCC CAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAA GCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAG CTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATC CCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAA CGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGAC CGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTG GAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGA CAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGC CGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGG ATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGAC GCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAG AAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCC GGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGA GTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATC GAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCT GATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCA AATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCT GGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCT GGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCTAAAGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGAGCGGCGGATCTACCCTGAACATCGAGGACGA GTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAA GCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAA GTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCG CGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGG CCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAG AAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACC AGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACC TGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAG GTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)3-SGGS-MMLVRT5M C3(G504X)	RNA	136	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCG GCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAU AAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCG GGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGC AGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACG ACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCAC CACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAU GGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGG GAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCA UCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAG GCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU CAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAU ACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAA GCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCA GAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGG CGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAG AGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACA AAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCA CGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUC

Sequence description	Type	SEQ ID No	SEQUENCE
			UUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCUAAAGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 34: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3-SGGS-SV40BPNLS1	Polypeptide	137	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDAEAAAKEAAAKEAAAKEAAAKATLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3	DNA	138	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCA

Sequence description	Type	SEQ ID No	SEQUENCE
			AATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACGCCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGGAAGCCGCCGCTAAAGAGGCCGCTGCCAAGGCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3	RNA	139	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACGCCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGGAAGCCGCCGCUAAAGAGGCCGCUGCCAAGGCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 35: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
SV40BPNLS-Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3-SGGS-SV40BPNLS1(G504X)	Polypeptide	140	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDAEAAAKEAAAKEAAAKEAAAKATLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Polynucleotide encoding Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3(G504X)	DNA	141	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACGCCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGGAAGCCGCCGCTAAAGAGGCCGCTGCCAAGGCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Polynucleotide encoding Cas9H840A-A-(EAAAK)4-A-MMLVRT5M C3(G504X)	RNA	142	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAG

Sequence description	Type	SEQ ID No	SEQUENCE
			GCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACGCCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGGAAGCCGCCGCUAAAGAGGCCGCUGCCAAGGCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 36: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5M C3	Polypeptide	143	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5M C3	DNA	144	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGAC

Sequence description	Type	SEQ ID No	SEQUENCE
			CGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCCAAGGAGGCCGCCGCTAAGGAAGCCGCCGCCAAGGAGGCCGCCGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5M C3	RNA	145	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCCAAGGAGGCCGCCGCUAAGGAAGCCGCCGCCAAGGAGGCCGCCGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAG

Sequence description	Type	SEQ ID No	SEQUENCE
			AAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 37: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5M C3(G504X)	Polypeptide	146	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSEAAAKEAAAKEAAAKEAAAKEAAAKEAAAKSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5M C3(G504X)	DNA	147	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCTGCCAAGGAGGCCGCTGCCAAGGAGGCCGCCGCTAAGGAAGCCGCCGCCAAGGAGGCCGCCGCTAAAAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCT

Sequence description	Type	SEQ ID No	SEQUENCE
			GAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-(EAAAK)6-SGGS-MMLVRT5MC3(G504X)	RNA	148	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCGAGGCCGCCGCCAAGGAAGCCGCUGCCAAGGAGGCCGCUGCCAAGGAGGCCGCCGCUAAGGAAGCCGCCGCCAAGGAGGCCGCCGCUAAAAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 38: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5MC3	Polypeptide	149	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAI

Sequence description	Type	SEQ ID No	SEQUENCE
			KKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5M C3	DNA	150	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTCCAGCCCCCGCCCCTGCCCCTGCCCCTGCTCCCAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5M C3	RNA	151	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU

Sequence description	Type	SEQ ID No	SEQUENCE
			CAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUCCAGCCCCCGCCCCUGCCCCUGCCCCUGCUCCCAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 39: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5M C3(G504X)	Polypeptide	152	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5M C3(G504X)	DNA	153	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAA

Sequence description	Type	SEQ ID No	SEQUENCE
			CGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTCCAGCCCCCGCCCCTGCCCCTGCCCCTGCTCCCAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-(PAPA)2-PAP-SGGS-MMLVRT5MC3(G504X)	RNA	154	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUCCAGCCCCCGCCCCUGCCCCUGCCCCUGCUCCCAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCG

Sequence description	Type	SEQ ID No	SEQUENCE
			GAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 40: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)4-P-SGGS-MMLVRT5M C3	Polypeptide	155	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-(PAPA)4-P-SGGS-MMLVRT5M C3	DNA	156	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTCCTGCCCCCGCCCCTGCCCCTGCTCCCGCTCCAGCCCCTGCCCCTGCCCCCAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGA

Sequence description	Type	SEQ ID No	SEQUENCE
			CAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-(PAPA)4-P-SGGS-MMLVRT5M C3	RNA	157	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUCCUGCCCCGCCCCUGCCCCUGCUCCCGCUCCAGCCCCUGCCCCUGCCCCCAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 41: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)4-P-SGGS-	Polypeptide	158	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVD

Sequence description	Type	SEQ ID No	SEQUENCE
MMLVRT5M C3(G504X)			LLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-(PAPA)4-P-SGGS-MMLVRT5M C3(G504X)	DNA	159	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTCCTGCCCCCGCCCCTGCCCCTGCTCCCGCTCCAGCCCCTGCCCCTGCCCCCAGCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-(PAPA)4-P-SGGS-MMLVRT5M C3(G504X)	RNA	160	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCA

Sequence description	Type	SEQ ID No	SEQUENCE
			GAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUCCUGCCCCCGCCCCUGCCCCUGCUCCCGCUCCAGCCCCUGCCCCUGCCCCCAGCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 42: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3	Polypeptide	161	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3	DNA	162	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCC

Sequence description	Type	SEQ ID No	SEQUENCE
			GGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCCCCGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCTCCCGCCCCAGCCCCTGCTCCAGCCCCTGCTCCCGCCCCCAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3	RNA	163	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCCCCGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCUCCCGCCCCAGCCCCUGCUCCAGCCCCUGCUCCCGCCCCCAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAA

Sequence description	Type	SEQ ID No	SEQUENCE
			CAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 43: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3(G504X)	Polypeptide	164	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3(G504X)	DNA	165	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCCCCGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCTCCCGCCCCAGCCCCTGCTCCAGCCCCTGCTCCCGCCCCCAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGG

Sequence description	Type	SEQ ID No	SEQUENCE
			AGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-(PAPA)6-P-SGGS-MMLVRT5M C3(G504X)	RNA	166	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCCCCGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCUCCCGCCCCAGCCCCUGCUCCAGCCCCUGCUCCCGCCCCCAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 44: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3	Polypeptide	167	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG

Sequence description	Type	SEQ ID No	SEQUENCE
			WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3	DNA	168	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCCCCGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCTCCCGCCCCTGCTCCCGCCCCTGCTCCAGCCCCTGCCCCAGCACCCGCCCCCAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3	RNA	169	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACA

Sequence description	Type	SEQ ID No	SEQUENCE
			AAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCCCCGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCUCCCGCCCCUGCUCCCGCCCCUGCUCCAGCCCCUGCCCCAGCACCCGCCCCCAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 45: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3(G504X)	Polypeptide	170	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3(G504X)	DNA	171	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGG

Sequence description	Type	SEQ ID No	SEQUENCE
			ATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCCCCGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCCCCTGCTCCCGCCCCTGCTCCCGCCCCTGCTCCAGCCCCTGCCCCAGCACCCGCCCCCAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-(PAPA)8-P-SGGS-MMLVRT5M C3(G504X)	RNA	172	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCCCCGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCCCCUGCUCCCGCCCCUGCUCCCGCCCCUGCUCCAGCCCCUGCCCCAGCACCCGCCCCCAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 46: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-XTEN-MMLVRT5M C3	Polypeptide	173	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGSETPGTSESATPESTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-XTEN-MMLVRT5M C3	DNA	174	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCAGCGAAACCCCTGGCACCAGCGAGAGCGCCACACCCGAGTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-XTEN-MMLVRT5M C3	RNA	175	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAU

Sequence description	Type	SEQ ID No	SEQUENCE
			AAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCAGCGAAACCCCUGGCACCAGCGAGAGCGCCACACCCGAGUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 47: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-XTEN-MMLVRT5M C3(G504X)	Polypeptide	176	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGSETPGTSESATPESTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-XTEN-MMLVRT5M C3(G504X)	DNA	177	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCAGCGAAACCCCTGGCACCAGCGAGAGCGCCACACCCGAGTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-XTEN-MMLVRT5M C3(G504X)	RNA	178	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAU

Sequence description	Type	SEQ ID No	SEQUENCE
			CCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCAGCGAAACCCCUGGCACCAGCGAGAGCGCCACACCCGAGUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCAUGCCUGCGGAUGGUGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 48: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-XTEN-MMLVRT5M C3	Polypeptide	179	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGSETPGTSESATPESTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-XTEN-MMLVRT5M C3	DNA	180	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCT

Sequence description	Type	SEQ ID No	SEQUENCE
			GGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGATCTGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-XTEN-MMLVRT5M C3	RNA	181	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGAUCUGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 49: Exemplary PE editor and PE editor construct sequences (Cas9H840A-SGGS-XTEN-MMLVRT5M C3(G504X))

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-XTEN-MMLVRT5M C3(G504X)	Polypeptide	182	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGSETPGTSESATPESTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-XTEN-MMLVRT5M C3(G504X)	DNA	183	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGATCTGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-XTEN-MMLVRT5M C3(G504X)	RNA	184	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU

Sequence description	Type	SEQ ID No	SEQUENCE
			CAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGAUCUGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 50: Exemplary PE editor and PE editor construct sequences (Cas9H840A-SGGS-XTEN-SGGS-MMLVRT$_{5M}$ C3)

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3	Polypeptide	185	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGSETPGTSESATPESSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3	DNA	186	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTG

Sequence description	Type	SEQ ID No	SEQUENCE
			GAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTAGCGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3	RNA	187	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUAGCGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGC

Sequence description	Type	SEQ ID No	SEQUENCE
			UGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 51: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3(G504X)	Polypeptide	188	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSETPGTSESATPESSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3(G504X)	DNA	189	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGATCTAGCGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTG

Sequence description	Type	SEQ ID No	SEQUENCE
			GCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-SGGS-XTEN-SGGS-MMLVRT5M C3(G504X)	RNA	190	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAUCUAGCGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 52: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3	Polypeptide	191	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEF

Sequence description	Type	SEQ ID No	SEQUENCE
			SKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3	DNA	192	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGCGGCTCTTCTGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCAGCGGCGGATCTAGCGGCGGCTCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3	RNA	193	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCA

Sequence description	Type	SEQ ID No	SEQUENCE
			GAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAAGCAGCGGCGGCUCUUCUGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCAGCGGCGGAUCUAGCGGCGGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 53: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3(G504X)	Polypeptide	194	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3(G504X)	DNA	195	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTG

Sequence description	Type	SEQ ID No	SEQUENCE
			GAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGCGGCTCTTCTGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCTGAGAGCAGCGGCGGATCTAGCGGCGGCTCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT5M C3(G504X)	RNA	196	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAAGCAGCGGCGGCUCUUCUGGCAGCGAGACACCCGGCACCAGCGAAAGCGCCACCCCUGAGAGCAGCGGCGGAUCUAGCGGCGGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 54: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)4-MMLVRT5M C3	Polypeptide	197	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)4-MMLVRT5M C3	DNA	198	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGCGGCAGCAGCGGCGGATCTAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)4-MMLVRT5M C3	RNA	199	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGCGGCAGCAGCGGCGGAUCUAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 55: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)4-MMLVRT5M C3(G504X)	Polypeptide	200	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGY

Sequence description	Type	SEQ ID No	SEQUENCE
			RASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)4-MMLVRT5M C3(G504X)	DNA	201	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGCGGCAGCAGCGGCGGATCTAGCGGCGGATCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)4-MMLVRT5M C3(G504X)	RNA	202	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGU

Sequence description	Type	SEQ ID No	SEQUENCE
			GGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGCGGCAGCAGCGGCGGAUCUAGCGGCGGAUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 56: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)4-MMLVRT5MC3(G504X)	Polypeptide	203	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)4-MMLVRT5MC3(G504X)	DNA	204	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCG

Sequence description	Type	SEQ ID No	SEQUENCE
			AGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGCGGCTCTAGCGGCGGAAGCAGCGGCGGATCTAGCGGCGGCTCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-(SGGS)4-MMLVRT5M C3(G504X)	RNA	205	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGCGGCUCUAGCGGCGGAAGCAGCGGCGGAUCUAGCGGCGGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 57: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)5-MMLVRT5M C3(G504X)	Polypeptide	206	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)5-MMLVRT5M C3(G504X)	DNA	207	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCAGCAGCGGCGGCTCTAGCGGCGGAAGCAGCGGCGGATCTAGCGGCGGCTCCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)5-MMLVRT5M C3(G504X)	RNA	208	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAG

Sequence description	Type	SEQ ID No	SEQUENCE
			GCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCAGCAGCGGCGGCUCUAGCGGCGGAAGCAGCGGCGGAUCUAGCGGCGGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 58: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)6-MMLVRT5M C3	Polypeptide	209	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)6-MMLVRT5M C3	DNA	210	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGAC

Sequence description	Type	SEQ ID No	SEQUENCE
			CGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACAGCGGCGGCAGCAGCGGCGGATCTAGCGGCGGCAGCAGCGGCGGATCTAGCGGAGGCTCCTCCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-(SGGS)6-MMLVRT5M C3	RNA	211	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACAGCGGCGGCAGCAGCGGCGGAUCUAGCGGCGGCAGCAGCGGCGGAUCUAGCGGAGGCUCCUCCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCC

Sequence description	Type	SEQ ID No	SEQUENCE
			AGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 59: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)6-MMLVRT5M C3(G504X)	Polypeptide	212	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)6-MMLVRT5M C3(G504X)	DNA	213	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACAGCGGCGGCAGCAGCGGCGGATCTAGCGGCGGCAGCAGCGGCGGATCTAGCGGAGGCTCCTCCGGCGGCAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGG

Sequence description	Type	SEQ ID No	SEQUENCE
			CGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)6-MMLVRT5M C3(G504X)	RNA	214	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACAGCGGCGGCAGCAGCGGCGGAUCUAGCGGCGGCAGCAGCGGCGGAUCUAGCGGAGGCUCCUCCGGCGGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 60: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)10-MMLVRT5M C3	Polypeptide	215	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSEL

Sequence description	Type	SEQ ID No	SEQUENCE
			DKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)10-MMLVRT5M C3	DNA	216	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCTTCTGGTGGCAGCAGCGGCGGAAGCAGCGGCGGCTCTAGCGGCGGCAGCAGCGGCGGCTCCTCCGGCGGATCTAGCGGCGGCAGCAGCGGAGGCAGCAGCGGCGGAAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-(SGGS)10-MMLVRT5M C3	RNA	217	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAU

Sequence description	Type	SEQ ID No	SEQUENCE
			ACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCUUCUGGUGGCAGCAGCGGCGGAAGCAGCGGCGGCUCUAGCGGCGGCAGCAGCGGCGGCUCCUCCGGCGGAUCUAGCGGCGGCAGCAGCGGAGGCAGCAGCGGCGGAAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 61: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)10-MMLVRT5MC3(G504X)	Polypeptide	218	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)10-MMLVRT5MC3(G504X)	DNA	219	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAA

Sequence description	Type	SEQ ID No	SEQUENCE
			CGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGCTCTTCTGGTGGCAGCAGCGGCGGAAGCAGCGGCGGCTCTAGCGGCGGCAGCAGCGGCGGCTCCTCCGGCGGATCTAGCGGCGGCAGCAGCGGAGGCAGCAGCGGCGGAAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)10-MMLVRT5MC3(G504X)	RNA	220	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGCUCUUCUGGUGGCAGCAGCGGCGGAAGCAGCGGCGGCUCUAGCGGCGGCAGCAGCGGCGGCUCCUCCGGCGGAUCUAGCGGCGGCAGCAGCGGAGGCAGCAGCGGCGGAAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGG

Sequence description	Type	SEQ ID No	SEQUENCE
			AGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 62: Exemplary PE editor and PE editor construct sequences (Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3)

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3	Polypeptide	221	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3	DNA	222	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGATCTGAAACCCCTGGCACCAGCGAATCTGCCACCCCTGAGTCCAGCGGCAGCGAGACACCAGGCACCAGCGAGAGCGCCACACCCGAGAGCAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAG

Sequence description	Type	SEQ ID No	SEQUENCE
			GCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Polynucleotide encoding	RNA		

Table 63: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3(G504X)	Polypeptide	224	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3(G504X)	DNA	225	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGATCTGAAACCCCTGGCACCAGCGAATCTGCCACCCCTGAGTCCAGCGGCAGCGAGACACCAGGCACCAGCGAGAGCGCCACACCCGAGAGCAGCGGCGGCTCTACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAG

Sequence description	Type	SEQ ID No	SEQUENCE
			GCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)-(XTEN)2-(SGGS)-MMLVRT5M C3(G504X)	RNA	226	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAAGCAGCGGAUCUGAAACCCCUGGCACCAGCGAAUCUGCCACCCCUGAGUCCAGCGGCAGCGAGACACCAGGCACCAGCGAGAGCGCCACACCCGAGAGCAGCGGCGGCUCUACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 64: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)2-(XTEN)2-	Polypeptide	227	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGAS

Sequence description	Type	SEQ ID No	SEQUENCE
(SGGS)2-MMLVRT5M C3			QEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Cas9H840A-(SGGS)2-(XTEN)2-(SGGS)2-MMLVRT5M C3	DNA	228	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGAGGCAGCTCTGGCTCTGAAACCCCTGGCACCAGCGAATCTGCCACACCAGAGTCTAGCGGCAGCGAGACACCCGGCACCAGCGAGAGCGCCACCCCTGAGAGCAGCGGCGGCTCCTCCGGCGGAAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Cas9H840A-(SGGS)2-(XTEN)2-(SGGS)2-MMLVRT5M C3	RNA	229	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCA

Sequence description	Type	SEQ ID No	SEQUENCE
			UCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAG GCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAU CAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAU ACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAA GCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCA GAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGG CGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAG AGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACA AAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCA CGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUC UUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAG UGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGU GGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUA CUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAA CAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAU CCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGC UGGGAGGUGACUCCGGCGGAAGCAGCGGAGGCAGCUCUGGCUCUGAAACCCCUGGCACCAGCGAAUCUGCCACACCAGAGUCUAGCGGCAGCGAGACACCCGGCACCAGCGAGAGCGCCACCCCUGAGAGCAGCGGCGGCUCCUCCGGCGGAAGCACCCUGA ACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCA CCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCC CGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAG CCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGC UGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGA AGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGA CCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGAC CCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGG CCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGG GCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGA CCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUA CAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCC GACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

Table 65: Exemplary PE editor and PE editor construct sequences

Sequence description	Type	SEQ ID No	SEQUENCE
Cas9H840A-(SGGS)2-(XTEN)2-(SGGS)2-MMLVRT5M C3(G504X)	Polypeptide	230	DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKL FIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGAS QEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVD LLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAI KKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSEL DKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNI VKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEF SKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGSETPGTSESATPESSGGSSGGSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMG LAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILL QYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
Cas9H840A-(SGGS)2-(XTEN)2-(SGGS)2-MMLVRT5M C3(G504X)	DNA	231	GACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGAGCCCTGCTGTTCGACAGCGGCGA AACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATACACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACAGCTTCTTCCACAGACTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAGCA CGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCCACCATCTACCACCTGAGAAAGAAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCACATGATCAAGTTCCGGGGCCACTTCCT GATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCCAAGGCCATCCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATC TGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAACCTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCC CAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACCAGGACCTGACCCTGCTGAAA

Sequence description	Type	SEQ ID No	SEQUENCE
			GCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGACGGCACCGAGGAACTGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTCCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTCGCCTGGATGACCAGAAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAGCCCGCCTTCCTGAGCGGCGAGCAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAAACCTATGCCCACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTCGCCAACAGAAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCCGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCCGTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGGCTGTCCGACTACGATGTGGACGCTATCGTGCCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGCGGCCTGAGCGAACTGGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTCGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCGTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGCATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGCAAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATATGTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCTGGGAGGTGACTCCGGCGGAAGCAGCGGAGGCAGCTCTGGCTCTGAAACCCCTGGCACCAGCGAATCTGCCACACCAGAGTCTAGCGGCAGCGAGACACCCGGCACCAGCGAGAGCGCCACCCCTGAGAGCAGCGGCGGCTCCTCCGGCGGAAGCACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Cas9H840A-(SGGS)2-(XTEN)2-(SGGS)2-MMLVRT5M C3(G504X)	RNA	232	GACAAGAAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAUCGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGGAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUGGACGCUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAAGAACCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUCCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCACAAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUCCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCUGGGAGGUGACUCCGGCGGAAGCAGCGGAGGCAGCUCUGGCUCUGAAACCCCUGGCACCAGCGAAUCUGCCACACCAGAGUCUAGCGGCAGCGAGACACCCGGCACCAGCGAGAGCGCCACCCCUGAGAGCAGCGGCGGCUCCUCCGGCGGAAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGC

Sequence description	Type	SEQ ID No	SEQUENCE
			UGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC

Table 66: Exemplary codon optimized reverse transcriptase with linker and NLS([(SGGS)2-XTEN-(SGGS)2-S]-MMLVRT5M -SSGS-KRTADGSEFEPKKKRKV) nucleotide sequences

SEQ ID NO.	SEQUENCE
412	AGCGGCGGCUCAUCUGGCGGCAGCAGCGGCUCCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCUAGCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCUGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCCGAAACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGAUCAGGGAAUCCUGGUGCCUUGUCAGAGCCCUUGGAACACCCCUCUGCUGCCUGUGAAGAAACCAGGAACCAACGACUACAGACCAGUGCAGGACCUGAGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCAGGCCUGCCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGCCUGAGACUGCACCCCACUAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGACUGCCACAGGGCUUCAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCCGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUAUCCACUGACCAAGCCCGGCACCCUGUUUAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCUCCAUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGAUAGGUGGCUGUCUAACGCCAGGAUGACCCAUUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAAUCCCGCCACACUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACAGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCUCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCUCCGAAGGCAAAGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGGCUGUCUAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCUAUUACCGAGACCCCUGACACCUCCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGCUCCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA
413	UCCGGGGGAAGCAGCGGCGGCAGCAGCGGCUCAGAGACCCCCGGCACAUCCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAAUAUCGAGGACGAGUACAGACUGCACGAGACAAGCAAGGAACCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAACAGUACCCUAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCUUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCAAGCCACCAGUGGUACACAGUGCUGGACCUGAAAGACGCUUUCUUCUGCCUGAGGCUGCACCCAACAAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCUCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGCAUCCAGCAUCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGACAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGUCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACCAAACCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCACUGGGCCUGCCAGACCUGACCAAGCCCUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCUAAUGCCAGGAUGACACACUACCAGGCCCUGCUGCUGGAUACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAAGCCCACGGCACCAGACCUGACCUGACCGACCAGCCACUGCCUGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGAGCCGAGCUCAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACAAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGGCAUAGCGCCGAGGCCCGCGGCAACCGCAUGGCCGACCAGGCCGCCAGGAAGGCAGCCAUCACAGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCUGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
414	AGCGGCGGCAGCUCCGGCGGCAGCUCCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCUGGCGGCUCCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCAGACGUGUCCCUGGGCUCAACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCUCUGAAAGCCACAUCUACCCCUGUGUCCAUCAAGCAGUACCCAAUGUCACAGGAGGCCCGGCUGGGCAUCAAGCCACACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAACCUGGCACCAACGACUACAGACCCGUGCAGGACCUGCGCGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCAAGCCACCAGUGGUAUACCGUGCUGGACCUGAAGGACGCCUUCUUUUGCCUGAGGCUGCACCCUACCUCUCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCCGGCUGCCACAGGGCUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUUUGCAGGCUGUUCAUCCCAGGCUUUGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACUAAGCCUGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGAUGAAAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGUCCAAAAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAAGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGGUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCU

SEQ ID NO.	SEQUENCE
	GACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGAAGGGGCUGGCUGACUAGCGAGGGCAAGGAGAUUAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUUAUCCAUUGCCCAGGCCACCAGAAGGGCCACUCCGCCGAAGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACCCCCGACACCUCUACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA
415	AGCGGCGGCUCCUCCGGCGGCAGCAGCGGGUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGUUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGUACCUGGCUGAGCGACUUUCCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCACUGAAAGCCACCAGCACCCCAGUGUCCAUCAAGCAGUAUCCUAUGUCCCAGGAGGCCCGCCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGUCACCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAACGAUUACAGACCAGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGAUAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCCUCCCACCAGUGGUACACUGUGCUGGACCUGAAGGACGCCUUCUUUUGCCUGCGGCUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGAGAGAUCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGACAGCUGAGGGAGUUUCUGGGCAAGGCCGGCUUCUGUAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCCGGCACACUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACUGCCCCAGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGGCCUUGGCGGCGCCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGAGCAACGCCCGCAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCUCUCAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCAGGUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAAAGACUGUCUAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUCCUGAUCGAGAACAGCUCUCCAAGCGGAGGCAGCAAGAGAACAGCCGAUGGCAGCGAGUUCGAACCCAAGAAGAAGAGAAAGGUGUGA
416	AGCGGGGGCUCUAGCGGCGGCAGCAGCGGGUCUGAGACCCCUGGGACCAGCGAGUCCGCCACCCCCGAGUCCUCUGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGAUGUGAGCCUGGGGUCCACCUGGCUGUCUGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACACCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUCCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCAUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGCACAAACGAUUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCUGGCCUGCCACCCUCCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUUGAGUGGCGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGAAUCCAGCACCCUGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGGUUCUGCAGACUGUUCAUUCCCGGCUUUGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGAAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACAAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCCGCAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUCGCCGAGGCCCAUGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCUCUGCUGCAGGAGGGCCAGAGGAAGGCUGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCUCUGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGUCCAGGCCACCAGAAGGGCCAUAGCGCCGAGGCCAGAGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAAUUCCAGCCCCUCCGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUUGAGCCAAAAAAGAAGAGGAAGGUGUGA
417	AGCGGCGGCUCCAGCGGCGGCUCCAGCGGAUCCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGGGGCAGCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGACUGGGCAUCAAGCCCCAUAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACCGGCCCGUGCAGGAUCUGCGCGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACAGUGCCCAAUCCUUACAACCUGCUGAGCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCUACCAGCCAGCCACUGUUUGCCUUCGAAUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCUACUCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUUAGAAUCCAGCACCCAGACCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCUCCCCUGUACCCUCUGACCAAGCCUGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACAGCCCCAGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGACGGCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUUGCCGUGCUGACCAAAGAUGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCAUGCCGUGGAGGCCCUGGUCAAGCAGCCUCCCGAUAGAUGGCUGUCCAACGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGAUCACACUUGGUACACAGACGGCAGCUCUCUGCUGCAGGAGGGACAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCAUAUCCACGGAGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCUUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCUCCAAGCGCACAGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
418	UCCGGCGGCUCUUCCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACUAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCUCCUCUACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCUGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGGAUCAAGCCUCACAUUCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCUUGUCAGAGCCCCUGGAACACUCCCCUGCUGCCAGUCAAGAAGCCCGGCACCAACGACUACAGACCCGUGCAGGAUCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGCGAGACCCCGAAAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACCGGGAUCUGGCCGACUUCAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACAAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAACCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCUAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGACGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACGAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGUCUGGAUAUCCUGGCCGAGGCUCACGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGGAGCUCCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGAGCCGCCGUGACCACCGAGACAGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCC

SEQ ID NO.	SEQUENCE
	UGCCCAAGAGGCUGUCUAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCUAAGAAGAAGAGGAAGGUGUGA
419	UCCGGAGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACCAGCGAGAGCGCCACCCCAGAGUCCAGCGGAGGCUCUAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACUUCCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGAGCGAUUUUCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGGCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCUCAGGAGGCCCGCCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCAGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAAUCCAUACAACCUGCUGAGCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACUCUCCUACCCUGUUCAACGAGGCCCUGCAUCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGGUAUCGCGCCAGCGCCAAGAAGGCUCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACCCCAGACAGCUGAGAGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUCACCCAGAAGCUGGGCCCUUGGAGAAGGCCAGUGGCCUACCUGUCCAAGAAACUGGACCCAGUGGCCGCCGGCUGGCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUCGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUAGAGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUUGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUAUACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGACGGAGGGGCUGGCUGACCUCUGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAAGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAAACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA
420	AGCGGCGGCUCCAGCGGCGGCAGCAGCGGGUCCGAGACCCCUGGCACCUCCGAGUCCGCCACCCCCGAGAGCUCCGGAGGCAGCAGCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCUAUGUCUCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCUGGCACAAACGACUACAGGCCAGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGCCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACUAGACUGCCCCAGGGAUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGGAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCUCCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAAACCGUGAUGGGCCAGCCUACACCCAAGACCCCCAGACAGCUGCGGGAGUUUCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCCGACCUGACCAAACCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCAGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCCUGUCUGAGAAUGGUGGCUGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCUGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGAUCCUCCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAAUGUGUACACCGACAGCCGGUAUGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCAAAGAGAACAGCCGACGGCAGCGAGUUCGAGCCAAAGAAGAAGCGGAAGGUGUGA
421	UCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
422	AGCGGAGGCAGCUCCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACCAGCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUAUCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUUCCCCAGGCAUGGGCUGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGAUUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCAUACAACCUGCUGUCUGGCCUGCCUCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGGCUGCCCCAGGGCUUCAAGAAUAGCCCAACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACAAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCAGCUAAGAAAGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGGUGGCUGACAGAGGCCCGCAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCCGGCAGCUGAGAGAGUUCCUGGGCAAGGCCGGAUUCUGCAGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAAAAGCAGGGCUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGACCCGUGGCCUAUCUGUCCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCUCCCGACAGAUGGCUGUCUAACGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAAUUGCCUGGAUAUCCUGGCCGAGGCCCACGGGACACGGCCAGACCUGACCGAUCAGCCACUGCCCGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACUACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGGAAGAAGCUGAAUGUGUACACCGACUCUAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGCAGCAAGAGGACCGCCGACGGAAGCGAGUUCGAGCCUAAGAAGAAGAGAAAGGUGUGA

SEQ ID NO.	SEQUENCE
423	AGCGGCGGCUCCUCAGGCGGCUCCAGCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCUCCACUCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUUAAACAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAAUACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACAAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCUAAUCCCUACAACCUGCUGUCCGGGCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCAACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGGACCCCGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCCGCCUGCCUCAGGGCUUCAAGAAUUCCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGAUUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCAGGCUUCGCCGAAAUGGCUGCCCCCCUGUACCCACUGACCAAGCCUGGAACACUGUUCAACUGGGGCCCUGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAACCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGAAGGCCUGUGGCCUACCUGUCUAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCCUGUCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGAUGGCUGAGCAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAAGGCCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACAGAAGUGAUCUGGGCCAAGGCUCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUUGCCACCGCCCACAUCCAUGGCGAGAUCUACCGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGACUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGAAACCGCAUGGCCGACCAGGCUGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACUCUUCCCCCAGCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAACCCAAGAAAAAGCGGAAGGUGUGA
424	UCCGGCGGCUCCUCCGGCGGCAGCAGCGGCAGCGAGACUCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGCGGCUCCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAACCAGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUAUCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCAUAUCCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAACCCGGCACCAACGACUACCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCCACCGUGCCUAACCCCUACAACCUGCUGAGCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGAAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGGACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGAUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACACCCAGGCAGCUGAGGGAGUUCCUGGGCAAAGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCAGAUCUGACCAAGCCUUUCGAGCUGUUCGUGGAUGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGAGGAGACCUGUGGCCUACCUGAGCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCACCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAACAGCCCCCCGACAGAUGGCUGUCUAAUGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAAUUGUCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGAUCAGCCCCUGCCAGACGCCGACCACACCUGGUAUACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGAUUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGCGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCAGGCCACCAGAAGGGGCACUCCGCCGAGGCUCGCGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCUGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA
425	UCUGGCGGCAGCUCCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCUGCCACCCCAGAGAGCUCCGGAGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCAGAGACCGGCGGCAUGGGACUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUAUCCUAUGUCUCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCUGUGAAGAAGCCUGGCACCAACGACUACAGACCAGUGCAGGAUCUGAGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGACUGCCCCAGGGCUUCAAGAACAGUCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCUCAGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGACCCGUGGCCUACCUGUCAAAGAAGCUGGAUCCAGUGGCCGCCGGCUGGCCACCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCUAACGCCCGCAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAAUUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGAGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUUACCGAGACUCCAGACACCUCCACCCUGCUGAUCGAGAAUUCCUCCCCCAGCGGCGGGAGCAAGAGAACCGCAGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA
426	AGCGGAGGCUCCUCCGGCGGCAGCAGCGGGAGCGAGACCCCAGGGACCAGCGAGUCCGCCACCCCAGAGAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCACACUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAAGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCUCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGAACCAACGACUAUCGGCCAGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACAGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCCUCACACCAGUGGUACACCGUGCUGGACCUGAAAGACGCCUUCUUCUGCCUGAGGCUGCACCCAACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGCCUGUUUAUCCCUGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAACCAGGCACUCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGAGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCCAACGCCAGGAUGACUCACUACCAGGCCCUGCUGCUGGACACCGAUCGCGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAAGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUCACCGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGACGCAGGGGCUGGCUGACCAGCGAGGGUAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAACGGCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCCGGCGGCAGCAAGAGAACCGCCGAUGGCAGCGAGUUCGAGCCAAAGAAGAAACGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
427	UCUGGCGGCAGCAGCGGAGGAAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCUCCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCAGACGUGUCCCUGGGCUCCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCAGAGACCGGCGGAAUGGGCCUGGCCGUGAGGCAGGCCCCACUCAUCAUCCCCCUCAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAAUCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCACAGGGCUUCAAGAACUCCCCAACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCCGGAUUCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACAAGCGAGCUGGAUUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACAAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACAAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCAGUGGCCUAUCUGUCCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCAGUGGAGGCUCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCUAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACACGCCCCGACCUGACCGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAACUGAACGUGUACACCGACUCCAGGUAUGCCUUCGCCACCGCCCACAUUCACGGCGAGAUCUACAGGAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGCCCAGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGAAUGGCCGACCAGGCCGCCCGCAAGGCCGCCAUCACCGAGACCCCCGAUACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCAGCAAGGACCGCCGACGGCUCCGAGUUCGAGCCUAAGAAGAAGAGAAAGGUGUGA
428	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCUUCCGGCGGCUCCAAGAGGACUGCCGACGGCUCCGAGUUCGAGCCUAAGAAGAAGAGGAAGGUGUGA
429	AGCGGCGGAAGCAGCGGCGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCUCCACCCCAGUGUCCAUCAAACAGUACCCCAUGAGCCAGGAGGCCCGGCUGGGCAUCAAGCCACACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCAGUGCAGGAUCUGCGGGAGGUGAACAAGCGGGUGGAAGAUAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCUCCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGUCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACUUGGACCAGGCUGCCUCAGGGCUUUAAGAAUUCCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGAUUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACCCGCGCUCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGGUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACACCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCUGGAACCCUGUUUAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGGCCCUGGAGGAGACCCGUGGCCUACCUGUCUAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACAAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCUGUGGAGGCCCUGGUGAAGCAGCCUCCCGACCGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACAGAUCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGAAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGAGAGGCUGGCUGACUAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGCCUGAGCAUUAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCUCCAAGAGGACAGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGCGCAAGGUGUGA
430	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCUAGCGGCGGCAGCAGCGGCGGGAGCAGCACUCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAAGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCUCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUAUCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACAGACCCGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACAAGCCAGCCACUGUUCGCCUUCGAGUGGAGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUCACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCAACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUUCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACACCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCACUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCUCCCUGUCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCUCUGCCUGAAGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAAGGACAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCAUGGCGAGAUCUAUAGGCGGAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCUCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCAGACGGGAGCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
431	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGAAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGAAGCUCCGGCGGCUCUAGCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAACAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUUCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGAGUCCCUGGAACACCCCUCUGCUGCCUGUGAAGAAGCCAGGCACCAAUGACUACAGGCCUGUGCAGGAUCUGCGCGAGGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCAAACCCUUACAACCUGCUGUCCGGCCUGCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAGAAUUCCCCCACCCUGUUCAACGAAGCCCUGCACAGGGACCUGGCCGAUUUCCGGAUCCAGCACCCUGACCUGAUUCUGCUGCAGUAUGUGGAUGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGAUAUAGGGCCAGCGCCAAGAAAGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCAAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGAGAGAGUUCCUGGGCAAAGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUUGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGCCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCCAACGCCAGAAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUUGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAAACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGGUAUGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGACGCAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAAACCCCCGACACCUCAACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGAAAGGUGUGA
432	AGCGGAGGCUCCAGCGGCGGCAGCUCCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAAUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUUCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACAAGCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACAUGGACCCGCCUGCCCCAGGGCUUUAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUAUGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACUCGGGCCCUGCUGCAGACACUGGGCAAUCUGGGCUACAGGGCUUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGGUUCUGCAGACUGUUCAUCCCUGGCUUCGCCGAGAUGGCUGCCCCCCUGUACCCACUGACCAAGCCCGGCACCCUGUUUAAUUGGGGCCCAGACCAGCAGAAGGCCUACCAGGAAAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACAAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGCGGAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGAUGCCGAUCACACCUGGUACACAGACGGCUCCAGCCUGCUGCAGGAGGGGCAGAGAAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGCGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCACUGCUGAAGGCCCUGUUCCUGCCAAAACGCCUGUCUAUUAUCCACUGCCCGGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGAUACCAGCACCCUGCUGAUCGAGAAUUCCAGUCCAAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUAA
433	UCUGGCGGCAGCAGCGGCGGCAGCAGCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCUAAUCCCUACAACCUGCUGAGCGGCCUGCCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGACAGCUGACCUGGACCCGGCUGCCCCAGGGAUUCAAGAACAGCCCAACACUGUUUAACGAGGCCCUGCACCGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGAUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCUAAGACCCCCAGACAGCUGAGAGAGUUUCUGGGAAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAACCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCCUGGAGAAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCAUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGAUAGAUGGCUGUCCAACGCCCGGAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACUUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGACUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGACGCAGAGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGACUGUCUAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCUAAGAAGAAGCGCAAGGUGUGA
434	AGCGGCGGCUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCUGGCACCUCCGAGAGCGCCACACCCGAGUCCAGCGGCGGCAGCAGCGGCGGCUCCUCUACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAACAGUACCCCAUGUCCCAGGAGGCCCGCCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGUCAGUCUCCUUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAAUCCAUACAACCUGCUGAGCGGCCUGCCACCAUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCUGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCUCAGGGCUUUAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACAGAGAUCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACAAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCAACCCCCAAGACCCCCCGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCCGGAUUCGCCGAGAUGGCCGCCCCUCUGUAUCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAACUGGGCCCCUGGCGGCGCCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCUAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCUAACGCCAGAAUGACUCACUACCAGGCCCUGCUGCUGGACACCGAUCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCAGCCACACUGCUGCCACUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACUUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCUAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAAAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACUCCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUAUCGGAGGAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAACGCCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGAGGACAGCCGACGGCUCCGAGUUCGAGCCUAAGAAGAAAAGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
435	AGCGGCGGGUCCUCCGGCGGCUCCAGCGGCUCUGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGUCCAGCGGCGGCUCCUCCGGCGGAAGCUCCACCCUGAAUAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUUCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACACCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUAUAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGAGGGUGGAGGACAUCCAUCCUACCGUGCCUAAUCCCUACAAUCUGCUGUCUGGACUGCCUCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGCCUGCACCCAACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGAUCCUGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGAUUCAAGAAUAGCCCCACACUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGACUUCAGAAUCCAGCAUCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGAACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAAGAGACCGUGAUGGGCCAGCCCACCCCAAAGACCCCUCGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACAGCCCCCGCCCUGGGACUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCAGGAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUUGGCCCCGUGGUGGCCCUGAAUCCCGCCACACUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACAAGCGCCCAGAGGGCCGAGCUGAUUGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUUCACGGCGAGAUCUACAGGAGAAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCUAGGAAGGCCGCCAUCACCGAAACCCCCGACACCAGCACACUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCUAAGAAGAAGAGGAAGGUGUGA
436	UCCGGAGGCAGCUCUGGCGGCAGCAGCGGAAGCGAGACCCCCGGCACCAGCGAGAGCGCCACACCCGAGUCUAGCGGCGGCAGCAGCGGCGGCAGCUCCACCCUGAAUAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGAUGUGUCUCUGGGCAGCACCUGGCUGAGCGAUUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCUCUGAUUAUCCCACUGAAGGCCACCUCCACCCCUGUGAGCAUCAAGCAGUAUCCCAUGUCCCAGGAGGCCCGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCAGGCACCAACGACUACAGACCCGUGCAGGAUCUGCGCGAGGUGAACAAGAGAGUGGAGGAUAUCCACCCCACCGUGCCAAACCCAUACAACCUGCUGAGCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCUACCUCUCAGCCACUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAAUAGCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACACUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCAAGACAGCUGAGGGAGUUCCUGGGAAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAACCCGGCACCCUGUUCAAUUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGAAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCUGACAGAUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAAACCGAGGUCAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGUAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGAGCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGAAACCGGAUGGCCGAUCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCUAGCCCAAGCGGCGGCAGCAAGAGAACCGCCGACGGGUCCGAGUUCGAGCCAAAGAAGAAGAGAAAGGUGUGA
437	AGCGGCGGCUCUAGCGGCGGCAGCAGCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUAUAGACUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUUAAGCAGUACCCUAUGUCACAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCCUAUAACCUGCUGUCUGGCCUGCCUCCCAGCCACCAGUGGUACACAGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCUGGGCAGCUGACCUGGACCCGCCUGCCUCAGGGCUUCAAGAACUCCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUCCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACACGGGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUACCGCGCCAGCGCCAAGAAGGCUCAGAUCUGUCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCUAAGACCCCCAGGCAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACAAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGGCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGAAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCUCCCUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCUAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGACCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACAAGGCCUGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUCGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACUCAGCCGAGGCCCGGGGAAAUAGAAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAAAACAGCUCCCCCAGCGGCGGCAGCAAGAGGACCGCCGAUGGCAGCGAGUUCGAGCCCAAAAAGAAGAGGAAGGUGUGA
438	UCCGGGGGCUCCAGCGGCGGGUCCUCCGGCUCCGAGACCCCUGGCACAUCUGAGAGCGCCACCCCCGAGUCCUCCGGCGGCAGCAGCGGCGGCUCUAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCAGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGUCAGUCUCCUUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCCGGCACCAACGACUACCGGCCAGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAAUCCUUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAAAACUCCCCUACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACACUGGGCAAUCUGGGCUACAGGGCCUCCGCUAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACUCCAAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAAAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGACCCUGGCGGAGGCCCGUGGCCUAUCUGUCCAAGAAGCUGGAUCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGGCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAAUGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAAGCCCACGGCACCCGCCCCGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACUAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGACUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCUCCGGGGGCAGCAAGAGAACAGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGCGCAAGGUGUGA

SEQ ID NO.	SEQUENCE
439	UCCGGCGGCAGCUCUGGCGGCAGCUCCGGCAGCGAAACCCCAGGCACCAGCGAGAGCGCUACCCCCGAGAGCUCCGGCGGCUCCAGCGGCGGCAGCUCAACACUGAACAUCGAGGACGAGUAUCGGCUGCACGAGACAAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGAGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAAUGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGACAUUCACCCCACCGUGCCUAACCCCUACAACCUGCUGAGCGGGCUGCCCCCCUCCCACCAGUGGUAUACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACAUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGACUUCAGAAUUCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACUCCCCGGCAGCUGAGAGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUUAUCCCAGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACUCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAAAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCACUGGUGAUCCUGGCCCCCACGCAGUGGAGGCCCUGGUGAAGCAGCCCCCGACAGGUGGCUGAGCAACGCCAGAAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGAUAUUCUGGCCGAGGCCCACGGCACCCGCCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUUUACCGGAGAAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGGCUGUCCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACAGGAUGGCCGAUCAGGCCGCCAGAAAAGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAAUAGCUCCCCAUCCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGAAAGGUGUGA
440	UCCGGCGGCAGCAGCGGCGGCUCUAGCGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCUCUUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAAACAAGCAAGGAGCCAGACGUGUCCCUGGGGAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGAGGCAUGGGACUGGCCGUGCGGCAGGCCCCCUGAUCAUCCCCCUGAAAGCCACCUCCACCCCAGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCAUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACCGGCCUGUGCAGGACCUGCGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGAGCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACAAGCCAGCCUCUGUUCGCCUUUGAGUGGAGAGACCCCGAGAUGGGCAUUUCCGGCCAGCUGACCUGGACCCGCCUGCCACAGGGCUUUAAGAAUAGCCCCACACUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACACUGGGAAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCUACCCCCAAGACCCCUAGGCAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCAGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGGUCUAGCCUGCUGCAGGAAGGCCAGAGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGGAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUAGAAGGCGCGGCUGGCUGACCUCCGAGGGCAAGGAAAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCAGGCCAUCAGAAGGGCCACAGCGCAGAGGCCCGCGGAAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAAUAGCAGCCCCAGCGGCGGCAGCAAGAGAACCGCCGAUGGCAGCGAGUUCGAGCCUAAGAAGAAGCGGAAGGUGUGA
441	UCCGGCGGCAGCAGCGGCGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCUCCUCCGGCGGCUCUUCCACACUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGAGCCAGGAGGCCCGGCUGGGCAUCAAGCCUCACAUCCAGCGCCUGCUGGACCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACACCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACCGGCCCGUGCAGGAUCUGAGGGAGGUGAAUAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGAGCGGCCUGCCCCCCAGCCACCAGUGGUACACAGUGCUGGAUCUGAAGGACGCCUUCUUUUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAAAAUAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGACAGCUGAGGGAGUUCCUGGGCAAGGCAGGCUUCUGUAGGCUGUUCAUCCCCGGAUUUGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCUGAUCUGACAAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCCUGGAGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCUAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCUCCCGACAGAUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGAUGGAUCUAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGCGCGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAAUGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGACGGAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACUCCUGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGCAAGGUGUGA
442	UCCGGCGGCAGCAGCGGCGGCUCUUCCGGCAGCGAGACCCCAGGCACCUCCGAGAGCGCCACCCCAGAGUCCAGCGGCGGCUCCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCAGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCCCAGGCCUGGGCCGAGACUGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCUGAUCAUCCCACUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUUAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUAUAGACCCGUGCAGGACCUGAGAGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACCGUGCCAAACCCUUACAACCUGCUGAGCGGCCUGCCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCAGACUGCCUCAGGGCUUCAAGAACUCACCCACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUUAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACAAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACACCUAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCACUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAACUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGACGCCCAGUGGCCUAUCUGUCCAAGAAGCUGGAUCCCGUGGCCGCUGGAUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGAUACCGACAGAGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAAGGCCAGCGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGAACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAACUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACUAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGACUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACACCAGACACCAGCACCCUGCUGAUCGAGAAUAGCUCCCCCUCCGGCGGCAGCAAGAGGACUGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGAAAGGUGUGA

SEQ ID NO.	SEQUENCE
443	AGCGGCGGAAGCAGCGGGGGCAGCAGCGGAUCUGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUUAUUCCUCUGAAGGCCACAAGCACCCCCGUGUCUAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUUCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCUCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGGACCAACGACUACAGACCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAAUCUGCUGAGCGGCCUGCCACCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACACUGGGCAAUCUGGGCUAUCGCGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGGCAGCCUACACCCAAGACCCCUAGACAGCUGCGCGAGUUCCUGGGAAAGGCCGGCUUCUGCAGACUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACUAAGCCAGGCACACUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCUCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGACGGCCCGUGGCCUACCUGAGCAAGAAGCUGGAUCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCUGACAGAUGGCUGUCCAACGCCAGGAUGACCCAUUACCAGGCCCUGCUGCUGGACACCGACCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCUGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGAUAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGGUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAAUCGGAUGGCCGAUCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCUCUACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCAGCAAGAGAACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGAAAGGUGUGA
444	AGCGGCGGCAGCAGCGGCGGCAGCUCCGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGCUCUGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCUCCACUUGGCUGUCCGAUUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCCCUGAAAGCCACCUCCACACCCGUGUCCAUUAAGCAGUACCCUAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUACAGAGACUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGAGCCCUUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCUGGCACCAAUGACUACCGCCCCGUGCAGGACCUGAGAGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCUUACAAUCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCAUAGAGACCUCGCCGACUUUCGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCUCUGCUGCAGACCCUGGGCAACCUGGGCUACCGCGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCGGCAGCUGCGGGAGUUUCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAAUUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGUCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGCGGAGACCCGUGGCCUACCUGUCUAAAAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCUUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAAGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCCGCAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGCCCUGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGAUACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCUCCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUGUGA
445	AGCGGCGGCAGCUCCGGCGGCUCCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCUCCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCUGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAUCCACACCCGUGUCCAUCAAGCAGUACCCUAUGUCUCAGGAGGCCAGACUGGGCAUUAAACCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCUCCCUGGAAUACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGAGAGUGGAGGACAUCCACCCAACCGUGCCAAACCCAUAUAACCUGCUGUCUGGCCUGCCACCUUCCCACCAGUGGUACACCGUGCUGGACCUGAAAGACGCCUUCUUCUGCCUGCGGCUCCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCUCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAAGCCCUGCACAGGGAUCUGGCCGACUUUAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAACUGGAUUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAAGAGACAGUGAUGGGCCAGCCCACACCCAAGACCCCAAGACAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCUGGAUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACAAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGAAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCUCCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGUCCAGGCCACCAGAAGGGCCAUUCCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACAGAGACCCCCGACACCUCUACACUGCUGAUCGAGAACAGUAGCCCUAGCGGCGGAAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGAAAGGUGUGA
446	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCAGCGGCGGCAGCUCUACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGAGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCUCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGCAUUAAGCCACACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGAUUAGCGGGCAGCUGACCUGGACCAGACUGCCUCAGGGCUUCAAAAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAAGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCAAGGCAGCUGAGGGAGUUUCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCCGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACAAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCCGUGGCCUACCUGUCUAAAAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCAUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACAAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCUCCUCUCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCAGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAACGUGUAUACCGAUUCUAGGUAUGCCUUCGCCACCGCCCAUAUCCACGGCGAGAUCUACAGAAGAAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGGCUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCUCUGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
447	UCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUGUGA
448	UCUGGCGGCAGCUCUGGCGGUUCCAGCGGGUCCGAGACCCCUGGAACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCUGACGUGAGUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCUUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCGGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUAUCGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCUUACAACCUCCUGUCAGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUAUCCCCUGACCAAGCCUGGCACCCUGUUCAAUUGGGGGCCAGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUUAUACACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGGAGCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA
449	AGCGGCGGGAGCUCUGGUGGCAGCUCUGGGAGCGAGACUCCUGGCACCAGCGAGUCCGCCACCCCAGAGAGCUCUGGGGGAAGCUCAGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACUCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCCGGCCUGCCUCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCAUCCCACAUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUCAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCUCCGCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCAGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGUAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
450	AGCGGGGGGUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCUAGCGGCGGCUCCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGAGCGACUUUCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCUGUGCGGCAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGCCCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAAUCCUUACAACCUGCUGAGCGGCCUGCCACCCAGCCAUCAGUGGUACACGGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCUCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGGAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGCCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGGUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCUCCACCCUGCUCAUCGAGAACAGCUCCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
451	UCUGGGGGAAGCAGCGGCGGCAGCAGCGGCUCAGAGACACCGGGCACCAGCGAGUCUGCCACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGGAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCAGGUCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGCGCGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUAUCUGGGCUAUCUGCUGAAGGAGGGCCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUCAUUCCUGGCUUCGCUGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUCCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACACUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
452	UCAGGGGGAUCCAGCGGGGGCUCCUCCGGCUCUGAGACUCCCGGGACUAGCGAGAGCGCUACUCCCGAGAGCUCAGGGGGAAGCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACAGGCCUGUGCAGGAUCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCAAAUCCUUACAACCUGCUGUCCGGCCUGCCUCCUUCACACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGAUCUCAGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCCUGUCUGCGGAUGGUGGCUGCUAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCUGAGGCUCGGGGGAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACUGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
453	UCCGGCGGCUCCAGCGGCGGCAGCUCCGGGUCCGAGACCCCUGGGACCAGCGAGUCUGCCACCCCUGAGAGCUCCGGCGGCUCCUCUGGGGGAAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUCCACGAGACCAGCAAGGAGCCUGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGCCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCGGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAAUCCCUACAACCUGCUGAGCGGCCUGCCCCCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCUGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGAUGACCUGCUGCUGGCAGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGGUGGCUGACCGAGGCACGGAAGGAGACCGUGAUGGGUCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUCGGCAAGGCCGGGUUCUGCAGGCUGUUCAUCCCCGGCUUUGCCGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUCCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACGGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCUGGAGCCGCCGUGACCACCGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCUGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA
454	UCUGGGGGGAGCUCCGGAGGGAGCUCCGGGUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGAGCAGCGGGGGCAGCAGCGGCGGCAGCUCCACCCUCAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCAGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAAUCCCUACAACCUGCUGUCUGGCCUGCCCCCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGACAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUCCUCCUGGCCGCCACCUCUGAGCUCGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCACGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAAUUGGGGUCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACUCAGAAGCUGGGGCCCUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUCAGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUCGCCGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
455	AGCGGGGGCAGCUCCGGCGGCUCCUCUGGCAGCGAGACUCCCGGGACUAGCGAGAGCGCUACCCCCGAGAGCUCUGGGGGCUCCAGCGGCGGGAGCUCCACCCUCAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCGCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGUCCUUGGAGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUCAGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCACACGGACCAGGCCCGACCUGACAGACCAGCCCCUGCCAGACGCUGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCUCUCCCAGCGGGGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
456	AGCGGCGGCUCCAGCGGGGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGUCAGCCACCCCUGAGAGCUCCGGGGGCUCCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACCGUGCCUAAUCCUUACAACCUGCUGAGCGGCCUGCCUCCCAGCCAUCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUCUUUUGCCUGAGACUGCAUCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGAUGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCAGGCUGUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGGCCGGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUUUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCUGUCUGAGGAUGGUGGCUGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUCACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCUCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCAGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGGACCAGCGCCCAGCGGGCAGAGCUGAUUGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCUCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGGCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCGGCCAGAAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACAGCUCUCCCUCUGGCGGGAGCAAGAGAACCGCUGACGGCAGCGAGUUCGAGCCUAAGAAGAAGCGGAAGGUGUGA
457	AGCGGGGGCUCCUCCGGAGGCAGCUCCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCUACUCCCGAGUCCAGCGGCGGGAGUAGCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCCCUCAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCGGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCUCUGGGCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGCCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCAGGGUGGCCUCCAUGCCUGCGGAUGGUGGCCGCGAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGUCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCUACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCCGCUGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCUAGCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCAGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
458	AGCGGCGGGAGCUCUGGGGGCUCCUCUGGCUCCGAGACCCCCGGAACCUCCGAGAGCGCCACUCCGGAGAGCUCCGGGGGCUCCAGCGGCGGCAGCUCUACCUUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUUCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACUCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCUUACAACCUGCUGUCGGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCUACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCGGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACGGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACUAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACUCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGCUAUGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGCCUGAGCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCCGCUGAGGCCCGGGGCAAUAGGAUGGCCGAUCAGGCCGCCAGAAAGGCCGCCAUCACAGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGUUCUAAGAGAACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
459	AGCGGGGGCAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCAGCAGCGGCGGGAGCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUCUCCGACUUCCCACAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUUCCCAAUCCCUACAACCUGCUGUCCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCACUCUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGGCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCUGAGAUGGCUGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACUCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCUUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGAGCAUCAUUCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGUAGCAAGCGCACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
460	AGCGGGGGCAGCUCCGGAGGCUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCUCUGGGGGCUCCAGCACUCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCUGAGACCGGUGGCAUGGGCCUGGCUGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAAUGACUACCGGCCAGUCCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCACCCCACCUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCAGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCUCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCUGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGGUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGGACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACCGGCGCCGCGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGCGGCUGAGCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
461	AGCGGGGGCAGCUCCGGAGGCUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCUCCGGGGGCUCCUCUGGCGGCAGCAGUACUCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGAAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUUCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUCCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGAGCGGGCUGCCGCCCUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGUCCCACACUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGAUCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGAGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCACGGCAGCUGCGCGAGUUCCUGGGAAAGGCCGGCUUCUGCCGGCUGUUCAUCCCAGGAUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGGCCAGAUCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCAGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCUGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCUCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCUCCCUCCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCGGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCUCGGUACGCCUUCGCUACUGCCCACAUCCACGGGGAGAUCUAUCGGCGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCUGCUGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
462	UCCGGGGGCAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCACUGGGGAGCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACCGCCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGAGCGGCUUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCUCCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUUCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACAGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCAGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCUGAUCUGACCGACCAGCCCCUGCCCGACGCAGAUCACACCUGGUACACCGAUGGGUCUAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCCGGGGGGAGCAAGCGGACCGCCGACGGGUCCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
463	AGCGGCGGCAGCAGCGGCGGCUCCAGCGGCAGCGAGACCCCAGGGACCAGCGAGAGCGCCACCCCCGAGAGCUCUGGCGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGAGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACUGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCCCUGUUCGCAUUCGAGUGGCGGGAUCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCUGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUCACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGCCUGCAGCACAACUGUCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCAGACCUGACCGAUCAGCCUCUGCCCGAUGCCGACCACACCUGGUACACGGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCAGCCGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCAAGGAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
464	AGCGGGGGGAGCUCCGGCGGCUCCUCCGGGAGCGAGACUCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGGAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUCAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCUACGCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAAUUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCGGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCAGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA
465	UCAGGGGGGAGCAGCGGGGGGUCCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCUGAGAGCUCCGGGGGCUCCAGCGGGGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGGCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGUACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGAGCGGCCUGCCUCCCUCCCACCAGUGGUACACAGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCUACCAGCCAGCCACUGUUUGCCUUUGAGUGGAGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGGUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUCCUGGGGAAGGCUGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACGGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCACGGGGAGAUCUACCGGCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCAAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGCGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
466	AGCGGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGAGCUCUGGGGGGAGCUCCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGAGCGGGCUGCCGCCCUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCCGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCCGGCCUGAUCUGACCGAUCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCACGGGGAGAUCUACCGGCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCUCUGUUUCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGUUCUAAGAGAACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
467	AGCGGCGGGUCUAGCGGCGGGAGCUCCGGCAGCGAGACCCCAGGCACCAGCGAGUCCGCCACCCCCGAGUCUAGCGGCGGCAGCUCUGGGGGAAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAAUGAUUACAGGCCCGUGCAGGACCUCAGAGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCACUGUUUGCCUUCGAGUGGAGGGAUCCCGAGAUGGGCAUCAGUGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACUAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCUUCAGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUAUCUGGGCUAUCUGCUGAAGGAGGGGCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUCUUCAUUCCUGGCUUCGCAGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCGGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUAGCCUGCUGCAGGAGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUUCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCUAAGAAGAAGCGGAAGGUGUGA
468	AGCGGGGGCAGCUCCGGGGGAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGUCUGCCACCCCCGAGAGCUCUGGGGGAAGCAGCGGUGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUCCACGAGACCUCCAAGGAGCCUGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCUUGGGCCGAGACAGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAAGCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUAUCGCCCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGGCUGCCACCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGUCUGCGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAAUGGCGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACAUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCAGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCAGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUAUGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGGUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUAGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACCGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUCCUGCUGGACACAGACAGGGUGCAGUUCGGGCCAGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCAUGGCACCCGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGGACCAGCGCCCAGCGGGCAGAGCUGAUUGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACGGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGAGCAUCAUCCACUGCCCUGGGCACCAGAAGGGCCACUCAGCAGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCGGCCAGGAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
469	AGCGGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGGACCAGCGAGUCAGCCACUCCCGAGAGCUCCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUCGGGAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUCAUCAUCCCUCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCGGGCACCAAUGAUUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACCGUGCCCAAUCCUUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGACAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCGGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUCCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCUCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACGCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCCGGUAUGCCUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGAACCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACGGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
470	AGCGGAGGCAGCUCCGGGGGAAGCAGCGGCAGCGAGACCCCAGGGACCUCUGAGUCCGCCACCCCCGAGAGCAGCGGGGGAGCAGCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCAGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCUGAGACCGGCGGCAUGGGACUGGCAGUGCGCCAGGCUCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCAAUGAGCCAGGAGGCUCGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUCAAGAAGCCCGGGACCAACGACUACAGGCCAGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCUGGCCUGCCCCCCAGCCAUCAGUGGUACACGGUGCUGGAUCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAACCUGGGCUAUAGGGCCUCUGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUCGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGCACCCUGUUCAACUGGGGGCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUCCUGCUGGACACAGACAGAGUGCAGUUCGGGCCAGUGGUGGCCCUGAACCCUGCCACUCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCUCUGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACUCCCGGUACGCAUUCGCUACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGGCUGAGCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCAGCAGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGCAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
471	UCCGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGGACCAGCGAGAGUGCUACCCCAGAGAGCUCCGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGGAGCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCGGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGACUGCACCCUACCUCUCAGCCUCUGUUUGCCUUCGAGUGGAGGGAUCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGCCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCUGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGCCCUGUGGCCUAUCUCAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCUCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUCCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACAGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCGAAGGCUCUGCCCGCUGGGACCAGCGCCCAGCGGGCAGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACUGCCCACAUCCACGGCGAGAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGCGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGAAUCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCUAAGAAGAAGCGGAAGGUGUGA
472	AGCGGCGGGAGCUCCGGCGGCAGCUCCGGGAGCGAGACUCCUGGCACCAGCGAGUCCGCCACUCCCGAGAGCUCCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUCUCCGACUUCCCACAGGCCUGGGCCGAGACCGGGGGCAUGGGGCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCUCCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACCGGCCCGUGCAGGACCUGCGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGUGGCUUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCUCGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACUCCCCGGCAGCUGCGGGAGUUCUUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUUCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUCUUCAACUGGGGCCCAGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGCCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGGAAGCUGACCAUGGGGCAGCCCCUGGUCAUCCUGGCGCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACCGAUCAGCCUCUGCCCGACGCUGAUCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUUCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCUGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
473	AGCGGGGGAGCAGCGGGGGGAGCUCAGGGUCUGAGACCCCCGGCACCAGCGAGUCUGCCACCCCUGAGAGCAGCGGGGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUAUCGCCCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCUUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCUAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCUAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACUCCCCGGCAGCUGCGGGAGUUUCUCGGCAAGGCCGGGUUCUGCAGACUGUUCAUCCCCGGCUUUGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCGCUGAAUCCAGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCAGGCCGGACCUGACCGACCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCUGGAGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
474	AGCGGGGGGAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCUACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGUAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCUGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGGAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCGGUCAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUCCCCAAUCCUUACAACCUCCUGUCAGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUUUGGGGAAGGCUGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCGGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUCGACAUCCUGGCCGAGGCCCACGGCACCAGGCCUGAUCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCUGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCCGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCGGCCAUCACCGAGACCCCCGACACCUCCACUCUGCUGAUCGAGAACAGCAGCCCCAGUGGGGGCUCCAAGCGCACUGCCGACGGCAGUGAGUUUGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
475	AGCGGCGGCAGCUCUGGCGGCUCCUCUGGGAGCGAGACCCCUGGCACCAGCGAGUCCGCCACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGGUCCUCCACCCUGAACAUCGAGGACGAGUACCGCCUGCAUGAGACCUCUAAGGAGCCUGACGUGAGUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUUCCCAAUCCCUACAACCUGCUGUCAGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACAUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAGGCUCACGGCACCCGGCCCGACCUGACAGACCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCCGUGACCACCGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCUAAGAAGAAGCGGAAGGUGUGA
476	AGCGGAGGCUCCAGCGGCGGCAGCUCCGGCAGCGAGACUCCAGGGACUAGCGAGUCCGCUACCCCUGAGUCUAGCGGCGGCAGCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCUGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACAGGGGGGAUGGGGCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCACUGAAGGCCACUAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCCGCCUGGGCAUCAAGCCCCAUAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGAUCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCAAAUCCUUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACAGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUUUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCCCUGUACCCUCUGACCAAGCCGGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACAGACAGCCGCUAUGCCUUCGCCACUGCCCACAUCCACGGCGAGAUCUACCGCCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCCGCUGAGGCCCGGGGCAAUAGGAUGGCGGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGCAGCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA
477	AGCGGCGGCUCUAGCGGCGGGAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGUCCGCUACUCCCGAGAGCUCCGGCGGCUCCAGCGGCGGGUCUAGCACUCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCAAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAAUGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCUGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUUAUUCCUGGCUUCGCUGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUAUGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCUGAUCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCUCCAGCCUUCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCGGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGGACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCAGCAGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGACACUAGCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGGGGCUCUAAGCGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
478	UCCGGCGGCUCCUCAGGCGGCUCCUCUGGCAGCGAGACUCCUGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGGAGCACCUGGCUGUCUGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGUCUGGGCUGCCGCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACUUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCAGGCUUUGCAGAGAUGGCAGCCCCCCUGUACCCUCUGACAAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCAUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCCGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACAGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCAGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGAUAGCAGGUACGCAUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
479	AGCGGGGGCAGCUCUGGCGGCUCUUCUGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCAGAGAGCAGUGGCGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGGUCCACCUGGCUGUCCGACUUCCCGCAGGCCUGGGCAGAGACCGGUGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCAGGGACCAAUGACUACCGGCCUGUGCAGGACCUGCGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCAUCCAACCAGCCAGCCGCUGUUUGCCUUCGAGUGGAGAGAUCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUCGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUCUUGGGGAAGGCCGGCUUCUGCAGGUUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUAUGCCAAGGGGGUGCUGACCCAGAAGCUGGGGCCAUGGAGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUCAAGCAGCCACCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGGCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCUCACGGCACCAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCAGAGCUGAUUGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGAGCAUCAUUCACUGCCCUGGGCACCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCAAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCAAAGAAGAAGAGGAAGGUGUGA
480	AGCGGUGGCUCUUCAGGGGGAUCCAGUGGCAGCGAGACACCCGGCACCUCUGAGUCUGCUACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGUAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCGGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGGCUGGCCGUGCGCCAGGCUCCACUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAACAGUACCCUAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGGAUUCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCUGGCACCAACGACUAUAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACAGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGGCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUCGCCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCAAGGGGGAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCUCCACUCUUCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
481	UCCGGGGGGAGCAGCGGGGGGAGUUCCGGGAGCGAGACUCCCGGGACUAGCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCAGCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUCAGACAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCCUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCGGACUUCAGGAUCCAGCACCCAGAUCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCGGACCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCAGCUCCCUCCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCUCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGGGGCAGCAAGAGGACCGCUGACGGCAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
482	AGCGGGGGGUCCUCAGGGGGCAGCUCAGGCUCUGAGACCCCCGGCACCAGCGAGAGUGCUACCCCAGAGAGCAGCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGGAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCUGAGACCGGAGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCGGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUUCCCAAUCCCUACAACCUGCUGUCCGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGGUACCUGCUGAAGGAGGGGCAGCGGUGGCUGACCGAGGCACGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCUCUGUACCCACUGACCAAGCCGGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCAGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCUGGGACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCAAGGGGGAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAGGUGUGA

SEQ ID NO.	SEQUENCE
483	UCCGGGGGGAGCAGCGGGGGCAGCUCCGGCAGCGAGACCCCCGGAACCUCUGAGAGCGCCACUCCAGAGAGUUCCGGCGGGUCCAGCGGCGGGAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUCAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGUCCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGUCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAAUGACUAUAGGCCUGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCCUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUCAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUCAGGGAGUUUCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCCCUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCCUGGCGCAGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCAGCAGGGUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGGCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCGCCUGAUAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCUGAGGAGGGGCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGAUCUGACCGAUCAGCCUCUGCCCGAUGCCGACCACACCUGGUAUACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCUGCCCAGCGGGCAGAGCUGAUCGCCCUGACUCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCCGCUGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCCCGCAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGCGGAAGGUGUGA
484	AGCGGCGGCUCAUCUGGCGGCAGCAGCGGCUCCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCUAGCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCUGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCCGAAACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGAUCAGGGAAUCCUGGUGCCUUGUCAGAGCCCUUGGAACACCCCUCUGCUGCCUGUGAAGAAACCAGGAACCAACGACUACAGACCAGUGCAGGACCUGAGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCAGGCCUGCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGCCUGAGACUGCACCCCACUAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGACUGCCACAGGGCUUCAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUAUCCACUGACCAAGCCCGGCACCCUGUUUAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCUCCAUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGAUAGGUGGCUGUCUAACGCCAGGAUGACCCAUUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAAUCCCGCCACACUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACAGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCUCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCUCCGAAGGCAAAGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGGCUGUCUAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCUAUUACCGAGACCCCUGACACCUCCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
485	UCCGGGGGAAGCAGCGGCGGCAGCAGCGGCUCAGAGACCCCCGGCACAUCCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAAUAUCGAGGACGAGUACAGACUGCACGAGACAAGCAAGGAACCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAACAGUACCCUAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCUUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCAAGCCACCAGUGGUACACAGUGCUGGACCUGAAAGACGCUUUCUUCUGCCUGAGGCUGCACCCAACAAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCUCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGCAUCCAGCAUCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGACAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGUCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACCAAACCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCACUGGGCCUGCCAGACCUGACCAAGCCCUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCUAAUGCCAGGAUGACACACUACCAGGCCCUGCUGCUGGAUACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAAGCCCACGGCACCAGACCUGACCUGACCGACCAGCCACUGCCUGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGAGCCGAGCUCAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACAAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGGCAUAGCGCCGAGGCCCGCGGCAACCGCAUGGCCGACCAGGCCGCCAGGAAGGCAGCCAUCACAGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCUGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
486	AGCGGCGGCAGCUCCGGCGGCAGCUCCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCUGGCGGCUCCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCAGACGUGUCCCUGGGCUCAACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCUCUGAAAGCCACAUCUACCCCUGUGUCCAUCAAGCAGUACCCAAUGUCACAGGAGGCCCGGCUGGGCAUCAAGCCACACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAACCUGGCACCAACGACUACAGACCCGUGCAGGACCUGCGCGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCAAGCCACCAGUGGUAUACCGUGCUGGACCUGAAGGACGCCUUCUUUUGCCUGAGGCUGCACCCUACCUCUCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCCGGCUGCCACAGGGCUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUUUGCAGGCUGUUCAUCCCAGGCUUUGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACUAAGCCUGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGAUGAAAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGUCCAAAAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAAGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGGUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGAAGGGGCUGGCUGACUAGCGAGGGCAAGGAGAUUAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUUAUCCAUUGCCCAGGCCACCAGAAGGGCCACUCCGCCGAAGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACCCCCGACACCUCUACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
487	AGCGGCGGCUCCUCCGGCGGCAGCAGCGGGUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGUUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGUACCUGGCUGAGCGACUUUCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCUGAUCAUCCCACUGAAAGCCACCAGCACCCCAGUGUCCAUCAAGCAGUAUCCUAUGUCCCAGGAGGCCCGCCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGUCACCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAACGAUUACAGACCAGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGAUAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUCCCACCAGUGGUACACUGUGCUGGACCUGAAGGACGCCUUCUUUUGCCUGCGGCUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGAGAGAUCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGACAGCUGAGGGAGUUUCUGGGCAAGGCCGGCUUCUGUAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCUGUACCCUCUGACCAAGCCCGGCACACUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACUGCCCCAGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGGCCUUGGCGGCGCCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGAGCAACGCCCGCAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCUCUCAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCAGGUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAAAGACUGUCUAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUCCUGAUCGAGAACAGCUCUCCAAGCGGAGGCAGCAAGAGAACAGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
488	AGCGGGGGCUCUAGCGGCGGCAGCAGCGGGUCUGAGACCCCUGGGACCAGCGAGUCCGCCACCCCCGAGUCCUCUGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGAUGUGAGCCUGGGGUCCACCUGGCUGUCUGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACACCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUCCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCAUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGCACAAACGAUUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCUGGCCUGCCACCCUCCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUUGAGUGGCGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGAAUCCAGCACCCUGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGGUUCUGCAGACUGUUCAUUCCCGGCUUUGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGAAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACAAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCCGCAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUCGCCGAGGCCCAUGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCUCUGCUGCAGGAGGGCCAGAGGAAGGCUGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCUCUGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGUCCAGGCCACCAGAAGGGCCAUAGCGCCGAGGCCAGAGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAAUUCCAGCCCCUCCGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
489	AGCGGCGGCUCCAGCGGCGGCUCCAGCGGAUCCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGGGGCAGCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGACUGGGCAUCAAGCCCCAUAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACCGGCCCGUGCAGGAUCUGCGCGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACAGUGCCCAAUCCUUACAACCUGCUGAGCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCUACCAGCCAGCCACUGUUUGCCUUCGAAUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCUACUCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUUAGAAUCCAGCACCCAGACCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCUCCCCUGUACCCUCUGACCAAGCCUGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACAGCCCCAGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGACGGCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUUGCCGUGCUGACCAAAGAUGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCAUGCCGUGGAGGCCCUGGUCAAGCAGCCUCCCGAUAGAUGGCUGUCCAACGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGAUCACACUUGGUACACAGACGGCAGCUCUCUGCUGCAGGAGGGACAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCAUAUCCACGGAGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCUUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCUCCAAGCGCACAGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
490	UCCGGCGGCUCUUCCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACUAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCUCCUCUACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCUGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGGAUCAAGCCUCACAUUCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCUUGUCAGAGCCCCUGGAACACUCCCCUGCUGCCAGUCAAGAAGCCCGGCACCAACGACUACAGACCCGUGCAGGAUCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGCGAGACCCCGAAAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACCGGGAUCUGGCCGACUUCAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACAAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAACCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCUAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGACGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACGAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGUCUGGAUAUCCUGGCCGAGGCUCACGGCACCAGGCCAGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGGAGCUCCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGAGCCGCCGUGACCACCGAGACAGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
491	UCCGGAGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACCAGCGAGAGCGCCACCCCAGAGUCCAGCGGAGGCUCUAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACUUCCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGAGCGAUUUUCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGGCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCUCAGGAGGCCCGCCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCAGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAAUCCAUACAACCUGCUGAGCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACUCUCCUACCCUGUUCAACGAGGCCCUGCAUCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGGUAUCGCGCCAGCGCCAAGAAGGCUCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACCCCCAGACAGCUGAGAGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUCACCCAGAAGCUGGGCCCUUGGAGAAGGCCAGUGGCCUACCUGUCCAAGAAACUGGACCCAGUGGCCGCCGGCUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUCGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUAGAGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUUGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUAUACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGACGGAGGGGCUGGCUGACCUCUGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAAGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAAACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
492	AGCGGCGGCUCCAGCGGCGGCAGCAGCGGGUCCGAGACCCCUGGCACCUCCGAGUCCGCCACCCCCGAGAGCUCCGGAGGCAGCAGCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCUAUGUCUCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCUGGCACAAACGACUACAGGCCAGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGCCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACUAGACUGCCCCAGGGAUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGGAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCUCCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAAACCGUGAUGGGCCAGCCUACACCCAAGACCCCCAGACAGCUGCGGGAGUUUCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCCGACCUGACCAAACCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCAGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCCUGUCUGAGAAUGGUGGCUGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCUGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGAUCCUCCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAAUGUGUACACCGACAGCCGGUAUGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCAAAGAGAACAGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
493	UCCGGCGGCAGCAGCGGAGGCAGCAGCGGCUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGAAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
494	AGCGGAGGCAGCUCCGGCGGCAGCAGCGGCAGCGAGACCCCAGGCACCAGCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAAUAUCGAGGACGAGUAUCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUUCCCCAGGCAUGGGCUGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGAUUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCAUACAACCUGCUGUCUGGCCUGCCUCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGGCUGCCCCAGGGCUUCAAGAAUAGCCCAACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACAAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCAGCUAAGAAAGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGGUGGCUGACAGAGGCCCGCAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCCGGCAGCUGAGAGAGUUCCUGGGCAAGGCCGGAUUCUGCAGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCACUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAAAAGCAGGGCUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGACCCGUGGCCUAUCUGUCCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCUCCCGACAGAUGGCUGUCUAACGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAAUUGCCUGGAUAUCCUGGCCGAGGCCCACGGGACACGGCCAGACCUGACCGAUCAGCCACUGCCCGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACUACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGGAAGAAGCUGAAUGUGUACACCGACUCUAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGCAGCAAGAGGACCGCCGACGGAAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
495	AGCGGCGGCUCCUCAGGCGGCUCCAGCGGCUCCGAGACCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCUCCACUCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUUAAACAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAAUACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACAAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCUAAUCCCUACAACCUGCUGUCCGGGCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCAACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGGACCCCGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCCGCCUGCCUCAGGGCUUCAAGAAUUCCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGAUUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCAGGCUUCGCCGAAAUGGCUGCCCCCCUGUACCCACUGACCAAGCCUGGAACACUGUUCAACUGGGGCCCUGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAACCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGAAGGCCUGUGGCCUACCUGUCUAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCCUGUCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGAUGGCUGAGCAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAAGGCCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACAGAAGUGAUCUGGGCCAAGGCUCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUUGCCACCGCCCACAUCCAUGGCGAGAUCUACCGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGACUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGAAACCGCAUGGCCGACCAGGCUGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACUCUUCCCCCAGCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
496	UCCGGCGGCUCCUCCGGCGGCAGCAGCGGCAGCGAGACUCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGCGGCUCCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAACCAGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUAUCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCAUAUCCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAACCCGGCACCAACGACUACCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCCACCGUGCCUAACCCCUACAACCUGCUGAGCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGAAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGGACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGAUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACACCCAGGCAGCUGAGGGAGUUCCUGGGCAAAGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCAGAUCUGACCAAGCCUUUCGAGCUGUUCGUGGAUGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGAGGAGACCUGUGGCCUACCUGAGCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCACCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAACAGCCCCCCGACAGAUGGCUGUCUAAUGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAAUUGUCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGAUCAGCCCCUGCCAGACGCCGACCACACCUGGUAUACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGAUUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGCGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCAGGCCACCAGAAGGGGCACUCCGCCGAGGCUCGCGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCUGGCGGCUCCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
497	UCUGGCGGCAGCUCCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCUGCCACCCCAGAGAGCUCCGGAGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCAGAGACCGGCGGCAUGGGACUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUAUCCUAUGUCUCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCUGUGAAGAAGCCUGGCACCAACGACUACAGACCAGUGCAGGAUCUGAGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACAAGACUGCCCCAGGGCUUCAAGAACAGUCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGUCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCUCAGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGACCCGUGGCCUACCUGUCAAAGAAGCUGGAUCCAGUGGCCGCCGGCUGGCCACCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCUAACGCCCGCAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAAUUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGAGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUUACCGAGACUCCAGACACCUCCACCCUGCUGAUCGAGAAUUCCUCCCCCAGCGGCGGGAGCAAGAGAACCGCAGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
498	AGCGGAGGCUCCUCCGGCGGCAGCAGCGGGAGCGAGACCCCAGGGACCAGCGAGUCCGCCACCCCAGAGAGCAGCGGCGGAAGCAGCGGCGGCAGCAGCACACUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAAGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCUCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGAACCAACGACUAUCGGCCAGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACAGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUCACACCAGUGGUACACCGUGCUGGACCUGAAAGACGCCUUCUUCUGCCUGAGGCUGCACCCAACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGCCUGUUUAUCCCUGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAACCAGGCACUCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGAGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCCAACGCCAGGAUGACUCACUACCAGGCCCUGCUGCUGGACACCGAUCGCGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAAGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUCACCGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGACGCAGGGGCUGGCUGACCAGCGAGGGUAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAACGGCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCCGGCGGCAGCAAGAGAACCGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
499	UCUGGCGGCAGCAGCGGAGGAAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCCAGCGGCGGCUCCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCAGACGUGUCCCUGGGCUCCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCAGAGACCGGCGGAAUGGGCCUGGCCGUGAGGCAGGCCCCACUCAUCAUCCCCCUCAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAAUCCUUACAACCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCACAGGGCUUCAAGAACUCCCCAACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCCGGAUUCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACAAGCGAGCUGGAUUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACAAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACAAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCAGUGGCCUAUCUGUCCAAGAAGCUGGACCCUGUGGCCGCCGGCUGGCCUCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAACUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCAGUGGAGGCUCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCUAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACACGCCCCGACCUGACCGACCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAACUGAACGUGUACACCGACUCCAGGUAUGCCUUCGCCACCGCCCACAUUCACGGCGAGAUCUACAGGAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGCCCAGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGAAUGGCCGACCAGGCCGCCCGCAAGGCCGCCAUCACCGAGACCCCCGAUACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
500	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCAAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCUUCCGGCGGCUCCAAGAGGACUGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
501	AGCGGCGGAAGCAGCGGCGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCUCCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCUCCACCCCAGUGUCCAUCAAACAGUACCCCAUGAGCCAGGAGGCCCGGCUGGGCAUCAAGCCACACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCAGUGCAGGAUCUGCGGGAGGUGAACAAGCGGGUGGAAGAUAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCUCCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGUCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACUUGGACCAGGCUGCCUCAGGGCUUUAAGAAUUCCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGAUUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACCCGCGCUCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGGUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACACCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCUGGAACCCUGUUUAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGGCCCUGGAGGAGACCCGUGGCCUACCUGUCUAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACAAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCUGUGGAGGCCCUGGUGAAGCAGCCUCCCGACCGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACAGAUCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGAAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGAGAGGCUGGCUGACUAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGCCUGAGCAUUAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCUCCAAGAGGACAGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
502	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCUAGCGGCGGCAGCAGCGGCGGGAGCAGCACUCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAAGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCUCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUAUCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACAGACCCGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACAAGCCAGCCACUGUUCGCCUUCGAGUGGAGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUCACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCAACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUUCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACACCCAGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCACUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCUCCCUGUCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCAGACAGGUGGCUGUCCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCUCUGCCUGAAGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAAGGACAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACCGCCCACAUCCAUGGCGAGAUCUAUAGGCGGAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCUCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCAGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
503	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGAAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGAAGCUCCGGCGGCUCUAGCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAACAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUUCAGAGGCUGCUGGAUCAGGGCAUCCUGGUGCCUUGCCAGAGUCCCUGGAACACCCCUCUGCUGCCUGUGAAGAAGCCAGGCACCAAUGACUACAGGCCUGUGCAGGAUCUGCGCGAGGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCAAACCCUUACAACCUGCUGUCCGGCCUGCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAGAAUUCCCCCACCCUGUUCAACGAAGCCCUGCACAGGGACCUGGCCGAUUUCCGGAUCCAGCACCCUGACCUGAUUCUGCUGCAGUAUGUGGAUGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGAUAUAGGGCCAGCGCCAAGAAAGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCAAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGAGAGAGUUCCUGGGCAAAGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUUGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGCCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCCAACGCCAGAAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUUGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAAACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGGUAUGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGACGCAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAAACCCCCGACACCUCAACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
504	AGCGGAGGCUCCAGCGGCGGCAGCUCCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAAUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUUCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACAAGCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACAUGGACCCGCCUGCCCCAGGGCUUUAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUAUGUGGACGAUCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACUCGGGCCCUGCUGCAGACACUGGGCAAUCUGGGCUACAGGGCUUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGGUUCUGCAGACUGUUCAUCCCUGGCUUCGCCGAGAUGGCUGCCCCCCUGUACCCACUGACCAAGCCCGGCACCCUGUUUAAUUGGGGCCCAGACCAGCAGAAGGCCUACCAGGAAAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACAAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGCGGAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGAUGCCGAUCACACCUGGUACACAGACGGCUCCAGCCUGCUGCAGGAGGGCAGAGAAAGGCCGGCGCCGCCGUGACCACAGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGCGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCACUGCUGAAGGCCCUGUUCCUGCCAAAACGCCUGUCUAUUAUCCACUGCCCGGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGAUACCAGCACCCUGCUGAUCGAGAAUUCCAGUCCAAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
505	UCUGGCGGCAGCAGCGGCGGCAGCAGCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCAGCUCCACACUGAAUAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGAGUGGAGGACAUCCACCCCACCGUGCCUAAUCCCUACAACCUGCUGAGCGGCCUGCCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCUACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGACAGCUGACCUGGACCCGGCUGCCCCAGGGAUUCAAGAACAGCCCAACACUGUUUAACGAGGCCCUGCACCGGGACCUGGCCGACUUCCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGAUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCUAAGACCCCCAGACAGCUGAGAGAGUUUCUGGGAAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAACCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCCUGGAGAAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCAUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGAUAGAUGGCUGUCCAACGCCCGGAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGACCACACUUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACACAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGACUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGACGCAGAGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGACUGUCUAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGGAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
506	AGCGGCGGCUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCUGGCACCUCCGAGAGCGCCACACCCGAGUCCAGCGGCGGCAGCAGCGGCGGCUCCUCUACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAACAGUACCCCAUGUCCCAGGAGGCCCGCCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGUCAGUCUCCUUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAAUCCAUACAACCUGCUGAGCGGCCUGCCACCAUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCUGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCUCAGGGCUUUAAGAACAGCCCUACCCUGUUCAACGAGGCCCUGCACAGAGAUCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGCACAAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCAACCCCCAAGACCCCCCGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUUAUCCCCGGAUUCGCCGAGAUGGCCGCCCCUCUGUAUCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAACUGGGCCCCUGGCGGCGCCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGCGGAUGGUGGCCGCUAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCUAACGCCAGAAUGACUCACUACCAGGCCCUGCUGCUGGACACCGAUCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCAGCCACACUGCUGCCACUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACUUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCUAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAAAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACUCCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUAUCGGAGGAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAACGCCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGAGGACAGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
507	AGCGGCGGGUCCUCCGGCGGCUCCAGCGGCUCUGAGACCCCCGGCACCAGCGAGUCCGCCACCCCCGAGUCCAGCGGCGGCUCCUCCGGCGGAAGCUCCACCCUGAAUAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUUCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACACCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUAUAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGAGGGUGGAGGACAUCCAUCCUACCGUGCCUAAUCCCUACAAUCUGCUGUCUGGACUGCCUCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGCCUGCACCCAACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGAUCCUGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGAUUCAAGAAUAGCCCCACACUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGACUUCAGAAUCCAGCAUCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGACUGCCAGCAGGGAACCCGCGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAAGAGACCGUGAUGGGCCAGCCCACCCCAAAGACCCCUCGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACAGCCCCCGCCCUGGGACUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGAUGGCUGUCCAACGCCAGGAUGACACACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUUGGCCCCGUGGUGGCCCUGAAUCCCGCCACACUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAAGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACAAGCGCCCAGAGGGCCGAGCUGAUUGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUUCACGGCGAGAUCUACAGGAGAAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCUAGGAAGGCCGCCAUCACCGAAACCCCCGACACCAGCACACUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
508	UCCGGAGGCAGCUCUGGCGGCAGCAGCGGAAGCGAGACCCCCGGCACCAGCGAGAGCGCCACACCCGAGUCUAGCGGCGGCAGCAGCGGCGGCAGCUCCACCCUGAAUAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGAUGUGUCUCUGGGCAGCACCUGGCUGAGCGAUUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGACUGGCCGUGCGGCAGGCCCCUCUGAUUAUCCCACUGAAGGCCACCUCCACCCCUGUGAGCAUCAAGCAGUAUCCCAUGUCCCAGGAGGCCCGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCAGGCACCAACGACUACAGACCCGUGCAGGAUCUGCGCGAGGUGAACAAGAGAGUGGAGGAUAUCCACCCCACCGUGCCAAACCCAUACAACCUGCUGAGCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCUACCUCUCAGCCACUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAAUAGCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGUCAGCAGGGCACCAGGGCCCUGCUGCAGACACUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCAAGACAGCUGAGGGAGUUCCUGGGAAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAACCCGGCACCCUGUUCAAUUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGAAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCUGACAGAUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAAACCGAGGUCAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGUAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAAGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGAGCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGAAACCGGAUGGCCGAUCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCUAGCCCAAGCGGCGGCAGCAAGAGAACCGCCGACGGGUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
509	AGCGGCGGCUCUAGCGGCGGCAGCAGCGGCUCCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUAUAGACUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGUCCGACUUUCCACAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUUAAGCAGUACCCUAUGUCACAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCCUAUAACCUGCUGUCUGGCCUGCCUCCCAGCCACCAGUGGUACACAGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCUGGGCAGCUGACCUGGACCCGCCUGCCUCAGGGCUUCAAGAACUCCCCUACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUCCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCCGAGCUGGAUUGCCAGCAGGGCACACGGGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUACCGCGCCAGCGCCAAGAAGGCUCAGAUCUGUCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCUAAGACCCCCAGGCAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACAAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGGCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGAAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGAUCCUGUGGCCGCCGGCUGGCCUCCCUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCUAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGACCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACAAGGCCUGACCUGACCGAUCAGCCCCUGCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUCGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCUGGCCACCAGAAGGGCCACUCAGCCGAGGCCCGGGGAAAUAGAAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAAAACAGCUCCCCCAGCGGCGGCAGCAAGAGGACCGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
510	UCCGGGGGCUCCAGCGGCGGGUCCUCCGGCUCCGAGACCCCUGGCACAUCUGAGAGCGCCACCCCCGAGUCCUCCGGCGGCAGCAGCGGCGGCUCUAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCAGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGUCAGUCUCCUUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCCGGCACCAACGACUACCGGCCAGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAAUCCUUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGACUGCCCCAGGGCUUCAAAAACUCCCCUACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACACUGGGCAAUCUGGGCUACAGGGCCUCCGCUAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACUCCAAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAAAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGACCCUGGCGGAGGCCCGUGGCCUAUCUGUCCAAGAAGCUGGAUCCCGUGGCCGCCGGCUGGCCCCCUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGGCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAAUGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCCCUGCCUGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAAGCCCACGGCACCCGCCCCGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACAGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACUAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGACUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCUCCGGGGGCAGCAAGAGAACAGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
511	UCCGGCGGCAGCUCUGGCGGCAGCUCCGGCAGCGAAACCCCAGGCACCAGCGAGAGCGCUACCCCCGAGAGCUCCGGCGGCUCCAGCGGCGGCAGCUCAACACUGAACAUCGAGGACGAGUAUCGGCUGCACGAGACAAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGAGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGAAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAAUGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGACAUUCACCCCACCGUGCCUAACCCCUACAACCUGCUGAGCGGGCUGCCCCCUCCCACCAGUGGUAUACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACAUCCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGACUUCAGAAUUCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGAUUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACUCCCCGGCAGCUGAGAGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUUAUCCCAGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACUCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUUAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCAGACCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAAAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGAUGGCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCACUGGUGAUCCUGGCCCCCCACGCAGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGAAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACACUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGAUAUUCUGGCCGAGGCCCACGGCACCCGCCCCGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUUUACCGGAGAAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAAAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGGCUGUCCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACUCCGCCGAGGCCCGGGGCAACAGGAUGGCCGAUCAGGCCGCCAGAAAAGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAAUAGCUCCCCAUCCGGCGGCAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
512	UCCGGCGGCAGCAGCGGCGGCUCUAGCGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCUCUUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAAACAAGCAAGGAGCCAGACGUGUCCCUGGGGAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGAGGCAUGGGACUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAAGCCACCUCCACCCCAGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCUUGCCAGAGCCCAUGGAAUACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUACCGGCCUGUGCAGGACCUGCGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGAGCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACAAGCCAGCCUCUGUUCGCCUUUGAGUGGAGAGACCCCGAGAUGGGCAUUUCCGGCCAGCUGACCUGGACCCGCCUGCCACAGGGCUUUAAGAAUAGCCCCACACUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACACUGGGAAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCUACCCCCAAGACCCCUAGGCAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGGCUGCCAGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGAGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGAUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCCCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGGUCUAGCCUGCUGCAGGAAGGCCAGAGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGGAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUAGAAGGCGCGGCUGGCUGACCUCCGAGGGCAAGGAAAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCAGGCCAUCAGAAGGGCCACAGCGCAGAGGCCCGCGGAAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGACACCAGCACCCUGCUGAUCGAGAAUAGCAGCCCCAGCGGCGGCAGCAAGAGAACCGCCGAUGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
513	UCCGGCGGCAGCAGCGGCGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCUCCUCCGGCGGCUCUUCCACACUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGAGCCAGGAGGCCCGGCUGGGCAUCAAGCCUCACAUCCAGCGCCUGCUGGACCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACACCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACCGGCCCGUGCAGGAUCUGAGGGAGGUGAAUAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUACAACCUGCUGAGCGGCCUGCCCCCCAGCCACCAGUGGUACACAGUGCUGGAUCUGAAGGACGCCUUCUUUUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAAAAUAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUAGACAGCUGAGGGAGUUCCUGGGCAAGGCAGGCUUCUGUAGGCUGUUCAUCCCCGGAUUUGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCUGAUCUGACAAAGCCAUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCCUGGAGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCUAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCUCCCGACAGAUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUUGGCCCUGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAGGCCCACGGCACCAGACCCGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGAUGGAUCUAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGCGCGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGAAAGAAGCUGAAUGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGGGAGAUCUACAGACGGAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGCAAUAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACUCCUGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
514	UCCGGCGGCAGCAGCGGCGGCUCUUCCGGCAGCGAGACCCCAGGCACCUCCGAGAGCGCCACCCCAGAGUCCAGCGGCGGCUCCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCAGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCCCAGGCCUGGGCCGAGACUGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUUAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCCCCAUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGCACCAACGAUUAUAGACCCGUGCAGGACCUGAGAGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCUACCGUGCCAAACCCUUACAACCUGCUGAGCGGCCUGCCCCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGACUGCACCCCACCAGCCAGCCCCUGUUUGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACAUGGACCAGACUGCCUCAGGGCUUCAAGAACUCACCCACCCUGUUCAACGAGGCCCUGCACAGAGACCUGGCCGACUUUAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACAAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAAUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCCACCCCAAAGACACCUAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCACUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAACUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGACGCCCAGUGGCCUAUCUGUCCAAGAAGCUGGAUCCCGUGGCCGCUGGAUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGAGCAACGCCAGAAUGACCCACUACCAGGCCCUGCUGCUGGAUACCGACAGAGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCACUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAAGGCCAGCGGAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGAACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAACUGAACGUGUACACCGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACUAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGACUGUCCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCCGCCGAGGCCAGAGGCAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACACCAGACACCAGCACCCUGCUGAUCGAGAAUAGCUCCCCCUCCGGCGGCAGCAAGAGGACUGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
515	AGCGGCGGAAGCAGCGGGGGCAGCAGCGGAUCUGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGUCCAGCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUUAUUCCUCUGAAGGCCACAAGCACCCCCGUGUCUAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGACUGGGCAUCAAGCCCCACAUUCAGCGCCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCUCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGGACCAACGACUACAGACCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAAUCUGCUGAGCGGCCUGCCACCCUCCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUUAACGAGGCCCUGCACAGAGACCUGGCCGACUUCCGCAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACACUGGGCAAUCUGGGCUAUCGCGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGGCAGCCUACACCCAAGACCCCUAGACAGCUGCGCGAGUUCCUGGGAAAGGCCGGCUUCUGCAGACUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACUAAGCCAGGCACACUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCUCCUGCCCUGGGCCUGCCCGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGAGACGGCCCGUGGCCUACCUGAGCAAGAAGCUGGAUCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUUCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCUGACAGAUGGCUGUCCAACGCCAGGAUGACCCAUUACCAGGCCCUGCUGCUGGACACCGACCGCGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCAGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGGCCCGACCUGACCGACCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCUGCCGUGACCACCGAGACCGAGGUGAUUUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGAUAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGGUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAAUCGGAUGGCCGAUCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCAGACACCUCUACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCAGCAAGAGAACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
516	AGCGGCGGCAGCAGCGGCGGCAGCUCCGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCCGAGAGCUCCGGCGGCAGCUCUGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCUCCACUUGGCUGUCCGAUUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCCCUGAAAGCCACCUCCACACCCGUGUCCAUUAAGCAGUACCCUAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUACAGAGACUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGAGCCCUUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCUGGCACCAAUGACUACCGCCCCGUGCAGGACCUGAGAGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCUUACAAUCUGCUGUCCGGCCUGCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCAACCCUGUUCAACGAGGCCCUGCAUAGAGACCUCGCCGACUUUCGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCUCUGCUGCAGACCCUGGGCAACCUGGGCUACCGCGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCUACCCCCAAGACCCCCGGCAGCUGCGGGAGUUUCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAAUUGGGGCCCCGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGUCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGACCCUGGCGGAGACCCGUGGCCUACCUGUCUAAAAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCUUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAAGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCCGCAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCCGCCCUGACCUGACCGACCAGCCCCUGCCAGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCAGCGCCCAGAGAGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACAGAAGGAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCAGAUACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGCUCCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
517	AGCGGCGGCAGCUCCGGCGGCUCCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCAGCGGCGGCUCCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCUGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAUCCACACCCGUGUCCAUCAAGCAGUACCCUAUGUCUCAGGAGGCCAGACUGGGCAUUAAACCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGUCUCCCUGGAAUACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACAGACCCGUGCAGGACCUGCGCGAGGUGAACAAGAGAGUGGAGGACAUCCACCCAACCGUGCCAAACCCAUAUAACCUGCUGUCUGGCCUGCCACCUUCCCACCAGUGGUACACCGUGCUGGACCUGAAAGACGCCUUCUUCUGCCUGCGGCUCCACCCCACCUCCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCUCAGGGCUUCAAGAACUCCCCCACCCUGUUUAACGAAGCCCUGCACAGGGAUCUGGCCGACUUUAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAACUGGAUUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGAUGGCUGACCGAGGCCAGAAAAGAGACAGUGAUGGGCCAGCCCACACCCAAGACCCCAAGACAGCUGCGCGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCUGGAUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACAAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGAAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACCGGUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGAGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGAUGGCAGCUCCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCCAUCAUCCACUGUCCAGGCCACCAGAAGGGCCAUUCCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACAGAGACCCCCGACACCUCUACACUGCUGAUCGAGAACAGUAGCCCUAGCGGCGGAAGCAAGAGAACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
518	AGCGGCGGCAGCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCAGCGGCGGCAGCUCUACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCCCAGGCCUGGGCCGAGACCGGAGGCAUGGGCCUGGCCGUGCGGCAGGCCCCACUGAUCAUCCCUCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGCAUUAAGCCACACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCCGGCACCAACGACUACAGACCCGUGCAGGACCUGAGAGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCCCCUAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGCCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGAUUAGCGGGCAGCUGACCUGGACCAGACUGCCUCAGGGCUUCAAAAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAAGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAAGAGGGCCAGAGAUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCAAGGCAGCUGAGGGAGUUUCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCCGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACAAAGCCAGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGCCUGCCCGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGACCCGUGGCCUACCUGUCUAAAAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCAUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGUCCAAUGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGAUAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACAAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCUCCUCUCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCAGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAAAAGCUGAACGUGUAUACCGAUUCUAGGUAUGCCUUCGCCACCGCCCAUAUCCACGGCGAGAUCUACAGAAGAAGAGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGAGGCUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGAAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCUCCCCCUCUGGCGGCAGCAAGAGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
519	UCCGGCGGCUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCAGAGAGCUCCGGCGGCAGCAGCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAG CGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCU GGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACC GUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUG GCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAG UAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCU GACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCC CUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGC CUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGG CCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCU GACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCU GCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAACGCACCGCCGAC GGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
520	UCUGGCGGCAGCUCUGGCGGUUCCAGCGGGUCCGAGACCCCUGGAACCAGCGAGAGCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCUGACGUGAGUCUGGGCAGCACCUGGCUGUC CGACUUCCCUCAGGCUUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCGGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCC UGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUAUCGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCUUACAACCUCCUGUCAGGCCUGCCACCCAGCCAUCAGUGGUACAC CGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCU GGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAA GUACCUGGGCUAUCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUAUCCCC UGACCAAGCCUGGCACCCUGUUCAAUUGGGGGCCAGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCC CUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCA GCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUC GGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCC CUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUC CUGCCCAAGCGGCUGUCCAUUAUACACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGCGGACCGCC GACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
521	
522	
523	AGCGGCGGGAGCUCUGGUGGCAGCUCUGGGAGCGAGACUCCUGGCACCAGCGAGUCCGCCACCCCAGAGAGCUCUGGGGGAAGCUCAGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUC UGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACUCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCC UGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCCGGCCUGCCUCCUAGCCACCAGUGGUACA CCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCAUCCCACAUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACC UGGCCGACUUCAGGAUCCAGCACCCCGACCUCAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGA AGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCU CUGACCAAGCCAGGCACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGC CCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCUCCGCACGCCGUGGAGGCCCUGGUGAAGC AGCCACCAGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCAGAGGCCCACGGCACCC GGCCUGACCUGACCGACCAGCCCCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCC CUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUC CUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGUAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGCGGACCGCC GACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
524	AGCGGGGGGUCCAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCCGAGUCUAGCGGCGGCUCCAGCGGCGGCAGCUCCACCCUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGAG CGACUUUCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCUGUGCGGCAGGCCCCUCUGAUCAUCCCACUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCC UGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGCCCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAAUCCUUACAACCUGCUGAGCGGCCUGCCACCCAGCCAUCAGUGGUACA CGGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGAC CUGGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGAUCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUG AAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCUCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCAGGCAGCUGAGGGAGUUCCUGGGGAAGGCCGGCUUCUGCAGACUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCACUGUACCC CCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGG CCCUUGGCGGCGCCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGGUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAG CAGCCACCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACC

SEQ ID NO.	SEQUENCE
	AGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCUCCACCCUGCUCAUCGAGAACAGCUCCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
525	UCUGGGGGAAGCAGCGGCGGCAGCAGCGGCUCAGAGACACCGGGCACCAGCGAGUCUGCCACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGGAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACAGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCAGGUCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCACUGUUCGCCUUCGAGUGGCGCGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUAUCUGGGCUAUCUGCUGAAGGAGGGCCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUCAUUCCUGGCUUCGCUGAGAUGGCCGCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUCCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACACUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
526	UCAGGGGGAUCCAGCGGGGGCUCCUCCGGCUCUGAGACUCCCGGGACUAGCGAGAGCGCUACUCCCGAGAGCUCAGGGGGAAGCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACAGGCCUGUGCAGGAUCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCAAAUCCUUACAACCUGCUGUCCGGCCUGCCUCCUUCACACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGGAUCUCAGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCCUGUCUGCGGAUGGUGGCUGCUAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACAGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCUGAGGCUCGGGGGAACAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACUGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
527	UCCGGCGGCUCCAGCGGCGGCAGCUCCGGGUCCGAGACCCCUGGGACCAGCGAGUCUGCCACCCCUGAGAGCUCCGGCGGCUCCUCUGGGGGAAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUCCACGAGACCAGCAAGGAGCCUGACGUGUCCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGCCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCGGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAAUCCCUACAACCUGCUGAGCGGCCUGCCCCCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACAGGGACCUGGCUGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGAUGACCUGCUGCUGGCAGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGCGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGGUGGCUGACCGAGGCACGGAAGGAGACCGUGAUGGGUCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUCGGCAAGGCCGGGUUCUGCAGGCUGUUCAUCCCCGGCUUUGCCGAGAUGGCUGCCCCUCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCUGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUCCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACGGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCUGGAGCCGCCGUGACCACCGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCUGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
528	UCUGGGGGGAGCUCCGGAGGGAGCUCCGGGUCCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGAGCAGCGGGGGCAGCAGCGGCGGCAGCUCCACCCUCAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCAGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAAUCCCUACAACCUGCUGUCUGGCCUGCCCCCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGACAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGAUCUCCUCCUGGCCGCCACCUCUGAGCUCGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCACGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAAUUGGGGUCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACUCAGAAGCUGGGGCCCUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUCAGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGACCCGAUCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUCGCCGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCU

SEQ ID NO.	SEQUENCE
	GCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
529	AGCGGGGGCAGCUCCGGCGGCUCCUCUGGCAGCGAGACUCCCGGGACUAGCGAGAGCGCUACCCCCGAGAGCUCUGGGGGCUCCAGCGGCGGGAGCUCCACCCUCAACAUCGAGGACGAGUACCGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCGCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGUCCUUGGAGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUCAGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCACACGGACCAGGCCCGACCUGACAGACCAGCCCCUGCCAGACGCUGACCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCUCUCCCAGCGGGGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
530	AGCGGCGGCUCCAGCGGGGGCUCCUCCGGCAGCGAGACCCCCGGCACCAGCGAGUCAGCCACCCCUGAGAGCUCCGGGGGCUCCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGAGCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACCGUGCCUAAUCCUUACAACCUGCUGAGCGGCCUGCCUCCCAGCCAUCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUCUUUUGCCUGAGACUGCAUCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGAUGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCAGGCUGUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGGCCGGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUUUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCCUGUCUGAGGAUGGUGGCUGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUCACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCUCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCAGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGGACCAGCGCCCAGCGGGCAGAGCUGAUUGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCUCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGGCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCGGCCAGAAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACAGCUCUCCCUCUGGCGGGAGCAAGAGAACCGCUGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
531	AGCGGGGGCUCCUCCGGAGGCAGCUCCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCUACUCCCGAGUCCAGCGGCGGGAGUAGCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCCCUCAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCGGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCUCUGGGCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGCCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCAGGGUGGCCUCCAUGCCUGCGGAUGGUGGCCGCGAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGUCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCUACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCCGCUGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCUAGCCCCAGCGGCGGCUCCAAGCGGACCGCCGACGGCUCAGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
532	AGCGGCGGGAGCUCUGGGGGCUCCUCUGGCUCCGAGACCCCCGGAACCUCCGAGAGCGCCACUCCGGAGAGCUCCGGGGGCUCCAGCGGCGGCAGCUCUACCUUGAACAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUUCCUCAGGCCUGGGCCGAGACCGGGGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACUCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCUUACAACCUGCUGUCGGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCUACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCGGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACGGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCUGCCACCCUGCUGCCUCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUCCCCGACGCCGACCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGCAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACUAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACUCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGCUAUGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGAGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGCGCCUGAGCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCCGCUGAGGCCCGGGGCAAUAGGAUGGCCGAUCAGGCCGCCAGAAAGGCCGCCAUCACAGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGUUCUAAGAGAACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
533	AGCGGGGGCAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCAGCAGCGGCGGGAGCUCCACCCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUCUCCGACUUCCCACAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUUCCCAAUCCCUACAACCUGCUGUCCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCACUCUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUAUCUGCUGAAGGAGGGGCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCUGAGAUGGCUGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACUCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCUUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUCCCCAAGCGGCUGAGCAUCAUUCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGUAGCAAGCGCACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
534	AGCGGGGGCAGCUCCGGAGGCUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCUCUGGGGGCUCCAGCACUCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCUGAGACCGGUGGCAUGGGCCUGGCUGUGCGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACAAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAAUGACUACCGGCCAGUCCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCACCCCACCUCUCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCAGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUACCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCUCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCUAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCUGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCCGGCACCCUGUUCAAUUGGGGCCCCGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGGUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGUUCCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGGACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCAGAUACGCCUUCGCCACAGCCCACAUCCACGGCGAGAUCUACCGGCGCCGCGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGCGGCUGAGCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
535	AGCGGGGGCAGCUCCGGAGGCUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCUCCGGGGGCUCCUCUGGCGGCAGCAGUACUCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGAAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUUCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUCCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGAGCGGGCUGCCGCCCUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGUCCCACACUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGAUCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGAAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGAGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCACGGCAGCUGCGCGAGUUCCUGGGAAAGGCCGGCUUCUGCCGGCUGUUCAUCCCAGGAUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGGCCAGAUCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUUGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCUGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCAGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCUGAGGAGGGGCUGCAGCACAACUGUCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCUCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCUCCCUCCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCGGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCUCGGUACGCCUUCGCUACUGCCCACAUCCACGGGGAGAUCUAUCGGCGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCUGCUGAGGCCCGGGGCAAUAGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
536	UCCGGGGGCAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCACUGGGGAGCACCUGGCUGUCAGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACCGCCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCCUACAACCUGCUGAGCGGCUUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGCAUCUCCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCCGGAUUCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACAGAGGCCAGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCUCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCCCCUUGCCUGCGGAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCAGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCUGAUCUGACCGACCAGCCCCUGCCCGACGCAGAUCACACCUGGUACACCGAUGGGUCUAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCUCCCCCUCCGGGGGGAGCAAGCGGACCGCCGACGGGUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
537	AGCGGCGGCAGCAGCGGCGGCUCCAGCGGCAGCGAGACCCCAGGGACCAGCGAGAGCGCCACCCCCGAGAGCUCUGGCGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGAUGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCACAGGCCUGGGCCGAGACCGGAGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCAGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACUGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCCCUGUUCGCAUUCGAGUGGCGGAUCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUAUGUGGACGACCUGCUGCUGGCUGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCCCCCUGCCUGAGGAUGGUGGCUGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUCACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACAGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGCCUGCAGCACAACUGUCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCAGACCUGACCGAUCAGCCUCUGCCCGAUGCCGACCACACCUGGUACACGGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACUCCAGGUACGCCUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCAGCCGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCAAGGAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
538	AGCGGGGGGAGCUCCGGCGGCUCCUCCGGGAGCGAGACUCCCGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGGAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGGAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUCAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCUACGCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCCGGAAGGAGACCGUCAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAAUUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCGGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCAGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
539	UCAGGGGGGAGCAGCGGGGGGUCCAGCGGCAGCGAGACCCCCGGCACCAGCGAGAGCGCCACCCCUGAGAGCUCCGGGGGCUCCAGCGGGGGCAGCUCCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUGGGCUCCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGGCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGUACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGAGCGGCCUGCCUCCCUCCCACCAGUGGUACACAGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGAGGCUGCAUCCUACCAGCCAGCCACUGUUUGCCUUUGAGUGGAGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGAAUCCAGCACCCCGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGGUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUCCUGGGGAAGGCUGGCUUCUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCACUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACGGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCACGGGGAGAUCUACCGGCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCAAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGCGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
540	AGCGGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGCACCUCCGAGAGCGCCACCCCAGAGAGCUCUGGGGGGAGCUCCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCUCUGAUCAUCCCUCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGAGCGGGCUGCCGCCCUCUCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUUAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCCGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCCGGCCUGAUCUGACCGAUCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACCGCCCACAUCCACGGGGAGAUCUACCGGCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCUCUGUUUCUGCCUAAGAGACUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGUUCUAAGAGAACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
541	AGCGGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGGACCAGCGAGUCAGCCACUCCCGAGAGCUCCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGCCUCGGGAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUCAUCAUCCCUCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCGGGCACCAAUGAUUACAGGCCCGUGCAGGACCUGAGGGAGGUGAACAAGCGGGUGGAGGAUAUCCACCCCACCGUGCCCAAUCCUUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGACAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAAUCUGGGGUACAGGGCCUCGGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUCCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCUCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACGCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCUGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUAUACCGACAGCCGGUAUGCCUUCGCCACCGCCCACAUCCAUGGAGAGAUCUAUAGGAGGCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAAUAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGAACCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACGGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
542	AGCGGAGGCAGCUCCGGGGGAAGCAGCGGCAGCGAGACCCCAGGGACCUCUGAGUCCGCCACCCCCGAGAGCAGCGGGGGAGCAGCGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCAGACGUGUCCCUGGGGUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCUGAGACCGGCGGCAUGGGACUGGCAGUGCGCCAGGCUCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCAAUGAGCCAGGAGGCUCGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGUCCCCCUGGAACACCCCACUGCUGCCCGUCAAGAAGCCCGGGACCAACGACUACAGGCCAGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCUGGCCUGCCCCCCAGCCAUCAGUGGUACACGGUGCUGGAUCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAACCUGGGCUAUAGGGCCUCUGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCUCGGCAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCAGGCUGUUCAUCCCCGGGUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCAGGCACCCUGUUCAACUGGGGGCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUCCUGCUGGACACAGACAGAGUGCAGUUCGGGCCAGUGGUGGCCCUGAACCCUGCCACUCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCAGCCGGCACCUCUGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACUCCCGGUACGCAUUCGCUACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGGAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCAAAGCGGCUGAGCAUCAUCCACUGCCCUGGCCACCAGAAGGGCCACUCAGCAGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCUCCGGCGGCAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
543	UCCGGGGGGUCUAGCGGCGGCAGCAGCGGCAGCGAGACCCCCGGGACCAGCGAGAGUGCUACCCCAGAGAGCUCCGGCGGCAGCUCCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGGAGCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCGGUGAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGACUGCACCCUACCUCUCAGCCUCUGUUUGCCUUCGAGUGGAGGGAUCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGCCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACCCUGGGCAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCUGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGCCCUGUGGCCUAUCUCAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCUCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUCCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCAGACCUGACAGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCGAAGGCUCUGCCCGCUGGGACCAGCGCCCAGCGGGCAGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGGUACGCAUUCGCCACUGCCCACAUCCACGGCGAGAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUUCUGCCCAAGCGGCUGAGCAUCAUCCACUGCCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCCGGGGAAUCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
544	AGCGGCGGGAGCUCCGGCGGCAGCUCCGGGAGCGAGACUCCUGGCACCAGCGAGUCCGCCACUCCCGAGAGCUCCGGCGGCAGCUCCGGCGGCAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUCUCCGACUUCCCACAGGCCUGGGCCGAGACCGGGGGCAUGGGGCUGGCCGUGAGGCAGGCCCCCCUGAUCAUCCCUCUGAAGGCCACCUCCACCCCCGUGUCUAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACCGGCCCGUGCAGGACCUGCGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGUGGCUUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCAGGCUGCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACCGAGGCUCGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACUCCCCGGCAGCUGCGGGAGUUCUUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUUCCCGGCUUCGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUCUUCAACUGGGGCCCAGACCAGCAGAAGGCUUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACUAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGCCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCUUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUCACCAAGGACGCCGGGAAGCUGACCAUGGGGCAGCCCCUGGUCAUCCUGGCGCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGACCUGACCGAUCAGCCUCUGCCCGACGCUGAUCACACCUGGUACACAGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUUCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCUGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACUGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
545	AGCGGGGGAGCAGCGGGGGAGCUCAGGGUCUGAGACCCCGGCACCAGCGAGUCUGCCACCCUGAGAGCAGCGGGGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUUCCUCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUAUCGCCCCGUGCAGGACCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCCAACCCUUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCUAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGCUGGCUGACCGAGGCUAGGAAGGAGACAGUGAUGGGGCAGCCAACCCCCAAGACUCCCCGGCAGCUGCGGGAGUUUCUCGGCAAGGCCGGGUUCUGCAGACUGUUCAUCCCCGGCUUUGCCGAGAUGGCUGCCCCACUGUACCCUCUGACCAAGCCCGGCACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCGCUGAAUCCAGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGAUAUCCUGGCCGAGGCCCACGGCACCAGGCCGGACCUGACCGACCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCUCCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCUGGAGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
546	AGCGGGGGAGCUCCGGAGGUUCCAGCGGGUCCGAGACCCCUGGAACCUCCGAGAGCGCUACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGUAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCUGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGUCUCAGGAGGCCAGGCUGGGGAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCGGUCAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGAGUGGAGGACAUCCACCCCACCGUCCCCAAUCCUUACAACCUCCUGUCAGGCCUGCCACCCAGCCACCAGUGGUACACCGUGCUGGAUCUGAAGGAUGCCUUUUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUUUGGGGAAGGCUGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGAUCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCGGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUCCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUCGACAUCCUGGCCGAGGCCCACGGCACCAGGCCUGAUCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGCACCUCUGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCCGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCGGCCAUCACCGAGACCCCCGACACCUCCACUCUGCUGAUCGAGAACAGCAGCCCCAGUGGGGGCUCCAAGCGCACUGCCGACGGCAGUGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
547	AGCGGCGGCAGCUCUGGCGGCUCCUCUGGGAGCGAGACCCCUGGCACCAGCGAGUCCGCCACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGGUCCUCCACCCUGAACAUCGAGGACGAGUACCGCCUGCAUGAGACCUCUAAGGAGCCUGACGUGAGUCUGGGCAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUUCCCAAUCCCUACAACCUGCUGUCAGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGAUCUGAAGGACGCCUUCUUCUGUCUGCGGCUGCACCCCACCUCCCAGCCACUGUUCGCCUUCGAGUGGCGGGACCCCGAGAUGGGGAUCAGCGGCCAGCUGACAUGGACCAGGCUCCCUCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUGUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCCGGGACCCUGUUCAACUGGGGUCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGUCUGGACAUCCUGGCCGAGGCUCACGGCACCCGGCCCGACCUGACAGACCAGCCUCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCCGUGACCACCGAGACAGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCCCGCGGCAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCAGCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
548	AGCGGAGGCUCCAGCGGCGGCAGCUCCGGCAGCGAGACUCCAGGGACUAGCGAGUCCGCUACCCCUGAGUCUAGCGGCGGCAGCAGCGGCGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCUGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCUCAGGCCUGGGCCGAGACAGGGGGGAUGGGGCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACUAGCACCCCAGUGAGCAUCAAGCAGUACCCCAUGAGCCAGGAGGCCCGCCUGGGCAUCAAGCCCCAUAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGAUCUGCGCGAGGUGAACAAGAGGGUGGAGGACAUCCACCCCACCGUGCCAAAUCCUUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUCCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACAGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUUUGCAGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCCCUGUACCCUCUGACCAAGCCGGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACUCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACAGACAGCCGCUAUGCCUUCGCCACUGCCCACAUCCACGGCGAGAUCUACCGCCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUCCAUUGCCCCGGGCACCAGAAGGGCCACUCCGCUGAGGCCCGGGGCAAUAGGAUGGCGGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGCGGCAGCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
549	AGCGGCGGCUCUAGCGGCGGGAGCAGCGGCUCCGAGACCCCGGCACCUCCGAGUCCGCUACUCCCGAGAGCUCCGGCGGCUCCAGCGGCGGGUCUAGCACUCUGAACAUCGAGGACGAGUACCGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGUCCGACUUCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGGCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCAAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAAUGACUACAGGCCCGUGCAGGACCUCAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGCCUGCCUCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGAGACCCAGAGAUGGGGAUCUCCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCUGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCAGCCACCAGUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGGCAGCGGUGGCUCACCGAGGCCAGGAAGGAGACAGUGAUGGGCCAGCCUACCCCAAAGACCCCCAGGCAGCUGCGGGAGUUUCUGGGGAAGGCUGGCUUCUGUCGGCUGUUUAUUCCUGGCUUCGCUGAGAUGGCUGCCCCUCUGUACCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUAUGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCUUGGAGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACCGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCUGAUCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCUCCAGCCUUCUGCAGGAGGGCCAGCGGAAGGCCGGAGCCGCGGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCCGGGACCAGCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCAGCAGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACAGAGACCCCCGACACUAGCACCCUGCUGAUCGAGAACAGCAGCCCUAGCGGGGGCUCUAAGCGGACCGCCGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
550	UCCGGCGGCUCCUCAGGCGGCUCCUCUGGCAGCGAGACUCCUGGCACCAGCGAGUCCGCCACCCCCGAGAGCAGCGGCGGCAGCUCCGGGGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGGAGCACCUGGCUGUCUGACUUCCCUCAGGCCUGGGCCGAGACCGGGGGGAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGAGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCAAACCCCUACAACCUGCUGUCUGGGCUGCCGCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACUCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACUUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUCAAGUACCUGGGCUAUCUGCUGAAGGAGGGGCAGCGCUGGCUCACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACUCCCCGGCAGCUGCGGGAGUUUCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCAGGCUUUGCAGAGAUGGCAGCCCCCCUGUACCCUCUGACAAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCAUUCGAGCUGUUUGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCCGACAGAUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUUCUGGACACAGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCGGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUUCUGGCAGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCUGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGAUAGCAGGUACGCAUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGUGCCGAGGCCCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
551	AGCGGGGGCAGCUCUGGCGGCUCUUCUGGCAGCGAGACCCCUGGCACCAGCGAGAGCGCCACCCCAGAGAGCAGUGGCGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUCUCUGGGGUCCACCUGGCUGUCCGACUUCCCGCAGGCCUGGGCAGAGACCGGUGGCAUGGGCCUGGCCGUGCGCCAGGCCCCCCUGAUCAUCCCACUGAAGGCCACCAGCACCCCGGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCAGGGACCAAUGACUACCGGCCUGUGCAGGACCUGCGGGAGGUCAACAAGAGGGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUUUUCUGUCUGCGGCUGCAUCCAACCAGCCAGCCGCUGUUUGCCUUCGAGUGGAGAGAUCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCAGACUUCAGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUCGACUGUCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAAUCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCCGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGAGGGAGUUCUUGGGGAAGGCCGGCUUCUGCAGGUUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCUCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUAUGCCAAGGGGGUGCUGACCCAGAAGCUGGGGCCAUGGAGGCGGCCGGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCCGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGUCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUCAAGCAGCCACCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGGCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCUCACGGCACCAGGCCCGACCUGACAGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCAGAGCUGAUUGCCCUCACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACUGACAGCAGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACCGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGAGCAUCAUUCACUGCCCUGGGCACCAGAAGGGCCACUCUGCUGAGGCCAGGGGCAAUCGGAUGGCCGACCAGGCCGCCAGGAAGGCCGCCAUCACCGAGACCCCUGACACCAGCACCCUGCUGAUCGAGAACUCCUCCCCAAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
552	AGCGGUGGCUCUUCAGGGGGAUCCAGUGGCAGCGAGACACCCGGCACCUCUGAGUCUGCUACCCCCGAGAGCUCCGGCGGGAGCUCCGGGGGUAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCGGACGUGUCUCUGGGCAGCACCUGGCUGUCCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGGCUGGCCGUGCGCCAGGCUCCACUGAUCAUCCCCCUGAAGGCCACCAGCACCCCUGUGUCCAUCAAACAGUACCCUAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGGAUUCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCUGUGAAGAAGCCUGGCACCAACGACUAUAGGCCUGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACAGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGAGGGACCCAGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACGCUGUUCAACGAGGCCCUGCACAGGGACCUGGCCGACUUUCGGAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCUCCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGACAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGGCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCAGCCCCUCUGUACCCUCUGACCAAGCCCGGGACCCUGUUCAACUGGGGGCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUCACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGAGGCCCGUGGCCUACCUGAGCAAGAAGCUGGACCCCGUGGCAGCCGGCUGGCCUCCUUGUCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUCAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUCCCCGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCCGGCCUGACCUGACCGACCAGCCCCUGCCCGACGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGUCAGAGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUAUCGCCGGAGGGGGUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGGCUGAGCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCAAGGGGGAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCUCCACUCUUCUGAUCGAGAACUCCUCCCCCAGCGGCGGCUCCAAGAGGACCGCCGACGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

SEQ ID NO.	SEQUENCE
553	UCCGGGGGGAGCAGCGGGGGGAGUUCCGGGAGCGAGACUCCCGGGACUAGCGAGAGCGCCACCCCCGAGAGCAGCGGGGGCAGCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUCAGACAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGUCCAUCAAGCAGUACCCCAUGUCCCAGGAGGCUCGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGGAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCCGGGACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAAUAAGAGGGUGGAGGACAUCCACCCUACCGUGCCUAACCCCUACAACCUGCUGAGCGGGCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGAGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAGUGGCGGGAUCCCGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCGGACUUCAGGAUCCAGCACCCAGAUCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCUCUGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCUACCCCAAAGACCCCUCGGCAGCUGAGGGAGUUUCUGGGGAAGGCUGGCUUCUGCCGGCUCUUCAUUCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCAGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGAUCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCAUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCUCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCUGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCUGAGGAGGGGCUGCAGCACAACUGCCUGGACAUCCUGGCAGAGGCCCACGGCACCAGGCCGGACCUGACCGAUCAGCCCCUGCCUGAUGCCGACCACACCUGGUACACCGACGGCAGCUCCCUCCUGCAGGAGGGGCAGCGGAAGGCCGGGGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCAGGGACCUCCGCCCAGAGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACUCUGCUGAGGCUCGGGGGAAUCGGAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCCUCCGGGGGCAGCAAGAGGACCGCUGACGGCAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
554	AGCGGGGGGUCCUCAGGGGGCAGCUCAGGCUCUGAGACCCCCGGCACCAGCGAGAGUGCUACCCCAGAGAGCAGCGGGGGCUCCUCUGGAGGCUCCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCUCCAAGGAGCCCGACGUGUCUCUGGGGAGCACCUGGCUGUCCGACUUCCCUCAGGCCUGGGCUGAGACCGGAGGCAUGGGCCUGGCCGUGCGCCAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGAGCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCCUGGAACACCCCACUGCUGCCAGUGAAGAAGCCUGGCACCAACGACUACAGGCCGGUGCAGGACCUGAGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUUCCCAAUCCCUACAACCUGCUGUCCGGCCUGCCUCCUAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGAUGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCUCUGUUCGCCUUCGAAUGGAGGGACCCAGAGAUGGGCAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGAUCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGGAAUCUGGGCUAUCGGGCCAGCGCCAAGAAGGCCCAGAUUUGCCAGAAGCAGGUGAAGUAUCUGGGGUACCUGCUGAAGGAGGGGCAGCGGUGGCUGACCGAGGCACGGAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGGAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCUGCCCCUCUGUACCCACUGACCAAGCCGGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCUUGGCGGCGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCCGUGGCCGCUGGCUGGCCUCCAUGCCUGCGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCUGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCACCCGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUCGACACCGACAGGGUGCAGUUCGGCCCAGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCUCUGCCAGAUGCCGACCACACCUGGUACACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGCGGAAGGCAGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCUGCUGGGACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCGUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGCAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGAUGAGAUCCUUGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGCCUGUCCAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCAGAGGCAAGGGGGAACCGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACUGAGACCCCCGACACCUCCACCCUGCUGAUCGAGAACAGCAGCCCCAGCGGCGGGAGCAAGCGCACCGCCGACGGCUCCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA
555	UCCGGGGGGAGCAGCGGGGGCAGCUCCGGCAGCGAGACCCCCGGAACCUCUGAGAGCGCCACUCCAGAGAGUUCCGGCGGGUCCAGCGGCGGGAGCAGCACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGUCUGGGCUCCACCUGGCUGUCUGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUCAGGCAGGCCCCCCUGAUCAUCCCCCUGAAGGCCACCAGCACCCCAGUGUCCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGUCCCUGGAACACCCCCCUGCUGCCCGUGAAGAAGCCUGGCACCAAUGACUAUAGGCCUGUGCAGGACCUGCGGGAGGUGAACAAGAGGGUGGAGGACAUCCACCCUACUGUGCCUAACCCCUACAACCUGCUGAGUGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUUUUCUGUCUGCGGCUGCACCCCACCUCUCAGCCUCUCUUCGCCUUCGAGUGGAGAGACCCUGAGAUGGGGAUCAGCGGGCAGCUGACCUGGACCCGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAAUGAGGCCCUGCACAGAGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACUAGUGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGGUACAGGGCCUCUGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUCAAGUACCUGGGCUACCUGCUGAAGGAGGGUCAGCGGUGGCUGACCGAGGCCCGCAAGGAGACCGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUCAGGGAGUUUCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCAGCCCCCCUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCAGACCAGCAGAAGGCCUAUCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCAGCCCUGGGCCUGCCUGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGGUACGCCAAGGGGGUGCUGACCCAGAAGCUGGGCCCCUGGCGCAGGCCAGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCAGCAGGGUGGCCACCAUGCCUGCGCAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGGAAGCUGACCAUGGGGCAGCCCCUGGUGAUCCUGGCCCCACACGCCGUGGAGGCCCUGGUGAAGCAGCCGCCUGAUAGGUGGCUGUCCAACGCCAGGAUGACCCACUAUCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCUGAGGAGGGGCUGCAGCACAACUGCCUGGACAUUCUGGCCGAGGCCCACGGCACUCGGCCAGAUCUGACCGAUCAGCCUCUGCCCGAUGCCGACCACACCUGGUAUACCGACGGCAGCAGCCUGCUGCAGGAGGGGCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCUCUGCCCAGCGGGCAGAGCUGAUCGCCCUGACUCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAAUGUGUACACCGACAGCCGCUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGGCGGCGGGGAUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGCGGCUGUCCAUCAUUCAUUGCCCCGGCCAUCAGAAGGGCCACUCCGCUGAGGCCAGGGGGAACAGGAUGGCCGACCAGGCCGCCCGCAAGGCCGCCAUCACCGAGACCCCCGAUACCAGCACCCUGCUGAUCGAGAACUCCUCUCCCAGCGGCGGCUCCAAGAGGACCGCCGAUGGGAGCGAGUUCGAGCCCAAGAAGAAGAGGAAAGUCUAA

Table 67: Exemplary MMLV-RT amino acid and nucleotide sequences

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
Wild type MMLV RT	Polypeptide	623	amino acids 659-1335 of NCBI accession no. NP_057933.2
Reference MMLV RT (H8Y)	Polypeptide	1	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			KLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
MMLVRT5M	Polypeptide	4	MTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
MMLVRT5Mwithout N-terminus methionine	Polypeptide	5	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
Polynucleotide encoding MMLVRT5M	DNA	28	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGGATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCC
Polynucleotide encoding MMLVRT5M	RNA	29	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCC
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C2)	DNA	245	ACACTGAATATCGAGGACGAGTACCGCCTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCCACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGAGACAGGCCCCTCTGATCATCCCCCTGAAGGCCACCTCCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCCCACATCCAGCGGCTGCTGGATCAGGGCATCCTGGTGCCCTGTCAGAGCCCCTGGAACACCCCCCTGCTGCCAGTGAAGAAGCCCGGCACCAACGACTATCGGCCTGTGCAGGACCTGCGGGAGGTGAACAAACGGGTGGAGGACATCCACCCCACCGTGCCTAACCCATACAACCTGCTGTCCGGCCTGCCCCCAAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGCGGCTGCACCCCACCAGCCAGCCCCTGTTCGCCTTCGAGTGGAGGGACCCCGAGATGGGCATCTCCGGCCAGCTGACCTGGACCAGGCTGCCCCAGGGCTTCAAGAACAGCCCCACCCTGTTCAACGAGGCCCTGCACCGCGACCTGGCCGATTTTAGAATCCAGCACCCTGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTGGACTGCCAGCAGGGCACCAGGGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGCGGTGGCTGACAGAGGCCAGAAAGGAGACCGTGATGGGCCAGCCCACACCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCCGGCTGTTCATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCCCTGACCAAGCCTGGGACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCG

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CCCCTGCCCTGGGACTGCCAGACCTGACCAAGCCCTTCGAGCTGTTCGTGGACGAGAAGCAGGGCTACGCCAAGGGCGTGCTGACACAGAAGCTGGGCCCATGGAGGAGACCCGTGGCCTACCTGTCCAAGAAGCTGGACCCAGTGGCCGCCGGCTGGCCACCCTGCCTGAGGATGGTGGCCGCCATCGCCGTGCTGACCAAGGATGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGACAGGTGGCTGAGCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCCCTGCCCGAGGAGGGCCTGCAGCACAATTGCCTGGACATCCTGGCCGAGGCCCACGGAACCCGCCCTGACCTGACCGACCAGCCTCTGCCCGACGCCGACCACACCTGGTATACCGACGGAAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGTGACAACCGAGACCGAGGTGATCTGGGCCAAGGCTCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACTCCCGGTACGCCTTCGCCACCGCCCACATCCACGGCGAAATCTACAGGCGGAGGGGCTGGCTGACCAGCGAGGGCAAGGAGATCAAGAACAAGGACGAGATCCTGGCCCTGCTGAAGGCCCTGTTCCTGCCCAAGAGGCTGTCTATCATCCACTGCCCCGGCCATCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGATGGCCGACCAGGCCGCCAGGAAAGCCGCCATCACCGAGACACCCGATACCTCCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C2)	RNA	246	ACACUGAAUAUCGAGGACGAGUACCGCCUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCCACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGAGACAGGCCCCUCUGAUCAUCCCCCUGAAGGCCACCUCCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCCCACAUCCAGCGGCUGCUGGAUCAGGGCAUCCUGGUGCCCUGUCAGAGCCCCUGGAACACCCCCCUGCUGCCAGUGAAGAAGCCCGGCACCAACGACUAUCGGCCUGUGCAGGACCUGCGGGAGGUGAACAAACGGUGGAGGACAUCCACCCCACCGUGCCUAACCCAUACAACCUGCUGUCCGGCCUGCCCCCAAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGCGGCUGCACCCCACCAGCCAGCCCCUGUUCGCCUUCGAGUGGAGGGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACCUGGACCAGGCUGCCCCAGGGCUUCAAGAACAGCCCCACCCUGUUCAACGAGGCCCUGCACCGCGACCUGGCCGAUUUUAGAAUCCAGCACCCUGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUGGACUGCCAGCAGGGCACCAGGGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGCGGUGGCUGACAGAGGCCAGAAAGGAGACCGUGAUGGGCCAGCCCACACCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCCGGCUGUUCAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCCCUGACCAAGCCUGGGACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCUGCCCUGGGACUGCCAGACCUGACCAAGCCCUUCGAGCUGUUCGUGGACGAGAAGCAGGGCUACGCCAAGGGCGUGCUGACACAGAAGCUGGGCCCAUGGAGGAGACCCGUGGCCUACCUGUCCAAGAAGCUGGACCCAGUGGCCGCCGGCUGGCCACCCUGCCUGAGGAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGAUGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGACAGGUGGCUGAGCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCCCUGCCCGAGGAGGGCCUGCAGCACAAUUGCCUGGACAUCCUGGCCGAGGCCCACGGAACCCGCCCUGACCUGACCGACCAGCCUCUGCCCGACGCCGACCACACCUGGUAUACCGACGGAAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGGGCCGCCGUGACAACCGAGACCGAGGUGAUCUGGGCCAAGGCUCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACUCCCGGUACGCCUUCGCCACCGCCCACAUCCACGGCGAAAUCUACAGGCGGAGGGGCUGGCUGACCAGCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUCCUGGCCCUGCUGAAGGCCCUGUUCCUGCCCAAGAGGCUGUCUAUCAUCCACUGCCCCGGCCAUCAGAAGGGCCACAGCGCCGAGGCCAGGGGCAACCGGAUGGCCGACCAGGCCGCCAGGAAAGCCGCCAUCACCGAGACACCCGAUACCUCCACCCUGCUGAUCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C3)	DNA	83	ACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGACCAGCCCCTGCCTGACGCCGACCACACCTGGTACACCGACGGCAGCTCCCTGCTGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAAGCCCTGCCTGCCGGCACCTCCGCCCAGCGGGCCGAGCTGATCGCCCTGACCCAGGCCCTGAAGATGGCTGAGGGCAAGAAGCTGAACGTGTACACCGATTCCAGATACGCCTTCGCCACCGCCCACATCCACGGCGAGATCTACAGAAGAAGGGGCTGGCTGACCTCCGAGGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGAGCATCATCCACTGTCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAATAGAATGGCCGACCAGGCCGCCAGAAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACAGCAGCCCC
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C3)	RNA	84	ACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGACCAGCCCCUGCCUGACGCCGACCACACCUGGUACACCGACGGCAGCUCCCUGCUGCAGGAGGGCCAGAGGAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAAGCCCUGCCUGCCGGCACCUCCGCCCAGCGGGCCGAGCUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCUGAGGGCAAGAAGCUGAACGUGUACACCGAUUCCAGAUACGCCUUCGCCACCGCCCACAUCCACGGCGAGAUCUACAGAAGAAGGGGCUGGCUGACCUCCGAGGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGAGCAUCAUCCACUGUCCCGGCCACCAGAAGGGCCACAGCGCCGAGGCCAGAGGCAAUAGAAUGGCCGACCAGGCCGCCAGAAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACAGCAGCCCC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C4)	DNA	257	ACCCTGAACATCGAGGACGAGTACAGACTGCACGAGACCAGCAAGGAGCCCGACGTGTCCCTGGGCTCTACCTGGCTGAGCGACTTCCCCCAGGCCTGGGCCGAGACCGGCGGAATGGGCCTGGCCGTGAGACAGGCCCCACTGATCATCCCACTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCTATGTCACAGGAGGCCAGACTGGGCATCAAGCCACACATCCAGAGACTGCTGGACCAGGGCATCCTGGTGCCCTGCCAGAGCCCATGGAACACCCCCCTGCTGCCCGTCAAGAAGCCCGGCACCAACGACTACAGGCCCGTGCAGGACCTGCGGGAGGTGAACAAGCGCGTGGAGGACATCCACCCTACCGTGCCCAACCCCTACAACCTGCTGTCCGGCCTGCCACCCAGCCATCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCCCAGCCTCTGTTCGCCTTCGAGTGGAGAGACCCCGAGATGGGCATCTCCGGCCAGCTGACTTGGACAAGACTGCCCCAGGGCTTCAAGAATTCTCCAACCCTGTTCAACGAGGCCCTGCACCGGGACCTGGCCGACTTCAGGATCCAGCACCCAGACCTGATCCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCCACCAGCGAGCTCGACTGCCAGCAGGGCACCCGGGCCCTGCTGCAGACTCTGGGCAACCTGGGCTACAGGGCCAGCGCCAAGAAGGCCCAGATCTGCCAGAAGCAGGTGAAGTACCTGGGCTACCTGCTGAAGGAGGGCCAGAGGTGGCTGACCGAGGCCAGGAAGGAGACCGTGATGGGCCAGCCAACCCCTAAGACCCCCAGACAGCTGAGGGAGTTCCTGGGCAAGGCCGGCTTCTGCCGGCTGTTCATCCCCGGCTTCGCCGAGATGGCCGCCCCCCTGTACCCCCTGACCAAGCCTGGCACCCTGTTCAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGATCTGACCAAGCCATTCGAGCTGTTCGTGGACGAGAAACAGGGCTACGCCAAGGGCGTGCTGACCCAGAAGCTGGGCCCCTGGAGGAGACCTGTGGCCTACCTGAGCAAAAAGCTGGACCCAGTGGCCGCCGGGTGGCCCCCCTGCCTGAGAATGGTGGCCGCCATCGCCGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGACAGCCTCTGGTGATCCTGGCCCCCCACGCCGTGGAGGCCCTGGTGAAGCAGCCCCCCGATAGGTGGCTGAGTAATGCCCGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACAGGGTGCAGTTCGGCCCCGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCACTGCCCGAGGAGGGCCTGCAGCATAACTGCCTGGACATCCTGGCCGAGGCCCACGGCACCAGGCCCGACCTGACCGATCAGCCTCTGCCCGACGCCGATCACACCTGGTACACCGATGGCAGCAGCCTGCTGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGTGACCACCGAGACCGAGGTGATCTGGGCCAAGGCCCTGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACTGATCGCCCTGACCCAGGCCCTGAAGATGGCCGAGGGCAAGAAGCTGAACGTGTACACCGACAGCCGGTACGCCTTCGCCACCGCTCACATCCACGGCGAGATTTACAGGAGAAGAGGCTGGCTGACCAGCGAAGGCAAGGAGATCAAGAACAAGGACGAGATTCTGGCCCTGCTGAAGGCCCTGTTCCTGCCTAAGAGACTGTCTATCATCCACTGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGATGGCCGACCAGGCCGCCCGGAAGGCCGCCATCACCGAGACCCCCGACACCAGCACCCTGCTGATCGAGAACTCCAGCCCT
Codon optimized polynucleotide encoding MMLVRT5M(MMLVRT5M C4)	RNA	258	ACCCUGAACAUCGAGGACGAGUACAGACUGCACGAGACCAGCAAGGAGCCCGACGUGUCCCUGGGCUCUACCUGGCUGAGCGACUUCCCCCAGGCCUGGGCCGAGACCGGCGGAAUGGGCCUGGCCGUGAGACAGGCCCCACUGAUCAUCCCACUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCUAUGUCACAGGAGGCCAGACUGGGCAUCAAGCCACACAUCCAGAGACUGCUGGACCAGGGCAUCCUGGUGCCCUGCCAGAGCCCAUGGAACACCCCCCUGCUGCCCGUCAAGAAGCCCGGCACCAACGACUACAGGCCCGUGCAGGACCUGCGGGAGGUGAACAAGCGCGUGGAGGACAUCCACCCUACCGUGCCCAACCCCUACAACCUGCUGUCCGGCCUGCCACCCAGCCAUCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCCCAGCCUCUGUUCGCCUUCGAGUGGAGAGACCCCGAGAUGGGCAUCUCCGGCCAGCUGACUUGGACAAGACUGCCCCAGGGCUUCAAGAAUUCUCCAACCCUGUUCAACGAGGCCCUGCACCGGGACCUGGCCGACUUCAGGAUCCAGCACCCAGACCUGAUCCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCCACCAGCGAGCUCGACUGCCAGCAGGGCACCCGGGCCCUGCUGCAGACUCUGGGCAACCUGGGCUACAGGGCCAGCGCCAAGAAGGCCCAGAUCUGCCAGAAGCAGGUGAAGUACCUGGGCUACCUGCUGAAGGAGGGCCAGAGGUGGCUGACCGAGGCCAGGAAGGAGACCGUGAUGGGCCAGCCAACCCCUAAGACCCCCAGACAGCUGAGGGAGUUCCUGGGCAAGGCCGGCUUCUGCCGGCUGUUCAUCCCCGGCUUCGCCGAGAUGGCCGCCCCCCUGUACCCCCUGACCAAGCCUGGCACCCUGUUCAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGAUCUGACCAAGCCAUUCGAGCUGUUCGUGGACGAGAAACAGGGCUACGCCAAGGGCGUGCUGACCCAGAAGCUGGGCCCCUGGAGGAGACCUGUGGCCUACCUGAGCAAAAAGCUGGACCCAGUGGCCGCCGGGUGGCCCCCCUGCCUGAGAAUGGUGGCCGCCAUCGCCGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGACAGCCUCUGGUGAUCCUGGCCCCCCACGCCGUGGAGGCCCUGGUGAAGCAGCCCCCCGAUAGGUGGCUGAGUAAUGCCCGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACAGGGUGCAGUUCGGCCCCGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCACUGCCCGAGGAGGGCCUGCAGCAUAACUGCCUGGACAUCCUGGCCGAGGCCCACGGCACCAGGCCCGACCUGACCGAUCAGCCUCUGCCCGACGCCGAUCACACCUGGUACACCGAUGGCAGCAGCCUGCUGCAGGAGGGCCAGAGAAAGGCCGGCGCCGCCGUGACCACCGAGACCGAGGUGAUCUGGGCCAAGGCCCUGCCCGCCGGCACCAGCGCCCAGCGGGCCGAACUGAUCGCCCUGACCCAGGCCCUGAAGAUGGCCGAGGGCAAGAAGCUGAACGUGUACACCGACAGCCGGUACGCCUUCGCCACCGCUCACAUCCACGGCGAGAUUUACAGGAGAAGAGGCUGGCUGACCAGCGAAGGCAAGGAGAUCAAGAACAAGGACGAGAUUCUGGCCCUGCUGAAGGCCCUGUUCCUGCCUAAGAGACUGUCUAUCAUCCACUGCCCCGGCCACCAGAAAGGCCACAGCGCCGAGGCCAGGGGCAACAGGAUGGCCGACCAGGCCGCCCGGAAGGCCGCCAUCACCGAGACCCCCGACACCAGCACCCUGCUGAUCGAGAACUCCAGCCCU
MMLVRT5MG504X	Polypeptide	36	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
polynucleotide encoding MMLVRT5MG504X	DNA	41	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGA
polynucleotide encoding MMLVRT5MG504X	RNA	42	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGA
Codon optimized polynucleotide encoding MMLVRT5MG504X (MMLVRT5M C3(G504X))	DNA	91	ACCCTGAACATCGAGGACGAGTACAGGCTGCACGAGACCAGCAAGGAGCCCGACGTGAGCCTGGGCAGCACCTGGCTGAGCGATTTCCCTCAGGCTTGGGCCGAGACCGGCGGCATGGGCCTGGCCGTGCGGCAGGCCCCCCTGATTATCCCCCTGAAGGCCACCAGCACCCCCGTGAGCATCAAGCAGTACCCAATGTCCCAGGAGGCCAGGCTGGGCATCAAGCCTCACATCCAGAGGCTGCTGGACCAGGGCATCCTGGTGCCATGCCAGTCCCCCTGGAACACCCCTCTGCTGCCCGTGAAGAAGCCTGGCACCAACGACTACCGGCCCGTGCAGGACCTGAGAGAAGTGAACAAGCGGGTGGAGGACATCCACCCAACCGTGCCCAACCCTTACAACCTGCTGTCCGGCCTGCCCCCCAGCCACCAGTGGTACACCGTGCTGGACCTGAAGGACGCCTTCTTCTGCCTGAGACTGCACCCCACCTCTCAGCCCCTGTTCGCCTTCGAGTGGCGCGACCCCGAGATGGGCATCAGCGGCCAGCTGACCTGGACCAGACTGCCACAGGGCTTTAAGAATAGCCCAACCCTGTTTAACGAGGCCCTGCACAGGGACCTGGCCGACTTCAGGATCCAGCACCCCGACCTGATTCTGCTGCAGTACGTGGACGACCTGCTGCTGGCCGCTACCAGCGAGCTGGACTGCCAGCAGGGCACCAGAGCCCTGCTGCAGACCCTGGGCAACCTGGGCTACAGAGCCAGCGCCAAGAAGGCCCAGATCTGTCAGAAGCAGGTGAAGTATCTGGGCTACCTGCTGAAGGAAGGCCAGAGATGGCTGACCGAGGCCAGAAAGGAGACTGTGATGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCTGCGGGAGTTCCTGGGCAAGGCCGGCTTTTGCAGACTGTTTATCCCTGGCTTCGCCGAGATGGCCGCCCCACTGTACCCTCTGACCAAGCCTGGCACCCTGTTTAACTGGGGCCCCGACCAGCAGAAGGCCTACCAGGAGATCAAGCAGGCCCTGCTGACCGCCCCCGCCCTGGGCCTGCCCGACCTGACCAAGCCTTTCGAGCTGTTCGTGGACGAGAAGCAGGGATACGCCAAAGGCGTGCTGACCCAGAAGCTGGGCCCCTGGCGGAGGCCCGTGGCCTACCTGAGCAAAAAACTGGACCCTGTGGCCGCCGGCTGGCCCCCATGCCTGCGGATGGTGGCCGCCATCGCTGTGCTGACCAAGGACGCCGGCAAGCTGACCATGGGCCAGCCCCTGGTGATCCTGGCCCCTCACGCCGTGGAGGCTCTGGTGAAGCAGCCTCCAGACAGGTGGCTGTCCAACGCCAGGATGACCCACTACCAGGCCCTGCTGCTGGACACCGACCGGGTGCAGTTCGGCCCTGTGGTGGCCCTGAACCCCGCCACCCTGCTGCCTCTGCCAGAGGAGGGCCTGCAGCACAACTGCCTGGACATCCTGGCCGAGGCCCACGGC
Codon optimized polynucleotide encoding MMLVRT5MG504X (MMLVRT5M C3(G504X))	RNA	92	ACCCUGAACAUCGAGGACGAGUACAGGCUGCACGAGACCAGCAAGGAGCCCGACGUGAGCCUGGGCAGCACCUGGCUGAGCGAUUUCCCUCAGGCUUGGGCCGAGACCGGCGGCAUGGGCCUGGCCGUGCGGCAGGCCCCCCUGAUUAUCCCCCUGAAGGCCACCAGCACCCCCGUGAGCAUCAAGCAGUACCCAAUGUCCCAGGAGGCCAGGCUGGGCAUCAAGCCUCACAUCCAGAGGCUGCUGGACCAGGGCAUCCUGGUGCCAUGCCAGUCCCCCUGGAACACCCCUCUGCUGCCCGUGAAGAAGCCUGGCACCAACGACUACCGGCCCGUGCAGGACCUGAGAGAAGUGAACAAGCGGGUGGAGGACAUCCACCCAACCGUGCCCAACCCUUACAACCUGCUGUCCGGCCUGCCCCCCAGCCACCAGUGGUACACCGUGCUGGACCUGAAGGACGCCUUCUUCUGCCUGAGACUGCACCCCACCUCUCAGCCCCUGUUCGCCUUCGAGUGGCGCGACCCCGAGAUGGGCAUCAGCGGCCAGCUGACCUGGACCAGACUGCCACAGGGCUUUAAGAAUAGCCCAACCCUGUUUAACGAGGCCCUGCACAGGGACCUGGCCGACUUCAGGAUCCAGCACCCCGACCUGAUUCUGCUGCAGUACGUGGACGACCUGCUGCUGGCCGCUACCAGCGAGCUGGACUGCCAGCAGGGCACCAGAGCCCUGCUGCAGACCCUGGGCAACCUGGGCUACAGAGCCAGCGCCAAGAAGGCCCAGAUCUGUCAGAAGCAGGUGAAGUAUCUGGGCUACCUGCUGAAGGAAGGCCAGAGAUGGCUGACCGAGGCCAGAAAGGAGACUGUGAUGGGCCAGCCCACCCCCAAGACCCCCAGGCAGCUGCGGGAGUUCCUGGGCAAGGCCGGCUUUUGCAGACUGUUUAUCCCUGGCUUCGCCGAGAUGGCCGCCCCACUGUACCCUCUGACCAAGCCUGGCACCCUGUUUAACUGGGGCCCCGACCAGCAGAAGGCCUACCAGGAGAUCAAGCAGGCCCUGCUGACCGCCCCCGCCCUGGGCCUGCCCGACCUGACCAAGCCUUUCGAGCUGUUCGUGGACGAGAAGCAGGGAUACGCCAAAGGCGUGCUGACCCAGAAGCUGGGCCCCUGGCGGAGGCCCGUGGCCUACCUGAGCAAAAAACUGGACCCUGUGGCCGCCGGCUGGCCCCCAUGCCUGCGGAUGGUGGCCGCCAUCGCUGUGCUGACCAAGGACGCCGGCAAGCUGACCAUGGGCCAGCCCCUGGUGAUCCUGGCCCCUCACGCCGUGGAGGCUCUGGUGAAGCAGCCUCCAGACAGGUGGCUGUCCAACGCCAGGAUGACCCACUACCAGGCCCUGCUGCUGGACACCGACCGGGUGCAGUUCGGCCCUGUGGUGGCCCUGAACCCCGCCACCCUGCUGCCUCUGCCAGAGGAGGGCCUGCAGCACAACUGCCUGGACAUCCUGGCCGAGGCCCACGGC
MMLVRT5M(G504X_L435K)	Polypeptide	63	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVIKAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG
polynucleotide encoding MMLVRT5M(G504X_L435K)	DNA	68	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTAAGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGA
polynucleotide encoding MMLVRT5M(G504X_L435K)	RNA	69	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			CAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUAAGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGA
MMLVRT5MD524N	Polypeptide	45	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTNGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
polynucleotide encoding MMLVRT5MD524N	DNA	50	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTCTTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTGAACCCGGCTACGCTGCTCCCACTGCCTGAGGAAGGGCTGCAACACAACTGCCTTGATATCCTGGCCGAAGCCCACGGAACCCGACCCGACCTAACGGACCAGCCGCTCCCAGACGCCGACCACACCTGGTACACGAATGGAAGCAGTCTCTTACAAGAGGGACAGCGTAAGGCGGGAGCTGCGGTGACCACCGAGACCGAGGTAATCTGGGCTAAAGCCCTGCCAGCCGGGACATCCGCTCAGCGGGCTGAACTGATAGCACTCACCCAGGCCCTAAAGATGGCAGAAGGTAAGAAGCTAAATGTTTATACTGATAGCCGTTATGCTTTTGCTACTGCCCATATCCATGGAGAAATATACAGAAGGCGTGGGTGGCTCACATCAGAAGGCAAAGAGATCAAAAATAAAGACGAGATCTTGGCCCTACTAAAAGCCCTCTTTCTGCCCAAAAGACTTAGCATAATCCATTGTCCAGGACATCAAAAGGGACACAGCGCCGAGGCTAGAGGCAACCGGATGGCTGACCAAGCGGCCCGAAAGGCAGCCATCACAGAGACTCCAGACACCTCTACCCTCCTCATAGAAAATTCATCACCC
polynucleotide encoding MMLVRT5MD524N	RNA	51	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGGUACACGAAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCACCC
MMLVRT5ML478X	Polypeptide	54	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVAL
polynucleotide encoding MMLVRT5ML478X	DNA	59	ACCCTAAATATAGAAGATGAGTATCGGCTACATGAGACCTCAAAAGAGCCAGATGTTTCTCTAGGGTCCACATGGCTGTCTGATTTTCCTCAGGCCTGGGCGGAAACCGGGGGCATGGGACTGGCAGTTCGCCAAGCTCCTCTGATCATACCTCTGAAAGCAACCTCTACCCCCGTGTCCATAAAACAATACCCCATGTCACAAGAAGCCAGACTGGGGATCAAGCCCCACATACAGAGACTGTTGGACCAGGGAATACTGGTACCCTGCCAGTCCCCCTGGAACACGCCCCTGCTACCCGTTAAGAAACCAGGGACTAATGATTATAGGCCTGTCCAGGATCTGAGAGAAGTCAACAAGCGGGTGGAAGATATCCACCCCACCGTGCCCAACCCTTACAACCTC

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
			TTGAGCGGGCTCCCACCGTCCCACCAGTGGTACACTGTGCTTGATTTAAAGGATGCCTTTTTCTGCCTGAGACTCCACCCCACCAGTCAGCCTCTCTTCGCCTTTGAGTGGAGAGATCCAGAGATGGGAATCTCAGGACAATTGACCTGGACCAGACTCCCACAGGGTTTCAAAAACAGTCCCACCCTGTTTAATGAGGCACTGCACAGAGACCTAGCAGACTTCCGGATCCAGCACCCAGACTTGATCCTGCTACAGTACGTGGATGACTTACTGCTGGCCGCCACTTCTGAGCTAGACTGCCAACAAGGTACTCGGGCCCTGTTACAAACCCTAGGGAACCTCGGGTATCGGGCCTCGGCCAAGAAAGCCCAAATTTGCCAGAAACAGGTCAAGTATCTGGGGTATCTTCTAAAAGAGGGTCAGAGATGGCTGACTGAGGCCAGAAAAGAGACTGTGATGGGGCAGCCTACTCCTAAGACCCCTCGACAACTAAGGGAGTTCCTAGGGAAGGCAGGCTTCTGTCGCCTCTTCATCCCTGGGTTTGCAGAAATGGCAGCCCCCCTGTACCCTCTCACCAAACCGGGGACTCTGTTTAATTGGGGCCCAGACCAACAAAAGGCCTATCAAGAAATCAAGCAAGCTCTTCTAACTGCCCCAGCCCTGGGGTTGCCAGATTTGACTAAGCCCTTTGAACTCTTTGTCGACGAGAAGCAGGGCTACGCCAAAGGTGTCCTAACGCAAAAACTGGGACCTTGGCGTCGGCCGGTGGCCTACCTGTCCAAAAAGCTAGACCCAGTAGCAGCTGGGTGGCCCCCTTGCCTACGGATGGTAGCAGCCATTGCCGTACTGACAAAGGATGCAGGCAAGCTAACCATGGGACAGCCACTAGTCATTCTGGCCCCCCATGCAGTAGAGGCACTAGTCAAACAACCCCCCGACCGCTGGCTTTCCAACGCCCGGATGACTCACTATCAGGCCTTGCTTTTGGACACGGACCGGGTCCAGTTCGGACCGGTGGTAGCCCTG
polynucleotide encoding MMLVRT5M L478X	RNA	60	ACCCUAAAUAUAGAAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAAGAUAUCCACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGGGCAGCCUACUCCUAAGACCCCUCGACAACUAAGGGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUCAAGCAAGCUCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUCAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCCCCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCCUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGCCCUG

Table 68: Exemplary promoter and UTR sequences

SEQUENCE DESCRIPTION	TYPE	SEQ ID NO.	SEQUENCE
T7 promoter	RNA	267	TAATACGACTCACTATA
5'UTR	RNA	268	AGGAAATAAGAGAGAAAAGAAGAGTAAGAAGAAATATAAGAGCCACC
stop codon 1	RNA	269	TAA
stop codon 2	RNA	270	TAG
stop codon 3	RNA	271	TGA
stop codon 4	RNA	272	TAATAGTGA
3' UTR	RNA	273	GCGGCCGCTTAATTAAGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCAAGCCCTTCTTCTCTCCCTTGCACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG
T7 promoter	RNA	639	UAAUACGACUCACUAUA
5'UTR	RNA	640	AGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC

stop codon 1	RNA	641	UAA
stop codon 2	RNA	642	UAG
stop codon 3	RNA	643	UGA
stop codon 4	RNA	644	UAAUAGUGA
3' UTR	RNA	645	GCGGCCGCUUAAUUAAGCUGCCUUCUGCGGGGCUUGCCUUCUGGCCAAGCCCUUCUUCUCUCCCUUGCACCUGUACCUCUUGGUCUUUGAAUAAAGCCUGAGUAGGAAG

EXAMPLES

[0574] The following examples are provided for illustrative purposes only and are not intended to limit the scope of the claims provided herein.

Example 1. Prime editors comprising a codon-optimized reverse transcriptase domain.

[0575] Polynucleotide sequences that encode a prime editor fusion protein having the structure of SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2-S]-MMLVRT5M-SGGS-SV40BPNLS1 (amino acid SEQ ID NO: 25) were engineered. Codon optimization was performed for the polynucleotide sequence encoding the C-terminal portion, [(SGGS)2-XTEN-(SGGS)2-S]-MMLVRT5M-SGGS-SV40BPNLS1] of the fusion protein. Codons encoding the indicated C-terminal portion of the fusion protein were optimized to use frequent codons in human genome and improve mRNA stability. For the remaining N-terminal portion (SV40BPNLS-Cas9H840A) of the fusion protein, the polynucleotide sequence that encode the same fusion protein as published in Anzalone Nature 576(7785):149-157 (2019) was used.

[0576] 144 codon optimized RNA sequences that encode the above-described prime editor fusion protein were designed, and the coding sequences are provided in SEQ ID Nos 412-555. Three codon optimized mRNAs, named PE-C2 (SEQ ID NO: 244), PE-C3 (SEQ ID NO: 234), and PE-C4 (SEQ ID NO: 256), were compared to the up-optimized control mRNA sequence that encodes the same fusion protein, which comprises the sequence of SEQ ID NO: 27 and is referred to here after as the PE-AA2019 mRNA. The codon optimized sequence encoding the RT portion of each of PE-C2, PE-C3, and PE-C4 are provided in SEQ ID Nos. 245, 83, and 257, respectively. The PE-C2, PE-C3, PE-C4, and PE-AA2019 mRNAs were in vitro transcribed. An mRNA encoding the Streptococcus pyogenes Cas9 (SpCas9) nuclease was also in vitro transcribed to serve as a negative control. RNA sequences and corresponding DNA sequences of each of PE-C2, PE-C3, PE-C4, and PE-AA2019, as well as sequences encoding each component, are provided in Table 15. For mRNA resulted from in vitro transcription, a 5'UTR was added to the 5' end and a "TAA" stop codon followed by a 3'UTR was added to the 3' end of each of the mRNAs. Sequence encoding UTR sequences are provided in SEQ ID Nos 640 and 645, Table 68.

[0577] Each mRNA was electroporated (ATx, Maxcyte) into healthy human donor CD34+ cells along with a prime editing guide RNA (pegRNA) and a nick guide RNA (ngRNA) designed to introduce a T>A nucleotide substitution (the sickle cell mutation that results in the amino acid substitution known as "E6V" associated with sickle cells disease) into a wild type HBB gene. Sequences of the pegRNA and the ngRNA are provided below:

[0578] pegRNA sequence: (5'-3')

mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCAGACUUCUCCACAGGAGUCAGGUGCACmU*mU*mU*U (SEQ ID NO: 559)

[0579] ngRNA sequence: (5'-3')

mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGG

CUAGUCCGUUAUCAACUUGAAAAAGUGGGACCGAGUCGGUGCmU*mU*mU*U (SEQ ID NO: 564)

[0580] In any instance where a guide RNA sequence is listed, * indicates phosphorothioate linkage, and 'm' indicates 2'OMe modification.

[0581] 200nM of the prime editor-encoding mRNAs, 20µM of pegRNA and 11µM of nick guide RNA were used for each electroporation. Prime editing efficiency was examined at three time points: 24 hours, 72 hours, and 120 hours post electroporation, respectively. For each time point, two biological replicates were included for each of the prime editor-encoding mRNAs, and one replicate was used for the SpCas9 control. Genomic DNA was extracted and sequenced with Illumina Miseq Next Generation Sequencing (NGS) at each of the three time points.

[0582] Prime editing efficiency of each of the prime editor encoding mRNA is summarized in Table 7. Improved prime editing efficiency with codon optimized constructs, particularly in PE-C3, was observed.

[0583] Table 7: prime editing efficiency (%) using prime editors encoded by codon-optimized mRNA

	Cas9	**PE-C2**		**PE-C3**		**PE-C4**		**PE AA2019**		**No treatment**	
Editing efficiency(%) 24h	0.02	2.45	2.21	4.5	3.53	2.57	2.98	3.65	1.33	0.24	0.33
Editing efficiency(%) 72h	0.03	6.59	5.35	11.17	10.72	9.73	7.04	7.77	3.97	0.08	0.02
Editing efficiency(%) 120h	0.03	8.37	8.28	13.85	13.06	9.09	8.57	8.79	5.07	0	0

[0584] The level of the prime editor protein (or the SpCas9 control) in the CD34+ cells were also accessed. 24 hours post electroporation, protein was harvested from the CD34+ cells and quantified by capillary Western blot assay (Jess, ProteinSimple) using an anti-Cas9 primary antibody. For PE-C3, only one of the two biological replicates was measured for prime editor protein level. Samples were normalized by total protein concentration using a bicinchoninic acid (BCA) quantification (ThermoFisher) prior to running the capillary Western blot. Protein was quantified by measuring the area under the curve for a detected peak at 160kDa (±10%) for Cas9 quantification or 230kDa (±10%) for the prime editor peak. The result is summarized in Table 8:

[0585] Table 8: protein expression level in CD34+ cells after electroporation

	Cas9	**PE-C2**		**PE-C3**	**PE-C4**		**PE AA2019**		**No treatment**	
Cas9 peak area (160kDa)	249365	n.d.	2173	436	887	n.d.	n.d.	n.d.	1138	623
Prime editor peak area (230kDa)	2613	13936	30682	48270	44067	11732	21140	6453	n.d.	387

Example 2. Prime editors with optimized linkers.

[0586] In this experiment, the peptide linker connecting the Cas9 domain and the RT domain of a prime editor fusion protein was optimized. 22 prime editor fusion proteins were designed, each having the following structure:

[0587] SV40BPNLS-Cas9H840A-[LINKER]-MMLVRT5M-SGGS-SV40BPNLS1

[0588] Where [LINKER] indicates a different peptide linker in each of the 22 fusion proteins. The prime editor fusion protein as described in Example 1, having the structure of SV40BPNLS-Cas9H840A-[(SGGS)2-XTEN-(SGGS)2-S]-MMLVRT5M-SGGS-SV40BPNLS1, was used as a control for comparison with the 22 prime editor fusion proteins having alternative linkers. An mRNA sequence encoding each of the 22 fusion proteins and the control fusion protein was in vitro transcribed. In each of the 22 mRNA sequences encoding the linker variant fusion proteins, the portion that encodes the MMLVRT was codon-optimized and has the same sequence as the sequence encoding the MMLVRT in PE-C3 as described in Example 1(SEQ ID NO: 234). The codon optimized RNA sequence encoding MMLVRT5M, referred to as MMLVRT-C3, is provided in SEQ ID No 84 and corresponding DNA sequence in SEQ ID No 83. The control prime editor fusion protein is encoded by the PE-C3 optimized mRNA, the coding sequence of which is in SEQ ID NO:234. For mRNA resulted from in vitro transcription, a 5'UTR was added to the 5' end and a "TAA" stop codon followed by a 3'UTR (sequence provided in Table 68) was added to the 3' end of each of the mRNAs.

[0589] A HEK293T cell line was generated to contain the sickle cell mutation in the HBB gene in a homozygous manner. A pegRNA and ngRNA pair were designed to edit the sickle cell mutation locus in the HEK293T cells and chemically synthesized:

[0590] pegRNA sequence: (5'-3')
mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUUCAGGAGUCAGGUGCACmU*mU*mU*U (SEQ ID NO: 569)

[0591] ngRNA sequence: (5'-3')
mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U (SEQ ID NO: 574)

[0592] mRNAs encoding the 22 fusion proteins and the control fusion protein were introduced into the HEK293T cells by lipofection, using MessengerMax^{TM} lipid reagent (ThermoFisher). 4000 ng of mRNA, 250ng of pegRNA and 75ng of ng RNA were used for each well. For each of the prime editor-encoding mRNAs, two technical replicates were examined. 3 days post lipofection, genomic DNA was harvested and sequenced using Illumina NGS as described above to measure prime editing efficiency and indel frequencies. The result is summarized in Table 9. Compared to the control linker (SGGS)2-XTEN(SGGS)2-S, prime editors with alternative linkers exhibit improved editing efficiency.

[0593] Table 9: prime editing efficiency with linker optimized prime editors

Linker SEQ ID	Editing efficiency (/%)		Indel Frequency (/%)		Corresponding Sequence Table No.
289	44.15	47.38	1	1.1	25
301	69.38	58.3	1.4	1.7	60
302	67.76	67.32	1.8	2.1	16
303	65.52	57.88	2	1.8	58
304	55.56	53.1	1.5	1.4	56
305	43.88	51.48	0.8	1.4	54
290	51.26	50.95	1.1	1.5	64
291	54.91	55.12	1.1	1.5	62
296	61.17	61.03	1.5	1.7	52
292	59.37	57.19	1.7	1.6	(SGGS)2-XTEN-SGGS linker control
293	61.06	62.86	1.5	1.2	50
294	62.06	65.11	1.4	1.5	48
295	69.17	60.85	1.6	1.7	46
297	53.92	48.54	1.2	1.2	44
298	50.25	48.56	1.2	1.4	42
299	57.39	50.25	1.3	1.5	40
300	59.97	50.37	1.7	1.4	38
306	41.63	53.61	1.2	1.5	28
307	51.56	53.23	1.3	1.3	36
309	40.85	53.22	1	1.3	34
308	47.17	45.13	1	1	34
310	59.45	64.25	1.2	1.9	32
311	63.93	60.9	1.9	1.9	30

[0594] A subset of the prime editors with optimized linkers were further tested in healthy human donor CD34+ cells for editing the HBB locus. a pegRNA and a ngRNA were designed to target the HBB locus:

[0595] pegRNA sequence: (5'-3')

mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGG CUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGU CAGGUGCACmU*mU*mU*U (SEQ ID NO: 579)

[0596] nickRNA sequence: (5'-3')

mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGG

CUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U (SEQ ID NO: 574)

[0597] 150nM of prime editor encoding mRNA, 20µM pegRNA, and 10µM ngRNA were used for each CD34+ cell electroporation. Prime editing efficiency and indel frequency was examined at 24 hours, 48 hours, and 96 hours after electroporation, respectively. Genomic DNA was extracted at each of the three time points and analyzed with Illumina MiSeq Next Generation Sequencing as described. The prime editing efficiency and indel frequency are summarized in Table 10. Up to 41% prime editing in CD34+ cells was observed at 96 hours post electroporation.

[0598] Table 10: prime editing efficiency (%) of linker-optimized prime editors (n=1):

	24h		**48h**		**96h**	
linker SEQ ID	**editing efficiency (%)**	**indel frequency (%)**	**editing efficiency (%)**	**indel frequency (%)**	**editing efficiency (%)**	**indel frequency (%)**
289	12.9	1.4	21.9	3.9	21.2	3.9
291	10.4	1.4	17.9	2.3	24.2	3.7
293	14	1.3	21.5	3.6	28.6	4.3
294	11	1.7	22.8	3.2	31.2	5.5
295	13.2	1.1	23.4	2.8	31.6	5.1
301	14.6	1.8	19.3	2.9	39.3	6.8
302	15.8	2.9	27.1	4.2	37.1	7
303	14.7	2.4	23.2	3	34.7	5.8
306	15.2	2.1	25	4	41.3	6.9
309	16.2	2.3	27.5	4	41.3	6.3
310	13.1	2.1	26.1	3.9	40.6	7.4
311	16.7	2.2	30.4	4.9	38.7	6.6
	0.1	0.1	0.1	0.1	0.1	0.2

Example 3. Prime editing with optimized pegRNAs

[0599] Chemically synthesized pegRNAs that lack 3' terminal Uracils were tested for editing efficiency in CD34+ cells, compared to chemically synthesized pegRNAs having 4 additional uracil nucleotides (5'-"UUUU"-3') at the 3' end. A pegRNA and an ngRNA were designed to target the HBB locus. The same pegRNA used in Example 2 were compared with a pegRNA generated by removing the 4 uracil nucleotides at the 3' end of the pegRNA. The ngRNA used in Example 2 above was paired with the pegRNAs with and without the four 3' uracil, respectively, to examine prime editing efficiency. The pegRNAs and the ngRNA were synthesized and chemically modified to protect the 5' and 3' ends, as shown below:

[0600] pegRNA sequence with terminal U: 5'-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACmU*mU*mU*U-3'(SEQ ID NO: 579)

[0601] pegRNA sequence without terminal U: 5’-mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUmG*mC*mA*C-3’(SEQ ID NO: 587)

[0602] nick guide RNA sequence: 5’-mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U-3’(SEQ ID NO: 574)

[0603] Two mRNAs encoding two different prime editors were used: 1) the PE-C3 codon optimized mRNA (SEQ ID NO: 233) as described in Example 1, and 2) the mRNA encoding a prime editor fusion protein with a (SGGS)8 linker having the structure (SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5MC3-SGGS-SV40BPNLS1) (SEQ ID NO: 80), with the MMLVRT5M portion codon optimized the same as in PE-C3 as described in Example 2. Different amounts of mRNA were also tested. The PE protein encoding mRNA, the pegRNA, and the ngRNA were electroporated in human healthy donor CD34+ cells. For each electroporation, 20µM pegRNA and11µMngRNAwere used. Prime editing efficiency and indel frequency were examined at 48 hours and 96 hours after electroporation, respectively. Genomic DNA was extracted at each time point, and prime editing efficiency and indel frequency were analyzed with Illumina Miseq Next Generation Sequencing. The editing conditions used, and prime editing efficiencies and indel frequencies are summarized in are summarized in Table 11.

[0604] Table 11: prime editing efficiency (%) of optimized pegRNAs

			48h		96h	
PE mRNA	**mRNA amount**	**pegRNA**	**Editing efficiency (%)**	**Indel frequency (%)**	**Editing efficiency (%)**	**Indel frequency (%)**
PE-C3 (SEQ ID NO: 233)	250uM	pegRNA plus terminal UUUU	28.75	5.2	30.59	5.2
PE-C3 (SEQ ID NO: 233)	250uM	pegRNA without terminal UUUU	30.14	6.6	32.89	6.8
PE with (SGGS)8 linker (SEQ ID NO: 80)	150uM	pegRNA plus terminal UUUU	29.01	6.1	36.66	6.7
PE with (SGGS)8 linker (SEQ ID NO: 80)	150uM	pegRNA without terminal UUUU	27.22	5.5	29.86	6.3
PE-C3 (SEQ ID NO: 233)	150uM	pegRNA without terminal UUUU	19.36	4.2	23.22	4.3
PE-C3 (SEQ ID NO: 233)	150uM	pegRNA plus terminal UUUU	20.42	3.4	24.63	3.2

Example 4. Prime editors with an engineered reverse transcriptase domain

[0605] Prime editor fusion proteins having an engineered reverse transcriptase domain, including truncations and mutations in the MMLVRT RNaseH domain, were examined for prime editing efficiency. Eleven prime editor fusion proteins were designed, modifications to the RT domain protein structure sequences are shown Table 12 below.

[0606] A pegRNA and an ngRNA were designed to target the sickle cell mutation in the HBB gene locus. Two different prime editing targeting strategies were used: i) incorporation of the sickle cell mutation; and ii) incorporation of a silent PAM mutation in addition to the sickle cell mutation. The DNA sequences encoding the pegRNA and ngRNA sequences are shown as below (a 5'Guanine and a 3' sequence TTTTTTT (SEQ ID NO: 646) in the DNA sequences encoding the pegRNAs and ngRNA related to transcription and are not involved in HBB targeting):

[0607] DNA sequence encoding for pegRNA sequence:
GCATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCAGACTTCTCCACAGGAGTCAGGTGCACTTTTTTT (SEQ ID NO: 588)

[0608] DNA sequence encoding for pegRNA sequence (with silent PAM mutation)
GCATGGTGCACCTGACTCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCAGACTTCTCTACAGGAGTCAGGTGCACTTTTTTT (SEQ ID NO: 589)

[0609] DNA sequence encoding for nickRNA sequence (with silent PAM mutation and ngRNA binding):
GCCTTGATACCAACCTGCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTGCTTTTTTT (SEQ ID NO: 590)

[0610] The prime editor coding sequences were each constructed in an expression plasmid under the control of a cytomegalovirus (CMV) promoter. The 5'UTR, and the "TAA" stop codon followed by 3' UTR as provided in Table 68 were also appended to the prime editor encoding sequence in the plasmids. The PEgRNA sequence and the ngRNA sequence were each constructed in a plasmid under the control of a hU6 promoter. The plasmids encoding the prime editors were each individually lipofected along with two additional plasmids, each encoding for the PEgRNA and the ngRNA, into wild type HEK293T cells. 750ng of the prime editor-encoding plasmid, 25ng of the PEgRNA-encoding plasmid, and 83ng of the ngRNA-encoding plasmid were used for lipofection per well (Lipofectamine 2000, Thermo Fisher). A plasmid encoding SpCas9 nuclease, and a plasmid encoding prime editor having full length MMLVRT5M having the sequence of SEQ ID NO: 25 were used as two controls. Genomic DNA was harvested three days post lipofection, PCR amplified and sequenced using Illumina MiseqNext Generation Sequencing. For each treatment, two technical replicates were examined. The results are summarized in Table 12 below. The MMLV-RT pentamutant (SEQ ID NO: 5) were further modified to generate constructs listed in Table 12. Amino acid substitutions are shown as "Original amino acid POSITION substituted amino acid". For example, D524N refers to an Asp to Asn substitution at position 524 compared to SEQ ID No

1, 5 or 623. The letter X and the number that precedes X indicate the position of truncation. For example, G504X refers to truncation after amino acid Gly504 compared to SEQ ID No 5; Gly504 is retained in the truncated amino acid sequence. 22aa_del_N-terimnus refers to a 22 amino acid deletion at the N terminus of SEQ ID No 5. The corresponding Cas9-RT fusion protein sequences and the RT variant sequences, as well as the polypeptide sequences encoding the same used in the experiment for variants G504X, D524N, and L478X are also provided in Tables 18-20, respectively. It should be noted that in this Example and following Examples 4 described herein, modifications to the MMLVRT are relative to MMLVRT5M, and mutations in MMLVRT5M, unless truncated, are retained in the MMLVRT variants.

[0611] The results are summarized in Table 12 below. Truncation of the prime editor to remove the RNAseH domain after positions G504 or L478 lead to an increase in activity as compared with the original full length construct, and inclusion of the L435K mutation is also well-tolerated.

[0612] Table 12. Prime editing efficiency using prime editors having engineered RT domains

MMLVRT modification in PE	**protein SEQ ID**	**Editing efficiency, no PAM mutation (%)**		**Editing efficiency, PAM mutation (%)**	
SpCas9	2	0.11	0.07	0.22	0.09
Control prime editor	25	15.3	14.58	31.57	24.35
G504X	34	18.76	18.8	31.81	27.9
D524N	43	16.18	14	26.67	21.02
L478X	52	18.06	14.83	28.76	22.28
L435K, G504X	61	20.49	16.76	30.97	22.8
M428X	70	3.66	2.93	5.39	4.52
Y133R, Y271R, P365X	71	0.04	0.02	0.09	0.08
P365X	72	0.04	0.04	0.07	0.07
K378X	73	0.07	0.04	0.08	0.05
T328X	74	0.04	0.03	0.07	0.03
R278X	75	0.41	0.37	0.51	0.69
22 aa_del_N-terminus,L435K, G504X	76	0.06	0.1	0.1	0.05

[0613] The experiment was repeated in HEK293T cells, with a different pair of pegRNA and ngRNA made by replacing the 84th nucleotide Guanine in SEQ ID Nos. 589 and 590 to be consistent with the canonical SpCas9 guide RNA scaffold. Three technical replicates were examined for each prime editor variant. The results are shown in Fig. 5.

[0614] Prime editors that comprise a M-MLV RT with truncation after position G504 in combination with multiple linker and NLS sequences were further tested for editing efficiency in CD34+ cells, in comparison to prime editors having the full length M-MLV RT of SEQ ID No 5. Components and structure of each of the fusion protein are indicated in the first column of Table 13. The amino acid sequences and corresponding DNA/RNA sequences that encode fusion protein are provided in Tables 15, 16, 17, 23, 24, 28, and 53. For Table 53, the NLS sequences are provided in Table 2. In the polynucleotide sequences encoding each of the prime editor fusion proteins, the portion that encodes the reverse transcriptase was codon optimized as the corresponding sequence (or portion thereof) encoding the

MMLVRT5M in PE-C3 (DNA and RNA sequence of the full-length codon-optimized MMLVRT5M as set forth in SEQ ID Nos 83 and 84). mRNA encoding each of the prime editor fusion proteins were in vitro transcribed. For in vitro transcription, a 5'UTR was added to the 5' end and a "TAA" stop codon followed by a 3'UTR (sequence provided in Table 68 was added to the 3' end of each of the mRNAs. A pegRNA and a ngRNA were synthesized, end protected PEgRNA and ngRNAs as follows were used to introduce the sickle cell mutation into the HBB gene mC*mA*mU*GGUGCACCUGACUCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAGACUUCUCUACAGGAGUCAGGUGCACmU*mU*mU*U (SEQ ID NO: 591)

[0615] nickRNA sequence: mC*mC*mU*UGAUACCAACCUGCCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCmU*mU*mU*U (SEQ ID NO: 574)

[0616] 150nM mRNA, 20μM PEgRNA, and 10μM ngRNA were used for electroporation in human healthy donor CD34+ cells. Genomic DNA was harvest 24 hours, 48 hours, 72 hours, and 96 hours after electroporation, respectively, and analyzed with Miseq-based sequencing methods. Editing efficiency and indel frequency are summarized in Table 13 below.

[0617] Table 13: prime editing efficiency (%) using prime editors having engineered RT domains

		24h		**48h**		**72h**		**96h**	
PE protein structure	**Corresponding sequence Table No.**	**Editing efficiency (%)**	**Indel frequency (%)**	**Editing efficiency (%)**	**Indel frequency (%)**	**Editing efficiency (%)**	**Indel frequency (%)**	**Editing efficiency (%)**	**Indel frequency (%)**
SV40BPNLS-Cas9H840A-(SGGS)2-XTEN-(SGGS)2-S-MMLVRT5M-SGGS-SV40BPNLS1	15	13.94	2.73	15.62	3.71	17.83	4.15	18.5	4.57
SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT5M-SGGS-SV40BPNLS1	16	19.91	4.05	27.52	7.08	31.15	7.85	24.33	5.55
cmycNLS-BPNLS-Cas9H840A-(SGGS)8-MMLVRT$_{5M}$-BPNLS-NLS	23	22.11	4.72	21.03	5.47	28.88	7.12	30.76	8.97
SV40BPNLS-Cas9H840A-SGGS-(EAAAK)$_8$-SGGS-MMLVRT$_{5M}$-SGGS-SV40BPNLS1	28	20.24	4.89	27.68	7.38	36.64	9.67	38.98	11.07
SV40BPNLS-Cas9H840A-(SGGS)$_2$-XTEN-(SGGS)$_2$-MMLVRT$_{5M}$ (G504X)-NLS	53	17.52	2.93	21.06	4.43	26.1	5.36	26.12	5.4
cmycNLS-BPNLS-Cas9H840A-(SGGS)8-MMLVRT$_{5M}$ (G504X)-BPNLS-NLS	24	26.5	5.17	31.55	8.07	34.68	8.26	37.15	9.82

SV40BPNLS-Cas9H840A-(SGGS)8-MMLVRT$_{5M}$ (G504X)-SGGS-BPNLS1	17	26.51	5.34	34.57	8.63	37.37	8.29	40.05	10.52
No treatment negative control	-	0.05	0.2	0.18	0.2	0.16	0.23	0.31	0.19

[0618] A mRNA dose response was further performed, using the PE-C3 mRNA and the mRNA encoding prime editor fusion proteins (SV40BPNLS-Cas9H840A-(SGGS)2-XTEN-(SGGS)2-MMLVRT(G504X)-NLS) in Table 13 above, which contains codon-optimized truncated MMLVRT(G504X) having the sequence of SEQ ID NO: 92. At 200nM mRNA, the full-length and truncated editor behaved similarly (means of 35.7% and 36.6% prime editing, 72h post-electroporation), but the truncated prime editor was slightly more efficient at 150nM mRNA than the full-length editor (mean of 28.7% for full-length and 34.3% for truncated prime editor).

CLAIMS

What is claimed is:

1. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos. 289, 291, 293, 294, 295, 301, 302, 303, 306, 309, 310, and 311.

2. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos. 286-411.

3. The prime editing composition of claim 1 or 2, wherein the amino acid sequence of the peptide linker has at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to the selected sequence.

4. The prime editing composition of any one of claims 1-3, wherein the selected sequence is SEQ ID NO: 302.

5. The prime editing composition of any one of claims 1-3, wherein the selected sequence is SEQ ID NO: 309.

6. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises at least 4 contiguous SGGS motifs.

7. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises 4 to 10 contiguous SGGS motifs.

8. The prime editing composition of claim 7, wherein the peptide linker comprises 4, 5, 6, 8, or 10 contiguous SGGS motifs.

9. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises at least 2 contiguous EAAAK motifs.

10. A prime editing composition that comprises a fusion protein or a polynucleotide encoding the fusion protein, wherein the fusion protein comprises a DNA binding domain and a DNA polymerase domain connected via a peptide linker, wherein the peptide linker comprises 2 to 8 contiguous EAAAK motifs.

11. The prime editing composition of claim 10, wherein the peptide linker comprises 2, 3, 4, 6, or 8 contiguous EAAAK motifs.

12. The prime editing composition of any one of claims 1-11, wherein the DNA polymerase domain comprises a reverse transcriptase (RT) domain.

13. The prime editing composition of claim 12, wherein the RT domain is a Moloney murine leukemia virus (M-MLV) RT domain.

14. The prime editing composition of claim 13, wherein the M-MLV RT domain comprises an amino acid having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 5.

15. The prime editing composition of claim 13, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1.

16. The prime editing composition of claim 15, wherein the M-MLV RT domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO: 36.

17. the prime editing composition of claim 13, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1.

18. The prime editing composition of claim 17, wherein the M-MLV RT domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 54.

19. A prime editing composition comprising: a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain comprises an amino acid sequence that is truncated at C terminus between positions corresponding to amino acids 504 and 505 as set forth in SEQ ID NO: 1.

20. A prime editing composition comprising a) a DNA binding domain or a polynucleotide encoding the DNA binding domain, and b) a Moloney Murine Leukemia reverse transcriptase (M-MLV RT) domain or a polynucleotide encoding the M-MLV RT domain, wherein the M-MLV RT domain is truncated at C terminus between positions corresponding to amino acids 478 and 479 as set forth in SEQ ID NO: 1.

21. The prime editing composition of claim 19 or 20, wherein the M-MLV RT domain comprises an amino acid substitution D200N, T306K, W313F, T330P, or any combination thereof as compared to a reference M-MLV RT as set forth in SEQ ID NO: 1.

22. The prime editing composition of any one of claims 19-21, wherein the DNA binding domain is connected to the M-MLV RT domain in a fusion protein.

23. The prime editing composition of claim 22, wherein the DNA binding domain and the M-MLV RT domain are connected by a peptide linker.

24. The prime editing composition of claim 23, wherein the peptide linker comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to a sequence selected from the group consisting of SEQ ID Nos 286-411.

25. The prime editing composition of any one of claims 1-24, wherein the DNA binding domain comprises a CRISPR associated (Cas) protein.

26. The prime editing composition of claim 25, wherein the Cas protein is a Type II Cas protein.

27. The prime editing composition of claim 26, wherein the Cas protein is Cas9.

28. The prime editing composition of claim 27, wherein the Cas9 protein is a nickase that comprises a mutation in a HNH domain.

29. The prime editing composition of claim 28, wherein the Cas9 protein comprises a H840A mutation compared to SEQ ID NO: 2.

30. The prime editing composition of claim 29, wherein the DNA binding domain comprises an amino acid sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or100% sequence identity to SEQ ID NO: 7.

31. The prime editing composition of claim 25, wherein the Cas protein is a Type V Cas protein.

32. The prime editing composition of claim 31, wherein the Cas protein is a Cas12a, Cas12b, Cas12c, Cas12d, or Cas12e.

33. The prime editing composition of any one of claims 1-18 and 22-32, wherein the fusion protein comprises the DNA polymerase domain and the DNA binding domain from N-terminus to C-terminus.

34. The prime editing composition of any one of claims 1-18 and 22-32, wherein the fusion protein comprises the DNA polymerase domain and the DNA binding domain from C-terminus to N-terminus.

35. The prime editing composition of claim 34, wherein the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 78, 105, 117, 125, 131, 137, 143, 149, 155, 161, 167, 173, 179, 185, 191, 197, 203, 209, 215, 221, and 227.

36. The prime editing composition of claim 35, wherein the selected sequence is SEQ ID NO 78.

37. The prime editing composition of claim 35, wherein the selected sequence is SEQ ID NO 105.

38. The prime editing composition of claim 34, wherein the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 86, 111, 122, 128, 134, 140, 146, 152, 158, 164, 170, 176, 182, 188, 194, 200, 206, 212, 218, 224, and 230.

39. The prime editing composition of claim 38, wherein the selected sequence is SEQ ID NO: 86.

40. The prime editing composition of claim 38, wherein the selected sequence is SEQ ID NO: 111.

41. The prime editing composition of any one of claims 35-40, wherein the fusion protein comprises an amino acid sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the selected sequence.

42. The prime editing composition of claim any one of claims 34-41, wherein the fusion protein comprises one or more nuclear localization signals (NLSs).

43. The prime editing composition of claim 42, wherein the one or more NLSs comprises an amino acid sequence selected from the group consisting of SEQ ID Nos 8-15 or 621.

44. The prime editing composition of claim 42, wherein the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 77, 93, 104, 116, and 620.

45. The prime editing composition of claim 44, wherein the selected sequence is SEQ ID NO: 77 or SEQ ID NO: 620.

46. The prime editing composition of claim 44, wherein the selected sequence is SEQ ID NO: 93.

47. The prime editing composition of claim 42, wherein the fusion protein comprises an amino acid sequence with at least 80% identity to a sequence selected from the group consisting of SEQ ID Nos 85, 96, 110, and 622.

48. The prime editing composition of claim 47, wherein the selected sequence is SEQ ID NO: 85 or SEQ ID NO: 622.

49. The prime editing composition of claim 48, wherein the selected sequence is SEQ ID NO: 110.

50. The prime editing composition of any one of claims 44-49, wherein the fusion protein comprises an amino acid sequence with at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to the selected sequence.

51. The prime editing composition of any one of claims 1-18 and 22-50, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, and 229.

52. The prime editing composition of claim 51, wherein the selected sequence is SEQ ID NO 81 or 82.

53. The prime editing composition of any one of claims 1-18 and 22-50, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232.

54. The prime editing composition of claim 53, wherein the selected sequence is SEQ ID NO 89 or 90.

55. The prime editing composition of any one of claims 1-18 and 22-50, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 94, 95, 106, 107, 118, and 119.

56. The prime editing composition of any one of claims 1-18 and 22-50, comprising the polynucleotide encoding the fusion protein, wherein the polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 87, 88, 97, 98, 100, 101, 112, and 113.

57. The prime editing composition of claim 55, wherein the selected sequence is SEQ ID NO 79 or 80.

58. The prime editing composition of claim 56, wherein the selected sequence is SEQ ID NO 87 or 88.

59. The prime editing composition of any one of claims 51-58, wherein the polynucleotide encoding the fusion protein further comprises a stop codon at the 3’ end.

60. The prime editing composition of claim 59, wherein the polynucleotide comprises the sequence of SEQ ID NO 276-279.

61. The prime editing composition of claim 59, wherein the polynucleotide comprises the sequence of SEQ ID NO 282-285.

62. The prime editing composition of any one of claims 51-61, further comprising a 5’ untranslated region (UTR) and/or a 3’ UTR.

63. The prime editing composition of claim 62, wherein the polynucleotide comprises the sequence of SEQ ID NO 274, 275, 592, or 593.

64. The prime editing composition of claim 62, wherein the polynucleotide comprises the sequence of SEQ ID NO 280, 281, 594, or 595.

65. The prime editing composition of any one of claims 51-64, wherein the polynucleotide comprises DNA.

66. The prime editing composition of any one of claims 51-64, wherein the polynucleotide comprises mRNA.

67. The prime editing composition of claim 65, further comprising a regulatory element sequence, optionally wherein the regulatory element sequence is a promoter.

68. A prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to a sequence corresponding to nucleotides 100-2130 of a sequence selected from the group consisting of to SEQ ID Nos 412-555.

69. A prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 83 or 84.

70. The prime editing composition of claim 69, wherein the second polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO 83 or 84.

71. A prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises the sequence of SEQ ID No 83 or 84.

72. A prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises a sequence having at least 80% identity to SEQ ID No 91 or 92.

73. The prime editing composition of claim 72, wherein the second polynucleotide comprises a sequence having at least about 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity to SEQ ID NO 91 or 92.

74. A prime editing composition comprising a first polynucleotide encoding a DNA binding domain and a second polynucleotide encoding a DNA polymerase domain, wherein the second polynucleotide comprises the sequence of SEQ ID No 91 or 92.

75. The prime editing composition of any one of claims 68-74, wherein the first polynucleotide encodes a CRISPR associated (Cas) protein.

76. The prime editing composition of claim 75, wherein the Cas protein is a Type II Cas protein.

77. The prime editing composition of claim 76, wherein the Cas protein is Cas9.

78. The prime editing composition of claim 77, wherein the Cas9 protein is a nickase that comprises a mutation in a HNH domain, optionally wherein the Cas9 protein comprises a H840A mutation compared to SEQ ID NO: 2.

79. The prime editing composition of claim 75, wherein the Cas protein is a Type V Cas protein.

80. the prime editing composition of claim 79, wherein the Cas protein is a Cas12a, Cas12b, Cas12c, Cas12d, or Cas12e.

81. The prime editing composition of any one of claims 68-80, wherein the first polynucleotide and the second polynucleotide are connected in a fusion polynucleotide.

82. The prime editing composition of claim 81, wherein the first polynucleotide and the second polynucleotide are connected by a sequence that encodes a peptide linker.

83. The prime editing composition of claims 82, wherein the polynucleotide encoding the peptide linker comprises the sequence of SEQ ID No 235, 236 or 633-636.

84. The prime editing composition of any one of claims 81-83, wherein the first polynucleotide is connected to the 5' end of the second polynucleotide.

85. The prime editing composition of any one of claims 81-83, wherein the first polynucleotide is connected to the 3' end of the second polynucleotide.

86. The prime editing composition of any one of claims 81-85, wherein the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 81, 82, 108, 109, 120, 121, 126, 127, 132, 133, 138, 139, 144, 145, 150, 151, 156, 157, 162, 163, 168, 169, 174, 175, 180, 181, 186, 187, 192, 193, 198, 199, 204, 205, 210, 211, 216, 217, 222, 223, 228, 229, 241, and 242.

87. The prime editing composition of claim 86, wherein the selected sequence is SEQ ID NO 81 or 82.

88. The prime editing composition of claim 86, wherein the selected sequence is SEQ ID NO 241 or 242.

89. The prime editing composition of any one of claims 81-85, wherein the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID Nos 89, 90, 102, 103, 114, 115, 123, 124, 129, 130, 135, 136, 141, 142, 147, 148, 153, 154, 159, 160, 165, 166, 171, 172, , 177, 178, 183, 184, 189, 190, 195, 196, 201, 202, 207, 208, 213, 214, 219, 220, 225, 226, 231, and 232.

90. The prime editing composition of claim 89, wherein the selected sequence is SEQ ID NO 89 or 90.

91. The prime editing composition of claim 89, wherein the selected sequence is SEQ ID NO 102 or 103.

92. The prime editing composition of claim 89, wherein the selected sequence is SEQ ID NO 114 or 115.

93. The prime editing composition of any one of claims 68-92, wherein the first polynucleotide, the second polynucleotide, or both further comprises a sequence encoding a nuclear localization signal (NLS).

94. The prime editing composition of any one of claims 68-93, wherein sequence encoding the NLS comprises the sequence of SEQ ID No 239 or 240 and is connected to the 3' end of the second polynucleotide.

95. The prime editing composition of any one of claims 81-94, wherein the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 94, 95, 106,107, 118, 119, 233, and 234.

96. The prime editing composition of claim 95, wherein the selected sequence is SEQ ID NO: 79 or 80.

97. The prime editing composition of any one of claims 81-94, wherein the fusion polynucleotide comprises a sequence having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from the group consisting of SEQ ID NOs: 87, 88, 97,98, 100, 101, 112, and 113.

98. The prime editing composition of claim 97, wherein the selected sequence is SEQ ID NO: 87 or 88.

99. The prime editing composition of any one of claims 81-98, wherein the fusion polynucleotide further comprises a stop codon at the 3' end.

100. The prime editing composition of claim 99, wherein the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO 276-279.

101. The prime editing composition of claim 99, wherein the fusion polynucleotide comprises a sequence selected from the group consisting of SEQ ID NO 282-285.

102. The prime editing composition of any one of claims 81-101, wherein the fusion polynucleotide comprises a 5' untranslated region (UTR) and/or a 3' UTR.

103. The prime editing composition of claim 102, wherein the polynucleotide comprises the sequence of SEQ ID NO 274, 275, 592, or 593.

104. The prime editing composition of claim 102, wherein the polynucleotide comprises the sequence of SEQ ID NO 280, 281, 594, or 595.

105. The prime editing composition of any one of claims 68-104, wherein the first polynucleotide, the second polynucleotide, and/or the fusion polynucleotide comprises DNA.

106. The prime editing composition of any one of claims 68-104, wherein the first polynucleotide, the second polynucleotide, and/or the fusion polynucleotide comprises mRNA.

107. The prime editing composition of claim 105, wherein the fusion polynucleotide further comprises a regulatory element sequence, optionally wherein the regulatory element sequence is a promoter.

108. The prime editing composition of any one of claims 1-107, wherein the sequence identities are determined by Needleman-Wunsch alignment of two sequences with Gap Costs set to Existence: 11 Extension: 1 where percent identity is calculated by dividing the number of identities by the length of the alignment.

109. The prime editing composition of any one of the claims 1-108, wherein the prime editing composition further comprises a prime editing guide RNA (PEgRNA) or a polynucleotide encoding the PEgRNA.

110. The prime editing composition of any one of claims 1-109, wherein the prime editing composition further comprises a nick guide RNA (ngRNA) or a polynucleotide encoding the ngRNA.

111. A vector comprising one or more of the polynucleotides of the prime editing composition of any one of claims 1-110.

112. The vector of claim 111, wherein the vector is a AAV vector.

113. The vector of claim 112, wherein the vector is a lipid nanoparticle (LNP).

114. A pharmaceutical composition comprising the prime editing composition of any one of claims 1-110 or the vector of claims 111-113, and a pharmaceutically acceptable excipient.

115. A method of editing a target gene, the method comprising contacting the target gene with the prime editing composition of any one of claims 1-110.

116. The method of claim 115, wherein the target gene is in a cell.

117. The method of claim 116, wherein the cell is a human cell.

118. The method of claim 116, wherein the cell is a (CD34+) hematopoietic stem cell or a hematopoietic stem progenitor cell.

119. The method of any one of claims 115-118, wherein the contacting is ex vivo.

120. The method of any one of claims 115-118, wherein the cell is in a subject.