

CROSS REFERENCE TO RELATED APPLICATIONS

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are uses of the gene editing systems disclosed herein, the pharmaceutical compositions and kits comprising such, and/or the genetically modified cells thus produced for treating neurodegenerative diseases (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a subject.

5 In some aspects, the present disclosure features system for genetic editing of a stathmin 2 (STMN2) gene, comprising (i) a Cas12i polypeptide or a first nucleic acid encoding the Cas12i polypeptide, and (ii) an RNA guide or a second nucleic acid encoding the RNA guide. The RNA guide comprises a spacer sequence specific to a target sequence within an STMN2 gene, the target sequence being adjacent to a protospacer adjacent motif (PAM) comprising the motif of
10 5'-TTN-3', which is located 5' to the target sequence.

 In some embodiments, the Cas12i is a Cas12i2 polypeptide. In other embodiments, the Cas12i is a Cas12i4 polypeptide.

 In some embodiments, the Cas12i polypeptide is a Cas12i2 polypeptide comprising an amino acid sequence at least 95% identical to SEQ ID NO: 448. In some instances, the Cas12i2
15 polypeptide may comprise one or more mutations relative to SEQ ID NO: 448. In some examples, the one or more mutations in the Cas12i2 polypeptide are at positions D581, G624, F626, P868, I926, V1030, E1035, and/or S1046 of SEQ ID NO: 448. In some examples, the one or more mutations are amino acid substitutions, which optionally is D581R, G624R, F626R, P868T, I926R, V1030G, E1035R, S1046G, or a combination thereof.

20 In one example, the Cas12i2 polypeptide comprises mutations at positions D581, D911, I926, and V1030 (*e.g.*, amino acid substitutions of D581R, D911R, I926R, and V1030G). In another example, the Cas12i2 polypeptide comprises mutations at positions D581, I926, and V1030 (*e.g.*, amino acid substitutions of D581R, I926R, and V1030G). In yet another example, the Cas12i2 polypeptide comprises mutations at positions D581, I926, V1030, and S1046 (*e.g.*, amino acid substitutions of D581R, I926R, V1030G, and S1046G). In still another example, the
25 Cas12i2 polypeptide comprises mutations at positions D581, G624, F626, I926, V1030, E1035, and S1046 (*e.g.*, amino acid substitutions of D581R, G624R, F626R, I926R, V1030G, E1035R, and S1046G). In another example, the Cas12i2 polypeptide comprises mutations at positions D581, G624, F626, P868, I926, V1030, E1035, and S1046 (*e.g.*, amino acid substitutions of
30 D581R, G624R, F626R, P868T, I926R, V1030G, E1035R, and S1046G).

 Exemplary Cas12i2 polypeptides for use in any of the gene editing systems disclosed herein may comprise the amino acid sequence of any one of SEQ ID NOs: 449-453. In one example, the exemplary Cas12i2 polypeptide for use in any of the gene editing systems disclosed herein comprises the amino acid sequence of SEQ ID NO: 450. In another example, the

exemplary Cas12i2 polypeptide for use in any of the gene editing systems disclosed herein comprises the amino acid sequence of SEQ ID NO: 453.

In some embodiments, the gene editing system may comprise the first nucleic acid encoding the Cas12i polypeptide (e.g., the Cas12i2 polypeptide). In some instances, the first
5 nucleic acid is located in a first vector (e.g., a viral vector such as an adeno-associated viral vector or AAV vector). In some instances, the first nucleic acid is a messenger RNA (mRNA). In some instances, the coding sequence for the Cas12i polypeptide is codon optimized.

In some embodiments, the target sequence may be within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene.

10 In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID NOs: 4508, 4512, 4559, and 4561, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4508, 4512, 4559, and 4561.

In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556,
15 4557, 4558, 4559, 4560, 4561, and 4562, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.

In some embodiments, the spacer sequence may be 20-30-nucleotides in length. In some examples, the spacer sequence is 20-nucleotides in length.

20 In some embodiments, the RNA guide comprises the spacer and a direct repeat sequence. In some examples, the direct repeat sequence is 23-36-nucleotides in length. In one example, the direct repeat sequence is at least 90% identical to any one of SEQ ID NOs: 1-10 or a fragment thereof that is at least 23-nucleotides in length. In some specific examples, the direct repeat sequence is any one of SEQ ID NOs: 1-10, or a fragment thereof that is at least 23-nucleotides in
25 length. By way of non-limiting example, the direct repeat sequence is 5'-AGAAAUCCGUCUUCAUUGACGG-3' (SEQ ID NO: 10).

In some embodiments, the system may comprise the second nucleic acid encoding the RNA guide. In some examples, the nucleic acid encoding the RNA guide may be located in a viral vector. In some examples, the viral vector comprises the both the first nucleic acid encoding
30 the Cas12i polypeptide (e.g., the Cas12i2 polypeptide) and the second nucleic acid encoding the RNA guide.

In some embodiments, any of the systems described herein may comprise the first nucleic acid encoding the Cas12i polypeptide (e.g., the Cas12i2 polypeptide), which is located in a first vector, and the second nucleic acid encoding the RNA guide, which is located on a second

vector. In some examples, the first and/or second vector is a viral vector. In some specific examples, the first and second vectors are the same vector.

In some embodiments, any of the systems described herein may comprise one or more lipid nanoparticles (LNPs), which encompass the Cas12i polypeptide (e.g., the Cas12i2 polypeptide) or the first nucleic acid encoding the Cas12i polypeptide, the RNA guide or the second nucleic acid encoding the RNA guide, or both.

In some embodiments, the system described herein may comprise an LNP, which encompasses the Cas12i polypeptide (e.g., the Cas12i2 polypeptide) or the first nucleic acid encoding the Cas12i polypeptide, and a viral vector comprising the second nucleic acid encoding the RNA guide. In some examples, the viral vector is an AAV vector. In other embodiments, the system described herein may comprise an LNP, which encompasses the RNA guide or the second nucleic acid encoding the RNA guide, and a viral vector comprising the first nucleic acid encoding the Cas12i polypeptide. In some examples, the viral vector is an AAV vector.

In some aspects, the present disclosure also provides a pharmaceutical composition comprising any of the gene editing systems disclosed herein, and a kit comprising the components of the gene editing system.

In other aspects, the present disclosure also features a method for editing a stathmin 2 (STMN2) gene in a cell, the method comprising contacting a host cell with any of the systems disclosed herein to genetically edit the STMN2 gene in the host cell. In some examples, the host cell is cultured *in vitro*. In other examples, the contacting step is performed by administering the system for editing the STMN2 gene to a subject comprising the host cell.

Also within the scope of the present disclosure is a cell comprising a disrupted a stathmin 2 (STMN2) gene, which can be produced by contacting a host cell with the system disclosed herein genetically edit the STMN2 gene in the host cell.

Still in other aspects, the present disclosure provides a method for treating neurodegenerative diseases (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a subject. The method may comprise administering to a subject in need thereof any of the systems for editing a stathmin 2 (STMN2) gene or any of the cells disclosed herein.

Also provided herein is an RNA guide, comprising (i) a spacer sequence as disclosed herein that is specific to a target sequence in a stathmin 2 (STMN2) gene, wherein the target sequence is adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3', which is located 5' to the target sequence; and (ii) a direct repeat sequence.

In some embodiments, the spacer may be 20-30-nucleotides in length. In some examples, the spacer is 20-nucleotides in length.

In some embodiments, the direct repeat sequence may be 23-36-nucleotides in length. In some examples, the direct repeat sequence is 23-nucleotides in length.

In some embodiments, the target sequence is within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene.

5 In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID NOs: 4508, 4512, 4559, and 4561, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4508, 4512, 4559, and 4561.

In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 10 4557, 4558, 4559, 4560, 4561, and 4562, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.

In some embodiments, the direct repeat sequence may be at least 90% identical to any one of SEQ ID NOs: 1-10 or a fragment thereof that is at least 23-nucleotides in length. In some 15 examples, the direct repeat sequence is any one of SEQ ID NOs: 1-10, or a fragment thereof that is at least 23-nucleotides in length. By way of non-limiting example, the direct repeat sequence is 5'-AGAAAUCCGUCUUUCAUUGACGG-3' (SEQ ID NO: 10).

Also provided herein are any of the gene editing systems disclosed herein, pharmaceutical compositions or kits comprising such, or genetically modified cells generated by the gene editing 20 system for use in treating neurodegenerative disease (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a subject, as well as uses of the gene editing systems disclosed herein, pharmaceutical compositions or kits comprising such, or genetically modified cells generated by the gene editing system for manufacturing a medicament for treatment of neurodegenerative disease (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a subject.

25 The details of one or more embodiments of the invention are set forth in the description below. Other features or advantages of the present invention will be apparent from the following drawings and detailed description of several embodiments, and also from the appended claims.

BRIEF DESCRIPTION OF THE DRAWINGS

30 The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present disclosure, which can be better understood by reference to the drawing in combination with the detailed description of specific embodiments presented herein.

FIG. 1 shows editing percentage of STMN2 intron target sequences by the indicated guides, as 35 described in Example 1.

FIG. 2A shows disruption of >15% of the cryptic splice site in STMN2 intron 1 by guides 4, 8, 55, and 57.

FIG. 2B shows disruption of >15% of at least one of 3 TDP-43 binding motifs in STMN2 intron 1 by guides 12, 46, 47, 48, and 49.

FIG. 2C shows disruption of >15% of the premature polyadenylation signal in STMN2 intron 1 by guides 17 and 18.

FIG. 3 is a schematic showing the positions where each of the indicated RNA guides binds intron 1 of STMN2 relative to the positions of the cryptic splice site, the TDP-43 binding motifs, and the premature polyadenylation signal.

FIG. 4 shows indel activity of the tested RNA guides in SH-SY5Y cells.

FIG. 5A is a plot comparing indel activity (% indels) demonstrated in HEK293T cells and SH-SY5Y cells from Example 1 and Example 2, respectively. **FIG. 5B** is a plot comparing splice site motif disruption demonstrated in HEK293T cells and SH-SY5Y cells from Example 1 and Example 2, respectively.

DETAILED DESCRIPTION

The present disclosure relates to a system for genetic editing of a stathmin 2 (STMN2) gene, which comprises (i) a Cas12i polypeptide or a first nucleic acid encoding the Cas12i2 polypeptide; and (ii) an RNA guide or a second nucleic acid encoding the RNA guide, wherein the RNA guide comprises a spacer sequence specific to a target sequence within a STMN2 gene, the target sequence being adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3', which is located 5' to the target sequence. Also provided in the present disclosure are a pharmaceutical composition or a kit comprising such a system as well as uses thereof. Further disclosed herein are a method for editing a STMN2 gene in a cell, a cell so produced that comprises a disrupted a STMN2 gene, a method of treating neurodegenerative disease in a subject, and an RNA guide that comprises (i) a spacer sequence that is specific to a target sequence in a STMN2 gene, wherein the target sequence is adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3', which is located 5' to the target sequence; and (ii) a direct repeat sequence, as well as uses thereof.

The Cas12i polypeptide for use in the gene editing system disclosed herein may be a Cas12i2 polypeptide, e.g., a wild-type Cas12i polypeptide or a variant thereof as those disclosed herein. In some examples, the Cas12i2 polypeptide comprises an amino acid sequence at least 95% identical to SEQ ID NO: 448 and comprises one or more mutations relative to SEQ ID NO: 448. In other examples, the Cas12i polypeptide may be a Cas12i4 polypeptide, which is also disclosed herein.

Definitions

The present disclosure will be described with respect to particular embodiments and with reference to certain Figures, but the present disclosure is not limited thereto but only by the claims. Terms as set forth hereinafter are generally to be understood in their common sense unless indicated otherwise.

As used herein, the term “activity” refers to a biological activity. In some embodiments, activity includes enzymatic activity, e.g., catalytic ability of a Cas12i polypeptide. For example, activity can include nuclease activity.

As used herein the term “STMN2” refers to “stathmin-2.” STMN2 is a neuron-specific member of the stathmin family of proteins and plays roles in regulation of microtubule stability and signal transduction. SEQ ID NO: 454 as set forth herein provides an example of a STMN2 gene sequence. Reference is also made to Gene ID: 11075 for this sequence (www.ncbi.nlm.nih.gov/gene/11075).

As used herein, the term “Cas12i polypeptide” (also referred to herein as Cas12i) refers to a polypeptide that binds to a target sequence on a target nucleic acid specified by an RNA guide, wherein the polypeptide has at least some amino acid sequence homology to a wild-type Cas12i polypeptide. In some embodiments, the Cas12i polypeptide comprises at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity with any one of SEQ ID NOs: 1-5 and 11-18 of U.S. Patent No. 10,808,245, which is incorporated by reference for the subject matter and purpose referenced herein. In some embodiments, a Cas12i polypeptide comprises at least 75%, at least 80%, at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity with any one of SEQ ID NOs: 4503, 448, 4504, and 482 of the present application. In some embodiments, a Cas12i polypeptide of the disclosure is a Cas12i2 polypeptide as described in WO/2021/202800, the relevant disclosures of which are incorporated by reference for the subject matter and purpose referenced herein. In some embodiments, the Cas12i polypeptide cleaves a target nucleic acid (*e.g.*, as a nick or a double strand break).

As used herein, the term “adjacent to” refers to a nucleotide or amino acid sequence in close proximity to another nucleotide or amino acid sequence. In some embodiments, a nucleotide sequence is adjacent to another nucleotide sequence if no nucleotides separate the two sequences (*i.e.*, immediately adjacent). In some embodiments, a nucleotide sequence is adjacent to another nucleotide sequence if a small number of nucleotides separate the two sequences (*e.g.*, about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleotides). In some

embodiments, a first sequence is adjacent to a second sequence if the two sequences are separated by about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 nucleotides. In some embodiments, a first sequence is adjacent to a second sequence if the two sequences are separated by up to 2 nucleotides, up to 5 nucleotides, up to 8 nucleotides, up to 10 nucleotides, up to 12 nucleotides, 5 or up to 15 nucleotides. In some embodiments, a first sequence is adjacent to a second sequence if the two sequences are separated by 2-5 nucleotides, 4-6 nucleotides, 4-8 nucleotides, 4-10 nucleotides, 6-8 nucleotides, 6-10 nucleotides, 6-12 nucleotides, 8-10 nucleotides, 8-12 nucleotides, 10-12 nucleotides, 10-15 nucleotides, or 12-15 nucleotides.

As used herein, the term “complex” refers to a grouping of two or more molecules. In 10 some embodiments, the complex comprises a polypeptide and a nucleic acid molecule interacting with (e.g., binding to, coming into contact with, adhering to) one another. For example, the term “complex” can refer to a grouping of an RNA guide and a polypeptide (e.g., a Cas12i polypeptide). Alternatively, the term “complex” can refer to a grouping of an RNA guide, a polypeptide, and the complementary region of a target sequence. As used herein, the term 15 “complex” can refer to a grouping of a STMN2-targeting RNA guide and a Cas12i polypeptide.

As used herein, the term “protospacer adjacent motif” or “PAM” refers to a DNA sequence adjacent to a target sequence (e.g., a STMN2 target sequence). In a double-stranded DNA molecule, the strand containing the PAM motif is called the “PAM-strand” and the complementary strand is called the “non-PAM strand.” The RNA guide binds to a site in the 20 non-PAM strand that is complementary to a target sequence disclosed herein.

In some embodiments, the PAM strand is a coding (e.g., sense) strand. In other embodiments, the PAM strand is a non-coding (e.g., antisense strand). Since an RNA guide binds the non-PAM strand via base-pairing, the non-PAM strand is also known as the target strand, while the PAM strand is also known as the non-target strand.

As used herein, the term “target sequence” refers to a DNA fragment adjacent to a PAM motif (on the PAM strand). The complementary region of the target sequence is on the non-PAM strand. A target sequence may be immediately adjacent to the PAM motif. Alternatively, the target sequence and the PAM may be separately by a small sequence segment (e.g., up to 5 nucleotides, for example, up to 4, 3, 2, or 1 nucleotide). A target sequence may be located at the 30 3’ end of the PAM motif or at the 5’ end of the PAM motif, depending upon the CRISPR nuclease that recognizes the PAM motif, which is known in the art. For example, a target sequence is located at the 3’ end of a PAM motif for a Cas12i polypeptide (e.g., a Cas12i2 polypeptide such as those disclosed herein). In some embodiments, the target sequence is a sequence within a STMN2 gene sequence, including, but not limited, to the sequence set forth in 35 SEQ ID NO: 454.

As used herein, the term “spacer” or “spacer sequence” is a portion in an RNA guide that is the RNA equivalent of the target sequence (a DNA sequence). The spacer contains a sequence capable of binding to the non-PAM strand via base-pairing at the site complementary to the target sequence (in the PAM strand). Such a spacer is also known as specific to the target
5 sequence. In some instances, the spacer may be at least 75% identical to the target sequence (e.g., at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, or at least 99%), except for the RNA-DNA sequence difference. In some instances, the spacer may be 100% identical to the target sequence except for the RNA-DNA sequence difference.

As used herein, the term “RNA guide” or “RNA guide sequence” refers to any RNA
10 molecule or a modified RNA molecule that facilitates the targeting of a polypeptide (e.g., a Cas12i polypeptide) described herein to a target sequence (e.g., a sequence of a STMN2 gene). For example, an RNA guide can be a molecule that is designed to be complementary to a specific nucleic acid sequence (a target sequence such as a target sequence within a STMN2 gene). An RNA guide may comprise a spacer sequence and a direct repeat (DR) sequence. In some
15 instances, the RNA guide can be a modified RNA molecule comprising one or more deoxyribonucleotides, for example, in a DNA-binding sequence contained in the RNA guide, which binds a sequence complementary to the target sequence. In some examples, the DNA-binding sequence may contain a DNA sequence or a DNA/RNA hybrid sequence. The terms CRISPR RNA (crRNA), pre-crRNA, and mature crRNA are also used herein to refer to an RNA
20 guide.

As used herein, the term “complementary” refers to a first polynucleotide (e.g., a spacer sequence of an RNA guide) that has a certain level of complementarity to a second polynucleotide (e.g., the complementary sequence of a target sequence) such that the first and second polynucleotides can form a double-stranded complex via base-pairing to permit an
25 effector polypeptide that is complexed with the first polynucleotide to act on (e.g., cleave) the second polynucleotide. In some embodiments, the first polynucleotide may be substantially complementary to the second polynucleotide, i.e., having at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% complementarity to the second polynucleotide. In some embodiments, the first polynucleotide is
30 completely complementary to the second polynucleotide, i.e., having 100% complementarity to the second polynucleotide.

The “percent identity” (a.k.a., sequence identity) of two nucleic acids or of two amino acid sequences is determined using the algorithm of Karlin and Altschul Proc. Natl. Acad. Sci. USA 87:2264-68, 1990, modified as in Karlin and Altschul Proc. Natl. Acad. Sci. USA 90:5873-
35 77, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version

2.0) of Altschul, et al. J. Mol. Biol. 215:403-10, 1990. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to the nucleic acid molecules of the present disclosure. BLAST protein searches can be performed with the XBLAST program, score=50, word length=3 to obtain amino acid sequences homologous to the protein molecules of the present disclosure. Where gaps exist between two sequences, Gapped BLAST can be utilized as described in Altschul et al., Nucleic Acids Res. 25(17):3389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used.

As used herein, the term “edit” refers to one or more modifications introduced into a target nucleic acid, e.g., within the STMN2 gene. The edit can be one or more substitutions, one or more insertions, one or more deletions, or a combination thereof. As used herein, the term “substitution” refers to a replacement of a nucleotide or nucleotides with a different nucleotide or nucleotides, relative to a reference sequence. As used herein, the term “insertion” refers to a gain of a nucleotide or nucleotides in a nucleic acid sequence, relative to a reference sequence. As used herein, the term “deletion” refers to a loss of a nucleotide or nucleotides in a nucleic acid sequence, relative to a reference sequence.

No particular process is implied in how to make a sequence comprising a deletion. For instance, a sequence comprising a deletion can be synthesized directly from individual nucleotides. In other embodiments, a deletion is made by providing and then altering a reference sequence. The nucleic acid sequence can be in a genome of an organism. The nucleic acid sequence can be in a cell. The nucleic acid sequence can be a DNA sequence. The deletion can be a frameshift mutation or a non-frameshift mutation. A deletion described herein refers to a deletion of up to several kilobases.

As used herein, the terms “upstream” and “downstream” refer to relative positions within a single nucleic acid (e.g., DNA) sequence in a nucleic acid molecule. “Upstream” and “downstream” relate to the 5' to 3' direction, respectively, in which RNA transcription occurs. A first sequence is upstream of a second sequence when the 3' end of the first sequence occurs before the 5' end of the second sequence. A first sequence is downstream of a second sequence when the 5' end of the first sequence occurs after the 3' end of the second sequence. In some embodiments, the 5'-NTTN-3' or 5'-TTN-3' sequence is upstream of an indel described herein, and a Cas12i-induced indel is downstream of the 5'-NTTN-3' or 5'-TTN-3' sequence.

I. Gene Editing Systems

In some aspects, the present disclosure provides gene editing systems comprising an RNA guide targeting a STMN2 gene. Such a gene editing system can be used to edit the STMN2 target gene, e.g., to disrupt the STMN2 gene.

5 As used herein the term “STMN2” refers to “stathmin-2.” STMN2 is a neuron-specific member of the stathmin family of proteins and plays roles in regulation of microtubule stability and signal transduction. SEQ ID NO: 454 as set forth herein provides an example of a STMN2 gene sequence. Reference is also made to Gene ID: 11075 for this sequence (www.ncbi.nlm.nih.gov/gene/11075).

10 In some embodiments, the RNA guide is comprised of a direct repeat component and a spacer sequence. In some embodiments, the RNA guide binds a Cas12i polypeptide. In some embodiments, the spacer sequence is specific to a STMN2 target sequence, wherein the STMN2 target sequence is adjacent to a 5'-NTTN-3' or 5'-TTN-3' PAM sequence as described herein. In the case of a double-stranded target, the RNA guide binds to a first strand of the target (i.e., the non-PAM strand) and a PAM sequence as described herein is present in the second,
15 complementary strand (i.e., the PAM strand).

 In some embodiments, the present disclosure provides compositions comprising a complex, wherein the complex comprises an RNA guide targeting a STMN2. In some embodiments, the present disclosure comprises a complex comprising an RNA guide and a Cas12i polypeptide. In some embodiments, the RNA guide and the Cas12i polypeptide bind to each other in a molar ratio of about 1:1. In some embodiments, a complex comprising an RNA guide and a Cas12i polypeptide binds to the complementary region of a target sequence within a STMN2 gene. In some embodiments, a complex comprising an RNA guide targeting a STMN2 and a Cas12i polypeptide binds to the complementary region of a target sequence within the STMN2 gene at a molar ratio of about 1:1. In some embodiments, the complex comprises
20 enzymatic activity, such as nuclease activity, that can cleave the STMN2 target sequence and/or the complementary sequence. The RNA guide, the Cas12i polypeptide, and the complementary region of the STMN2 target sequence, either alone or together, do not naturally occur. In some embodiments, the RNA guide in the complex comprises a direct repeat and/or a spacer sequence described herein.

30 In some embodiments, the present disclosure comprises compositions comprising an RNA guide as described herein and/or an RNA encoding a Cas12i polypeptide as described herein. In some embodiments, the RNA guide and the RNA encoding a Cas12i polypeptide are comprised together within the same composition. In some embodiments, the RNA guide and the RNA encoding a Cas12i polypeptide are comprised within separate compositions. In some

embodiments, the RNA guide comprises a direct repeat and/or a spacer sequence described herein.

Use of the gene editing systems disclosed herein has advantages over those of other known nuclease systems. Cas12i polypeptides are smaller than other nucleases. For example, 5 Cas12i2 is 1,054 amino acids in length, whereas *S. pyogenes* Cas9 (SpCas9) is 1,368 amino acids in length, *S. thermophilus* Cas9 (StCas9) is 1,128 amino acids in length, FxCpf1 is 1,300 amino acids in length, AsCpf1 is 1,307 amino acids in length, and LbCpf1 is 1,246 amino acids in length. Cas12i RNA guides, which do not require a trans-activating CRISPR RNA (tracrRNA), are also smaller than Cas9 RNA guides. The smaller Cas12i polypeptide and RNA 10 guide sizes are beneficial for delivery. Compositions comprising a Cas12i polypeptide also demonstrate decreased off-target activity compared to compositions comprising an SpCas9 polypeptide. See, WO/2021/202800, the relevant disclosures of which are incorporated by reference for the subject matter and purpose referenced herein. Furthermore, indels induced by compositions comprising a Cas12i polypeptide differ from indels induced by compositions 15 comprising an SpCas9 polypeptide. For example, SpCas9 polypeptides primarily induce insertions and deletions of 1 nucleotide in length. However, Cas12i polypeptides induce larger deletions, which can be beneficial in disrupting a larger portion of a gene such as STMN2.

Also provided herein is a system for genetic editing of a STMN2 gene, which comprises (i) a Cas12i polypeptide (e.g., a Cas12i2 polypeptide) or a first nucleic acid encoding the Cas12i 20 polypeptide (e.g., a Cas12i2 polypeptide comprises an amino acid sequence at least 95% identical to SEQ ID NO: 448, which may and comprises one or more mutations relative to SEQ ID NO: 448); and (ii) an RNA guide or a second nucleic acid encoding the RNA guide, wherein the RNA guide comprises a spacer sequence specific to a target sequence within the STMN2 gene (e.g., within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the 25 STMN2 gene), the target sequence being adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3' (5'-NTTN-3'), which is located 5' to the target sequence.

A. RNA Guides

In some embodiments, the gene editing system described herein comprises an RNA guide 30 targeting a STMN2 gene, for example, targeting exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene. In some embodiments, the gene editing system described herein may comprise two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or more) RNA guides targeting STMN2.

The RNA guide may direct the Cas12i polypeptide contained in the gene editing system 35 as described herein to an STMN2 target sequence. Two or more RNA guides may direct two or

more separate Cas12i polypeptides (e.g., Cas12i polypeptides having the same or different sequence) as described herein to two or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, or more) STMN2 target sequences. Those skilled in the art reading the below examples of particular kinds of RNA guides will understand that, in some embodiments, an RNA guide is STMN2 target-specific.

5 That is, in some embodiments, an RNA guide binds specifically to one or more STMN2 target sequences (e.g., within a cell) and not to non-targeted sequences (e.g., non-specific DNA or random sequences within the same cell).

In some embodiments, the RNA guide comprises a spacer sequence followed by a direct repeat sequence, referring to the sequences in the 5' to 3' direction. In some embodiments, the
10 RNA guide comprises a first direct repeat sequence followed by a spacer sequence and a second direct repeat sequence, referring to the sequences in the 5' to 3' direction. In some embodiments, the first and second direct repeats of such an RNA guide are identical. In some embodiments, the first and second direct repeats of such an RNA guide are different.

In some embodiments, the spacer sequence and the direct repeat sequence(s) of the RNA
15 guide are present within the same RNA molecule. In some embodiments, the spacer and direct repeat sequences are linked directly to one another. In some embodiments, a short linker is present between the spacer and direct repeat sequences, e.g., an RNA linker of 1, 2, or 3 nucleotides in length. In some embodiments, the spacer sequence and the direct repeat sequence(s) of the RNA guide are present in separate molecules, which are joined to one another
20 by base pairing interactions.

Additional information regarding exemplary direct repeat and spacer components of RNA guides is provided as follows.

(i). Direct Repeat

25 In some embodiments, the RNA guide comprises a direct repeat sequence. In some embodiments, the direct repeat sequence of the RNA guide has a length of between 12-100, 13-75, 14-50, or 15-40 nucleotides (e.g., 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).

In some embodiments, the direct repeat sequence is a sequence of Table 1 or a portion of
30 a sequence of Table 1. The direct repeat sequence can comprise nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 4 through nucleotide 36
35 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise

nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can comprise nucleotide 1 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 2 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 3 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 4 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 5 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 6 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 7 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 8 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 9 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 10 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 11 through nucleotide 34 of SEQ ID NO: 9. The direct repeat sequence can comprise nucleotide 12 through nucleotide 34 of SEQ ID NO: 9. In some embodiments, the direct repeat sequence is set forth in SEQ ID NO: 10. In some embodiments, the direct repeat sequence comprises a portion of the sequence set forth in SEQ ID NO: 10.

In some embodiments, the direct repeat sequence has at least 90% identity (*e.g.*, at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 1 or a portion of a sequence of Table 1. The direct repeat sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can have at least 90% identity to a sequence comprising 2 through nucleotide 36 of any one of SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, or 8. The direct repeat sequence can have at least 90% identity to a sequence comprising 3 through nucleotide 36 of any

15

In some embodiments, the direct repeat sequence has at least 90% identity (*e.g.*, at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to SEQ ID NO: 10. In some embodiments, the direct repeat sequence has at least 90% identity to a portion of the sequence set forth in SEQ ID NO: 10.

- 5 In some embodiments, compositions comprising a Cas12i2 polypeptide and an RNA guide comprising the direct repeat of SEQ ID NO: 10 and a spacer length of 20 nucleotides are capable of introducing indels into a STMN2 target sequence.

In some embodiments, the direct repeat sequence is at least 90% identical to the reverse complement of any one of SEQ ID NOs: 1-10 (*see*, Table 1). In some embodiments, the direct repeat sequence is the reverse complement of any one of SEQ ID NOs: 1-10.

Table 1. Cas12i2 Direct Repeat Sequences

Sequence identifier	Direct Repeat Sequence
SEQ ID NO: 1	GUUGCAAAACCCAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 2	AAUAGCGGCCCUAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 3	AUUGGAACUGGCGAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 4	CCAGCAACACCUAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 5	CGGCGCUCGAAUAGGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 6	GUGGCAACACCUAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 7	GUUGCAACACCUAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 8	GUUGCAAUGCCUAAGAAAUCCGUCUUUCAUUGACGG
SEQ ID NO: 9	GCAACACCUAAGAAAUCCGUCUUUCAUUGACGGG
SEQ ID NO: 10	AGAAAUCCGUCUUUCAUUGACGG

- In some embodiments, the direct repeat sequence is a sequence of Table 2 or a portion of a sequence of Table 2. The direct repeat sequence can comprise nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs:

462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can comprise nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479.

In some embodiments, the direct repeat sequence has at least 95% identity (e.g., at least 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 2 or a portion of a sequence of Table 2. The direct repeat sequence can have at least 95% identity to a sequence comprising nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 2 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 3 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 4 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 5 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 6 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 7 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476,

477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 8 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 9 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 10 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 11 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 12 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 95% identity to a sequence comprising 13 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479.

In some embodiments, the direct repeat sequence has at least 90% identity (e.g., at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 2 or a portion of a sequence of Table 2. The direct repeat sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 2 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 3 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 4 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 5 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 6 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 7 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90%

identity to a sequence comprising 8 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 9 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 10 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 11 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 12 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. The direct repeat sequence can have at least 90% identity to a sequence comprising 13 through nucleotide 36 of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479.

In some embodiments, the direct repeat sequence is at least 90% identical to the reverse complement of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. In some embodiments, the direct repeat sequence is at least 95% identical to the reverse complement of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479. In some embodiments, the direct repeat sequence is the reverse complement of any one of SEQ ID NOs: 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, or 479.

In some embodiments, the direct repeat sequence is at least 90% identical to SEQ ID NO: 480 or a portion of SEQ ID NO: 480. In some embodiments, the direct repeat sequence is at least 95% identical to SEQ ID NO: 480 or a portion of SEQ ID NO: 480. In some embodiments, the direct repeat sequence is 100% identical to SEQ ID NO: 480 or a portion of SEQ ID NO: 480.

Table 2. Cas12i4 Direct Repeat Sequences

Sequence identifier	Direct Repeat Sequence
SEQ ID NO: 462	UCUCAACGAUAGUCAGACAUGUGUCCUCAGUGACAC
SEQ ID NO: 463	UUUUAACAACACUCAGGCAUGUGUCCACAGUGACAC
SEQ ID NO: 464	UUGAACGGAUACUCAGACAUGUGUUUCCAGUGACAC
SEQ ID NO: 465	UGCCCUCAAUAGUCAGAUGUGUGUCCACAGUGACAC
SEQ ID NO: 466	UCUCAAUGAUACUAGAUACGUGUCCUCAGUGACAC
SEQ ID NO: 467	UCUCAAUGAUACUCAGACAUGUGUCCCCAGUGACAC
SEQ ID NO: 468	UCUCAAUGAUACUAAAGACAUGUGUCCUCAGUGACAC
SEQ ID NO: 469	UCUCAACUAAUACUCAGACAUGUGUCCUCAGUGACAC
SEQ ID NO: 470	UCUCAACGAUACUCAGACAUGUGUCCUCAGUGACAC
SEQ ID NO: 471	UCUCAACGAUACUAAAGAUUGUGUCCUCAGCGACAC

SEQ ID NO: 472	UCUCAACGAUACUAAGAU AUGUGUCCCCAGUGACAC
SEQ ID NO: 473	UCUCAACGAUACUAAGAU AUGUGUCCACAGUGACAC
SEQ ID NO: 474	UCUCAACAAUACUCAGACAUGUGUCCCCAGUGACAC
SEQ ID NO: 475	UCUCAACAAUACUAAGGCAUGUGUCCCCAGUGACCC
SEQ ID NO: 476	UCUCAAGAUACUCAGACACGUGUCCCCAGUGACAC
SEQ ID NO: 477	UCUCAAAAAUACUCAGACAUGUGUCCUCAGUGACAC
SEQ ID NO: 478	GCGAAACAACAGUCAGACAUGUGUCCCCAGUGACAC
SEQ ID NO: 479	CCUCAACGAUAUUAAGACAUGUGUCCGCAGUGACAC
SEQ ID NO: 480	AGACAUGUGUCCUCAGUGACAC

In some embodiments, the direct repeat sequence is a sequence of Table 3 or a portion of a sequence of Table 3. In some embodiments, the direct repeat sequence has at least 95% identity (e.g., at least 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 3 or a portion of a sequence of Table 3. In some embodiments, the direct repeat sequence has at least 90% identity (e.g., at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 3 or a portion of a sequence of Table 3. In some embodiments, the direct repeat sequence is at least 90% identical to the reverse complement of any one of SEQ ID NOs: 485-487. In some embodiments, the direct repeat sequence is at least 95% identical to the reverse complement of any one of SEQ ID NOs: 485-487. In some embodiments, the direct repeat sequence is the reverse complement of any one of SEQ ID NOs: 485-487.

Table 3. Cas12i1 Direct Repeat Sequences

Sequence identifier	Direct Repeat Sequence
SEQ ID NO: 485	GUUGGAAUGACUAAUUUUUGUGCCCCACCGUUGGCAC
SEQ ID NO: 486	AAUUUUUGUGCCCAUCGUUGGCAC
SEQ ID NO: 487	AUUUUUGUGCCCAUCGUUGGCAC

In some embodiments, the direct repeat sequence is a sequence of Table 4 or a portion of a sequence of Table 4. In some embodiments, the direct repeat sequence has at least 95% identity (e.g., at least 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 4 or a portion of a sequence of Table 4. In some embodiments, the direct repeat sequence has at least 90% identity (e.g., at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 4 or a portion of a sequence of Table 4. In some embodiments, the direct repeat sequence is at least 90% identical to the reverse complement of any one of SEQ ID NOs: 488-490. In some embodiments, the direct repeat sequence is at least 95% identical to the reverse complement of any one of SEQ ID NOs: 488-490. In some embodiments, the direct repeat sequence is the reverse complement of any one of SEQ ID NOs: 488-490.

Table 4. Cas12i3 Direct Repeat Sequences.

Sequence identifier	Direct Repeat Sequence
SEQ ID NO: 488	CUAGCAAUGACCUGAAUAGUGUGUCCUUAGUUGACAU
SEQ ID NO: 489	CCUACAAUACCUGAAGAAAUCCGUCCUAAGUUGACGG
SEQ ID NO: 490	AUAGUGUGUCCUUAGUUGACAU

In some embodiments, a direct repeat sequence described herein comprises a uracil (U). In some embodiments, a direct repeat sequence described herein comprises a thymine (T). In some
5 embodiments, a direct repeat sequence according to Tables 1-4 comprises a sequence comprising a thymine in one or more places indicated as uracil in Tables 1-4.

(ii). Spacer Sequences

In some embodiments, the RNA guide comprises a DNA targeting or spacer sequence. In
10 some embodiments, the spacer sequence of the RNA guide has a length of between 12-100, 13-75, 14-50, or 15-30 nucleotides (e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) and is complementary to a non-PAM strand sequence. In some embodiments, the spacer sequence is designed to be complementary to a specific DNA strand, e.g., of a genomic locus.

15 In some embodiments, the RNA guide spacer sequence is substantially identical to a complementary strand of a target sequence. In some embodiments, the RNA guide comprises a sequence having at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least
20 about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to a complementary strand of a reference nucleic acid sequence, e.g., target sequence. The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (e.g., BLAST, ALIGN, CLUSTAL) using standard parameters.

25 In some embodiments, the RNA guide comprises a spacer sequence that has a length of between 12-100, 13-75, 14-50, or 15-30 nucleotides (e.g., 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides) and at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a region on the non-PAM strand that is complementary to the target sequence. In some embodiments, the RNA guide comprises a
30 sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a target DNA sequence. In some embodiments, the RNA guide comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least

98%, at least 99% complementary to a target genomic sequence. In some embodiments, the RNA guide comprises a sequence, e.g., RNA sequence, that is a length of up to 50 and at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a region on the non-PAM strand that is complementary to the target sequence. In some
5 embodiments, the RNA guide comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a target DNA sequence. In some embodiments, the RNA guide comprises a sequence at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% complementary to a target genomic sequence.

10 In some embodiments, the spacer sequence is a sequence of Table 5A or 5B or a portion of a sequence of Table 5A or 5B. It should be understood that an indication of SEQ ID NOs: 229-446 or 2497-4502 should be considered as equivalent to a listing of SEQ ID NOs: 229-446 or 2497-4502, with each of the intervening numbers present in the listing, *i.e.*, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250,
15 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345,
20 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440,
25 441, 442, 443, 444, 445, and 446, or 2497, 2498, 2499, 2500, 2501, 2502, 2503, 2504, 2505, 2506, 2507, 2508, 2509, 2510, 2511, 2512, 2513, 2514, 2515, 2516, 2517, 2518, 2519, 2520, 2521, 2522, 2523, 2524, 2525, 2526, 2527, 2528, 2529, 2530, 2531, 2532, 2533, 2534, 2535, 2536, 2537, 2538, 2539, 2540, 2541, 2542, 2543, 2544, 2545, 2546, 2547, 2548, 2549, 2550, 2551, 2552, 2553, 2554, 2555, 2556, 2557, 2558, 2559, 2560, 2561, 2562, 2563, 2564, 2565,
30 2566, 2567, 2568, 2569, 2570, 2571, 2572, 2573, 2574, 2575, 2576, 2577, 2578, 2579, 2580, 2581, 2582, 2583, 2584, 2585, 2586, 2587, 2588, 2589, 2590, 2591, 2592, 2593, 2594, 2595, 2596, 2597, 2598, 2599, 2600, 2601, 2602, 2603, 2604, 2605, 2606, 2607, 2608, 2609, 2610, 2611, 2612, 2613, 2614, 2615, 2616, 2617, 2618, 2619, 2620, 2621, 2622, 2623, 2624, 2625, 2626, 2627, 2628, 2629, 2630, 2631, 2632, 2633, 2634, 2635, 2636, 2637, 2638, 2639, 2640,
35 2641, 2642, 2643, 2644, 2645, 2646, 2647, 2648, 2649, 2650, 2651, 2652, 2653, 2654, 2655,

2656, 2657, 2658, 2659, 2660, 2661, 2662, 2663, 2664, 2665, 2666, 2667, 2668, 2669, 2670,
2671, 2672, 2673, 2674, 2675, 2676, 2677, 2678, 2679, 2680, 2681, 2682, 2683, 2684, 2685,
2686, 2687, 2688, 2689, 2690, 2691, 2692, 2693, 2694, 2695, 2696, 2697, 2698, 2699, 2700,
2701, 2702, 2703, 2704, 2705, 2706, 2707, 2708, 2709, 2710, 2711, 2712, 2713, 2714, 2715,
5 2716, 2717, 2718, 2719, 2720, 2721, 2722, 2723, 2724, 2725, 2726, 2727, 2728, 2729, 2730,
2731, 2732, 2733, 2734, 2735, 2736, 2737, 2738, 2739, 2740, 2741, 2742, 2743, 2744, 2745,
2746, 2747, 2748, 2749, 2750, 2751, 2752, 2753, 2754, 2755, 2756, 2757, 2758, 2759, 2760,
2761, 2762, 2763, 2764, 2765, 2766, 2767, 2768, 2769, 2770, 2771, 2772, 2773, 2774, 2775,
2776, 2777, 2778, 2779, 2780, 2781, 2782, 2783, 2784, 2785, 2786, 2787, 2788, 2789, 2790,
10 2791, 2792, 2793, 2794, 2795, 2796, 2797, 2798, 2799, 2800, 2801, 2802, 2803, 2804, 2805,
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2821, 2822, 2823, 2824, 2825, 2826, 2827, 2828, 2829, 2830, 2831, 2832, 2833, 2834, 2835,
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4501, or 4502.

20 The spacer sequence can comprise nucleotide 1 through nucleotide 16 of any one of SEQ
ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through
nucleotide 17 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can
comprise nucleotide 1 through nucleotide 18 of any one of SEQ ID NOs: 229-446 or 2497-4502.
The spacer sequence can comprise nucleotide 1 through nucleotide 19 of any one of SEQ ID
25 NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through nucleotide
20 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise
nucleotide 1 through nucleotide 21 of any one of SEQ ID NOs: 229-446 or 2497-4502. The
spacer sequence can comprise nucleotide 1 through nucleotide 22 of any one of SEQ ID NOs:
229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through nucleotide 23 of
30 any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1
through nucleotide 24 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence
can comprise nucleotide 1 through nucleotide 25 of any one of SEQ ID NOs: 229-446 or 2497-
4502. The spacer sequence can comprise nucleotide 1 through nucleotide 26 of any one of SEQ
ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through
35 nucleotide 27 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can

comprise nucleotide 1 through nucleotide 28 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through nucleotide 29 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can comprise nucleotide 1 through nucleotide 30 of any one of SEQ ID NOs: 229-446 or 2497-4502.

5 In some embodiments, the spacer sequence has at least 90% identity (*e.g.*, at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity) to a sequence of Table 5A or 5B or a portion of a sequence of Table 5A or 5B. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 16 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising
10 nucleotide 1 through nucleotide 17 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 18 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 19 of any one of
15 SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 20 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 21 of any one of SEQ ID NOs: 229-446 or 2497-4502. The
20 spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 22 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 23 of any one of
25 SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 24 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 25 of any one of SEQ ID NOs: 229-446 or 2497-4502. The
30 spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 26 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 27 of any one of
35 SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 28 of any one of SEQ ID NOs: 229-446 or 2497-4502. The spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 29 of any one of SEQ ID NOs: 229-446 or 2497-4502. The
40 spacer sequence can have at least 90% identity to a sequence comprising nucleotide 1 through nucleotide 30 of any one of SEQ ID NOs: 229-446 or 2497-4502.

Table 5A. Target and Spacer Sequences - Exons

ref_id	Str and	PA M		target		spacer
STMN2_ exon1	+	TT TG	1 1	CCTTCGCCACTGCTCAGC GTCTGCACATCC	2 2 9	CCUUCGCCACUGCUCAGC GUCUGCACAUC
STMN2_ exon1	+	CT TC	1 2	GCCACTGCTCAGCGTCTG CACATCCCTACA	2 3 0	GCCACUGCUCAGCGUCU GCACAUCCCUACA
STMN2_ exon1	+	CT TT	1 3	GCCTTCGCCACTGCTCAG CGTCTGCACATC	2 3 1	GCCUUCGCCACUGCUCAG CGUCUGCACAUC
STMN2_ exon1	-	CT TA	1 4	CCCATTGCTGTTTTAGCC ATTGTAGGGATG	2 3 2	CCCAUUGCUGUUUUAGCC AUUGUAGGGAUG
STMN2_ exon1	-	AT TG	1 5	CTGTTTTAGCCATTGTAG GGATGTGCAGAC	2 3 3	CUGUUUUAGCCAUUGUAG GGAUGUGCAGAC
STMN2_ exon1	-	GT TT	1 6	TAGCCATTGTAGGGATGT GCAGACGCTGAG	2 3 4	UAGCCAUUGUAGGGAUGU GCAGACGCUGAG
STMN2_ exon1	-	TT TT	1 7	AGCCATTGTAGGGATGTG CAGACGCTGAGC	2 3 5	AGCCAUUGUAGGGAUGU GCAGACGCUGAGC
STMN2_ exon1	-	TT TA	1 8	GCCATTGTAGGGATGTGC AGACGCTGAGCA	2 3 6	GCCAUUGUAGGGAUGUG CAGACGCUGAGCA
STMN2_ exon1	-	AT TG	1 9	TAGGGATGTGCAGACGCT GAGCAGTGGCGA	2 3 7	UAGGGAUGUGCAGACGC UGAGCAGUGGCGA
STMN2_ exon1	+	GT TC	2 0	TCCGTCGGCTCTACCTGG AGCCCACCTCT	2 3 8	UCCGUCGGCUCUACCUG GAGCCCACCUCU
STMN2_ exon2	-	TT TG	2 1	GTTTTCTAAGCCAGGGAG GTTTTGAAAGAT	2 3 9	GUUUUCUAAGCCAGGGAG GUUUUGAAAGAU
STMN2_ exon2	+	CT TT	2 2	CAAAACCTCCCTGGCTTA GAAAACCAAATT	2 4 0	CAAAACCUCCUGGCUUA GAAAACCAAUUU
STMN2_ exon2	+	TT TC	2 3	AAAACCTCCCTGGCTTAG AAAACCAAATTT	2 4 1	AAAACCUCCUGGCUUAG AAAACCAAUUU
STMN2_ exon2	+	CT TA	2 4	GAAAACCAAATTTTGTAG AGAGAGATGGG	2 4 2	GAAAACCAAUUUUUGUA GAGAGAGAUGGG
STMN2_ exon2	-	AT TT	2 5	GGTTTTCTAAGCCAGGGA GGTTTTGAAAGA	2 4 3	GGUUUUCUAAGCCAGGGA GGUUUUGAAAGA
STMN2_ exon2	+	TT TT	2 6	TGTAGAGAGAGATGGGTA GAATCTAATTTT	2 4 4	UGUAGAGAGAGAUGGGUA GAAUCUAAUUUU
STMN2_ exon2	+	AT TT	2 7	TTGTAGAGAGAGATGGGT AGAATCTAATTT	2 4 5	UUGUAGAGAGAGAUGGG UAGAAUCUAAUUU

STMN2_ exon2	-	AT TA	2 8	GATTCTACCCATCTCTCTC TACAAAAATTT	2 4 6	GAUUCUACCCAUCUCUCU CUACAAAAUUU
STMN2_ exon2	-	AT TC	2 9	TACCCATCTCTCTCTACAA AAATTTGGTTT	2 4 7	UACCCAUCUCUCUCUACA AAAAUUUGGUUU
STMN2_ exon2	-	TT TA	3 0	GAATAAAATTAGATTCTAC CCATCTCTCTC	2 4 8	GAAUAAAAUJAGAUUCUA CCCAUCUCUCUC
STMN2_ exon2	-	CT TT	3 1	AGAATAAAATTAGATTCTA CCCATCTCTCT	2 4 9	AGAAUAAAAUJAGAUUCU ACCAUCUCUCUCU
STMN2_ exon2	-	AT TG	3 2	CTTTAGAATAAAATTAGAT TCTACCCATCT	2 5 0	CUUUAGAAUAAAAUJAGA UUCUACCCAUCU
STMN2_ exon2	+	AT TC	3 3	TAAAGCAATTAGCATTACA TCATCACAGCA	2 5 1	UAAAGCAAUJAGCAUUAC AUCAUCACAGCA
STMN2_ exon2	+	TT TA	3 4	TTCTAAAGCAATTAGCATT ACATCATCACA	2 5 2	UUCUAAAGCAAUJAGCAU UACAUCAUCACA
STMN2_ exon2	+	AT TT	3 5	TATTCTAAAGCAATTAGCA TTACATCATCA	2 5 3	UAUUCUAAAGCAAUJAGC AUUACAUCAUCA
STMN2_ exon2	+	TT TT	3 6	ATTCTAAAGCAATTAGCAT TACATCATCAC	2 5 4	AUUCUAAAGCAAUJAGCA UUACAUCAUCA
STMN2_ exon2	+	TT TT	3 7	GTAGAGAGAGATGGGTAG AATCTAATTTTA	2 5 5	GUAGAGAGAGAUGGGUA GAAUCUAAUUUUUA
STMN2_ exon2	+	TT TG	3 8	TAGAGAGAGATGGGTAGA ATCTAATTTTAT	2 5 6	UAGAGAGAGAUGGGUAGA AUCUAAUUUUUAU
STMN2_ exon2	+	AT TA	3 9	GCATTACATCATCACAGC AG	2 5 7	GCAUUACAUCAUCAAGC AG
STMN2_ exon2	-	GT TT	4 0	TCTAAGCCAGGGAGGTTT TGAAAGATT	2 5 8	UCUAAGCCAGGGAGGUUU UGAAAGAUU
STMN2_ exon2	-	TT TT	4 1	CTAAGCCAGGGAGGTTT GAAAGATT	2 5 9	CUAAGCCAGGGAGGUUUU GAAAGAUU
STMN2_ exon2	-	TT TC	4 2	TAAGCCAGGGAGGTTTTG AAAGATT	2 6 0	UAAGCCAGGGAGGUUUU GAAAGAUU
STMN2_ exon3	-	GT TG	4 3	CGAGGTTCCGGGTAAAAG CAAGAGCAGATC	2 6 1	CGAGGUUCCGGGUAAAAG CAAGAGCAGAUC
STMN2_ exon3	-	CT TG	4 4	TAGGCTGAAATGAAAAGC TGAAGATTAGTA	2 6 2	UAGGCUGAAAUGAAAAGC UGAAGAUUAGUA
STMN2_ exon3	-	GT TC	4 5	CGGGTAAAAGCAAGAGCA GATCAGTGACAG	2 6 3	CGGGUAAAAGCAAGAGCA GAUCAGUGACAG

STMN2_ exon3	-	TT TT	4 6	CCTTG TAGGCTGAAATGA AAAGCTGAAGAT	2 6 4	CCUUGUAGGCUGAAAUGA AAAGCUGAAGAU
STMN2_ exon3	-	TT TT	4 7	TCCTTG TAGGCTGAAATG AAAAGCTGAAGA	2 6 5	UCCUUGUAGGCUGAAAUG AAAAGCUGAAGA
STMN2_ exon3	-	TT TT	4 8	TTCCTTG TAGGCTGAAAT GAAAAGCTGAAG	2 6 6	UCCUUGUAGGCUGAAAU GAAAAGCUGAAG
STMN2_ exon3	-	AT TT	4 9	TTTCCTTG TAGGCTGAAAT GAAAAGCTGAA	2 6 7	UUUCCUUGUAGGCUGAAA UGAAAAGCUGAA
STMN2_ exon3	-	CT TC	5 0	ATTTTTTCCTTG TAGGCTG AAATGAAAAGC	2 6 8	AUUUUUCCUUGUAGGCU GAAAUGAAAAGC
STMN2_ exon3	+	AT TC	5 1	AGAAAAATGAAATATACT AATCTTCAGCT	2 6 9	AGAAAAAUGAAAUAUAC UAAUCUUCAGCU
STMN2_ exon3	+	CT TC	5 2	AGCTTTTCATTT CAGCCTA CAAGGAAAAAA	2 7 0	AGCUUUUCAUUUCAGCCU ACAAGGAAAAAA
STMN2_ exon3	+	CT TT	5 3	TCATTT CAGCCTACAAGG AAAAATGAAGG	2 7 1	UCAUUUCAGCCUACAAGG AAAAAUGAAGG
STMN2_ exon3	-	TT TC	5 4	CTTG TAGGCTGAAATGAA AAGCTGAAGATT	2 7 2	CUUGUAGGCUGAAAUGAA AAGCUGAAGAUU
STMN2_ exon3	+	TT TC	5 5	ATTT CAGCCTACAAGGAA AAAATGAAGGAG	2 7 3	AUUUCAGCCUACAAGGAA AAAAUGAAGGAG
STMN2_ exon3	+	TT TT	5 6	CATTT CAGCCTACAAGGA AAAAATGAAGGA	2 7 4	CAUUUCAGCCUACAAGGA AAAAAUGAAGGA
STMN2_ exon3	-	GT TA	5 7	CTCACCATCGTAAGTATA GATGTTGATGTT	2 7 5	CUCACCAUCGUAAGUAUA GAUGUUGAUGUU
STMN2_ exon3	-	TT TC	5 8	CAAATGATCTAGCTAGCA GGGGTATGTCTA	2 7 6	CAAUGAUCUAGCUAGCA GGGGUAUGUCUA
STMN2_ exon3	-	CT TT	5 9	CCAAATGATCTAGCTAGC AGGGGTATGTCT	2 7 7	CCAAUGAUCUAGCUAGC AGGGGUAUGUCU
STMN2_ exon3	+	CT TA	6 0	CGATGGTGAGTAACCTAG GATAGACATACC	2 7 8	CGAUGGUGAGUAACCUAG GAUAGACAUACC
STMN2_ exon3	+	TT TA	6 1	CCCGGAACCTCGCAACAT CAACATCTATAC	2 7 9	CCCGGAACCUCGCAACAU CAACAUCUAUAC
STMN2_ exon3	-	GT TG	6 2	ATGTTGCGAGGTTCCGGG TAAAAGCAAGAG	2 8 0	AUGUUGCGAGGUUCCGG GUAAAAGCAAGAG
STMN2_ exon3	+	CT TT	6 3	TACCCGGAACCTCGCAAC ATCAACATCTAT	2 8 1	UACCCGGAACCUCGCAAC AUCAACAUCUAU

STMN2_ exon3	+	CT TG	6 4	CTTTTACCCGGAACCTCG CAACATCAACAT	2 8 2	CUUUUACCCGGAACCUCG CAACAUCAACAU
STMN2_ exon3	+	TT TC	6 5	AGCCTACAAGGAAAAAAT GAAGGAGCTGTC	2 8 3	AGCCUACAAGGAAAAAAU GAAGGAGCUGUC
STMN2_ exon3	+	AT TT	6 6	CAGCCTACAAGGAAAAAA TGAAGGAGCTGT	2 8 4	CAGCCUACAAGGAAAAAA UGAAGGAGCUGU
STMN2_ exon3	+	TT TT	6 7	ACCCGGAACCTCGCAACA TCAACATCTATA	2 8 5	ACCCGGAACCUCGCAACA UCAACAUCUAUA
STMN2_ exon3	-	AT TA	6 8	GTATATTTTCATTTTTCTG AATTTCTC	2 8 6	GUAUAUUUCAUUUUUUUCU GAAUUUCUC
STMN2_ exon4	-	TT TC	6 9	TTCTGGATCTCCTCCAGG GACAGGTCTTTC	2 8 7	UUCUGGAUCUCCUCCAGG GACAGGUCUUUC
STMN2_ exon4	-	CT TC	7 0	TGGATCTCCTCCAGGGAC AGGTCTTTCTTC	2 8 8	UGGAUCUCCUCCAGGGAC AGGUCUUUCUUC
STMN2_ exon4	-	CT TT	7 1	CTTCTTTGGAGAAGCTAA AGTTCGTGGGGC	2 8 9	CUUCUUUGGAGAAGCUAA AGUUCGUGGGGC
STMN2_ exon4	-	TT TC	7 2	TTCTTTGGAGAAGCTAAA GTTCGTGGGGCT	2 9 0	UUCUUUGGAGAAGCUAAA GUUCGUGGGGCU
STMN2_ exon4	-	CT TC	7 3	TTTGGAGAAGCTAAAGTT CGTGGGGCTTCT	2 9 1	UUUGGAGAAGCUAAAGUU CGUGGGGCUUCU
STMN2_ exon4	-	CT TT	7 4	GGAGAAGCTAAAGTTCGT GGGGCTTCTGAG	2 9 2	GGAGAAGCUAAAGUUCGU GGGGCUUCUGAG
STMN2_ exon4	-	TT TG	7 5	GAGAAGCTAAAGTTCGTG GGGCTTCTGAGA	2 9 3	GAGAAGCUAAAGUUCGUG GGGCUUCUGAGA
STMN2_ exon4	-	GT TC	7 6	GTGGGGCTTCTGAGATAG GAGATGGTGGCT	2 9 4	GUGGGGCUUCUGAGAU GGAGAUGGUGGCU
STMN2_ exon4	-	CT TC	7 7	TGAGATAGGAGATGGTGG CTTCAAGATCAG	2 9 5	UGAGAUAGGAGAUUGGUG GCUUCAAGAUCA
STMN2_ exon4	-	TT TG	7 8	TTGATTTGCTTCACTTCCA TATCTGAAAAG	2 9 6	UUGAUUUGCUUCACUCC AUAUCUGAAAAG
STMN2_ exon4	-	GT TT	7 9	GTTGATTTGCTTCACTTCC ATATCTGAAAA	2 9 7	GUUGAUUUGCUUCACUUC CAUAUCUGAAAA
STMN2_ exon4	-	GT TG	8 0	ATTTGCTTCACTTCCATAT CTGAAAAGTGA	2 9 8	AUUUGCUUCACUCCAUA UCUGAAAAGUGA
STMN2_ exon4	-	AT TT	8 1	GCTTCACTTCCATATCTGA AAAGTGAACAT	2 9 9	GCUUCACUCCAUAUCUG AAAAGUGAACAU

STMN2_ exon4	-	TT TG	8 2	CTTCACTTCCATATCTGAA AAGTGAACATT	3 0 0	CUUCACUCCAUUAUCUGA AAAGUGAACAUU
STMN2_ exon4	-	CT TC	8 3	ACTTCCATATCTGAAAAGT GAACATTTGAG	3 0 1	ACUUCCAUAUCUGAAAAG UGAACAUUUGAG
STMN2_ exon4	-	CT TC	8 4	CATATCTGAAAAGTGAAC ATTTGAGAATGT	3 0 2	CAUAUCUGAAAAGUGAAC AUUUGAGAAUGU
STMN2_ exon4	-	AT TT	8 5	GAGAATGTTAAGCATACA AAGCTTGCAGCA	3 0 3	GAGAAUGUUAAGCAUACA AAGCUUGCAGCA
STMN2_ exon4	-	TT TG	8 6	AGAATGTTAAGCATACAAA GCTTGCAGCAT	3 0 4	AGAAUGUUAAGCAUACAA AGCUUGCAGCAU
STMN2_ exon4	-	GT TT	8 7	CTTCTGGATCTCCTCCAG GGACAGGTCTTT	3 0 5	CUUCUGGAUCUCCUCCAG GGACAGGUCUUU
STMN2_ exon4	-	CT TC	8 8	AAGATCAGCTCAAAAGCC TGGCCAGAGGCA	3 0 6	AAGAUCAGCUCAAAAGCC UGGCCAGAGGCA
STMN2_ exon4	-	TT TC	8 9	CTCTGCAGCCTCCAGTTT CTTCTGGATCTC	3 0 7	CUCUGCAGCCUCCAGUUU CUUCUGGAUCUC
STMN2_ exon4	+	TT TC	9 0	AGATATGGAAGTGAAGCA AATCAACAAACG	3 0 8	AGAUUAUGGAAGUGAAGCA AAUCAACAAACG
STMN2_ exon4	-	CT TC	9 1	TTTCCTCTGCAGCCTCCA GTTTCTTCTGGA	3 0 9	UUUCCUCUGCAGCCUCCA GUUUCUUCUGGA
STMN2_ exon4	+	TT TG	9 2	TATGCTTAACATTCTCAA TGTTCACTTTT	3 1 0	UAUGCUIAACAUIUCUCAA AUGUUCACUUUU
STMN2_ exon4	+	CT TA	9 3	ACATTCTCAAATGTTCACT TTTCAGATATG	3 1 1	ACAUUCUCAAUGUUCAC UUUUCAGAUUG
STMN2_ exon4	+	AT TC	9 4	TCAAATGTTCACTTTTCAG ATATGGAAGTG	3 1 2	UCAAUGUUCACUUUUA GAUAUGGAAGUG
STMN2_ exon4	+	GT TC	9 5	ACTTTTCAGATATGGAAGT GAAGCAAATCA	3 1 3	ACUUUUCAGAUUGGAAG UGAAGCAAUA
STMN2_ exon4	+	CT TT	9 6	TCAGATATGGAAGTGAAG CAAATCAACAAA	3 1 4	UCAGAUUGGAAGUGAAG CAAUAACAAA
STMN2_ exon4	+	TT TT	9 7	CAGATATGGAAGTGAAGC AAATCAACAAAC	3 1 5	CAGAUUGGAAGUGAAGC AAUAACAAAC
STMN2_ exon4	+	CT TT	9 8	TGAGCTGATCTTGAAGCC ACCATCTCCTAT	3 1 6	UGAGCUGAUCUUGAAGCC ACCAUCUCCUAU
STMN2_ exon4	+	TT TT	9 9	GAGCTGATCTTGAAGCCA CCATCTCCTATC	3 1 7	GAGCUGAUCUUGAAGCCA CCAUCUCCUAUC

STMN2_ exon4	+	TT TG	1 0 0	AGCTGATCTTGAAGCCAC CATCTCCTATCT	3 1 8	AGCUGAUCUUGAAGCCAC CAUCUCCUAUCU
STMN2_ exon4	+	CT TG	1 0 1	AAGCCACCATCTCCTATC TCAGAAGCCCCA	3 1 9	AAGCCACCAUCUCCUAUC UCAGAAGCCCCA
STMN2_ exon4	+	CT TT	1 0 2	AGCTTCTCCAAAGAAGAA AGACCTGTCCCT	3 2 0	AGCUUCUCCAAAGAAGAA AGACCUGUCCCU
STMN2_ exon4	+	TT TA	1 0 3	GCTTCTCCAAAGAAGAAA GACCTGTCCCTG	3 2 1	GCUUCUCCAAAGAAGAAA GACCUGUCCCU
STMN2_ exon4	+	CT TC	1 0 4	TCCAAAGAAGAAAGACCT GTCCCTGGAGGA	3 2 2	UCCAAAGAAGAAAGACCU GUCCCUUGGAGGA
STMN2_ exon4	+	CT TT	1 0 5	TTCCATAGGTTTTCTTCT CTCTCTCCCTC	3 2 3	UUCCAUAGGUUUUCCUUC UCUCUCUCCCU
STMN2_ exon4	+	TT TT	1 0 6	TCCATAGGTTTTCTTCTC TCTCTCCCTCC	3 2 4	UCCAUAGGUUUUCCUUCU CUCUCUCCCUCC
STMN2_ exon4	+	TT TT	1 0 7	CCATAGGTTTTCTTCTCT CTCTCCCTCCC	3 2 5	CCAUAGGUUUUCCUUCUC UCUCUCCCUCCC
STMN2_ exon4	+	TT TC	1 0 8	CATAGGTTTTCTTCTCTC TCTCCCTCCCC	3 2 6	CAUAGGUUUUCCUUCUCU CUCUCCCUCCCC
STMN2_ exon4	+	GT TT	1 0 9	TCCTTCTCTCTCTCCCTCC CCTGCTCCTCC	3 2 7	UCCUUCUCUCUCUCCCUCC CCCUGCUCCUCC
STMN2_ exon4	-	GT TA	1 1 0	CCTTTCTTCTTTCTCTGC AGCCTCCAGTT	3 2 8	CCUUUCUUCUUUCCUUCUG CAGCCUCCAGUU
STMN2_ exon4	-	CT TT	1 1 1	CTTCTTTCTCTGCAGCCT CCAGTTTCTTC	3 2 9	CUUCUUUCCUCUGCAGCC UCCAGUUUCUUC
STMN2_ exon4	-	TT TC	1 1 2	TTCTTTCTCTGCAGCCTC CAGTTTCTTCT	3 3 0	UUCUUUCCUCUGCAGCCU CCAGUUUCUUCU
STMN2_ exon4	-	CT TT	1 1 3	CCTCTGCAGCCTCCAGTT TCTTCTGGATCT	3 3 1	CCUCUGCAGCCUCCAGUU UCUUCUGGAUCU
STMN2_ exon4	+	CT TT	1 1 4	GTATGCTTAACATTCTCAA ATGTTCACTTT	3 3 2	GUAUGCUUAACAUCUCA AAUGUUCACUUU
STMN2_ exon4	+	TT TT	1 1 5	CCTTCTCTCTCTCCCTCC CCTGCTCCTCC	3 3 3	CCUUCUCUCUCUCCCUCC CCUGCUCCUCC
STMN2_ exon4	+	TT TC	1 1 6	CTTCTCTCTCTCCCTCCC CTGCTCCTCC	3 3 4	CUUCUCUCUCUCCCUCCC CUGCUCCUCC
STMN2_ exon4	+	CT TC	1 1 7	TCTCTCTCCCTCCCTGCTC TCCTCC	3 3 5	UCUCUCUCCCUCCCUCC UCCUCC

STMN2_ exon4	-	GT TA	1 1 8	AGCATACAAAGCTTGCAG CATGG	3 3 6	AGCAUACAAAGCUUGCAG CAUGG
STMN2_ exon5	+	GT TT	1 1 9	GTGTTTGGATAATTATAAG ATGGCTATGTT	3 3 7	GUGUUUGGAUAAUUUAUA GAUGGCUAUGUU
STMN2_ exon5	-	TT TC	1 2 0	CTGCAGACGTTCAATAAT AGCAGCTAGATT	3 3 8	CUGCAGACGUUCAUAUAU AGCAGCUAGAUU
STMN2_ exon5	-	TT TC	1 2 1	AGGATCAGCTTTTCCTCC GCCATCTTGCTG	3 3 9	AGGAUCAGCUUUUCCUCC GCCAUCUUGCUG
STMN2_ exon5	-	CT TT	1 2 2	TCCTCCGCCATCTTGCTG AAGTTGTTGTTC	3 4 0	UCCUCCGCCAUCUUGCUG AAGUUGUUGUUC
STMN2_ exon5	-	TT TT	1 2 3	CCTCCGCCATCTTGCTGA AGTTGTTGTTCT	3 4 1	CCUCCGCCAUCUUGCUGA AGUUGUUGUUCU
STMN2_ exon5	-	TT TC	1 2 4	CTCCGCCATCTTGCTGAA GTTGTTGTTCTC	3 4 2	CUCCGCCAUCUUGCUGAA GUUGUUGUUCUC
STMN2_ exon5	-	CT TG	1 2 5	CTGAAGTTGTTGTTCTCCT CCAAAGCCTTC	3 4 3	CUGAAGUUGUUGUUCUCC UCCAAAGCCUUC
STMN2_ exon5	-	GT TG	1 2 6	TTGTTCTCCTCCAAAGCCT TCTGAAGGACT	3 4 4	UUGUUCUCCUCCAAAGCC UUCUGAAGGACU
STMN2_ exon5	-	GT TG	1 2 7	TTCTCCTCCAAAGCCTTCT GAAGGACTTCT	3 4 5	UUCUCCUCCAAAGCCUUC UGAAGGACUUCU
STMN2_ exon5	-	GT TC	1 2 8	TCCTCCAAAGCCTTCTGA AGGACTTCTCGC	3 4 6	UCCUCCAAAGCCUUCUGA AGGACUUCUCGC
STMN2_ exon5	-	CT TC	1 2 9	TGAAGGACTTCTCGCTCG TGTTCCCTCTTC	3 4 7	UGAAGGACUUCUCGCUCG UGUUCCCUUCUUC
STMN2_ exon5	-	TT TT	1 3 0	CAGGATCAGCTTTTCCTC CGCCATCTTGCT	3 4 8	CAGGAUCAGCUUUUCCUC CGCCAUCUUGCUG
STMN2_ exon5	-	CT TC	1 3 1	TCGCTCGTGTTCCCTCTT CTCTGCCAATTG	3 4 9	UCGCUCGUGUUCCCUCU UCUCUGCCAAUUG
STMN2_ exon5	-	CT TC	1 3 2	TCTGCCAATTGTTTCAGCA CCTGGGCCTCC	3 5 0	UCUGCCAAUUGUUUCAGC ACCUGGGCCUCC
STMN2_ exon5	-	AT TG	1 3 3	TTTCAGCACCTGGGCCTC CTGAGACTGGGG	3 5 1	UUUCAGCACCUGGGCCUC CUGAGACUGGGG
STMN2_ exon5	-	GT TT	1 3 4	CAGCACCTGGGCCTCCTG AGACTGGGGAAG	3 5 2	CAGCACCUGGGCCUCCU GAGACUGGGGAAG
STMN2_ exon5	-	TT TC	1 3 5	AGCACCTGGGCCTCCTGA GACTGGGGAAGA	3 5 3	AGCACCUGGGCCUCCUGA GACUGGGGAAGA

STMN2_ exon5	-	GT TC	1 3 6	AATAATAGCAGCTAGATTA GCCTCACGGTT	3 5 4	AAUAAUAGCAGCUAGAUU AGCCUCACGGUU
STMN2_ exon5	-	TT TT	1 3 7	CCTGCAGACGTTCAATAA TAGCAGCTAGAT	3 5 5	CCUGCAGACGUUCAAUAA UAGCAGCUAGAU
STMN2_ exon5	-	CT TT	1 3 8	TCCTGCAGACGTTCAATA ATAGCAGCTAGA	3 5 6	UCCUGCAGACGUUCAUA AUAGCAGCUAGA
STMN2_ exon5	-	AT TA	1 3 9	CCTTTTCCTGCAGACGTT CAATAATAGCAG	3 5 7	CCUUUCCUGCAGACGUU CAAUAAUAGCAG
STMN2_ exon5	+	AT TG	1 4 0	AACGTCTGCAGGAAAAGG TAATCTCAGCAG	3 5 8	AACGUCUGCAGGAAAAGG UAAUCUCAGCAG
STMN2_ exon5	-	GT TC	1 4 1	CCTCTTCTCTGCCAATTGT TTCAGCACCTG	3 5 9	CCUCUUCUCUGCCAAUUG UUUCAGCACCUG
STMN2_ exon5	-	AT TT	1 4 2	TCAGGATCAGCTTTTCCT CCGCCATCTTGC	3 6 0	UCAGGAUCAGCUUUUCCU CCGCCAUCUUGC
STMN2_ exon5	-	GT TC	1 4 3	CATTTTCAGGATCAGCTTT TCCTCCGCCAT	3 6 1	CAUUUUCAGGAUCAGCUU UCCUCCGCCAU
STMN2_ exon5	+	CT TC	1 4 4	AGAAGGCTTTGGAGGAGA ACAACAACCTCA	3 6 2	AGAAGGCUUUGGAGGAGA ACAACAACUUA
STMN2_ exon5	+	TT TG	1 4 5	GATAATTATAAGATGGCTA TGTTTTCTTC	3 6 3	GAUAAUUAAGAUGGCU AUGUUUUUCUUC
STMN2_ exon5	+	AT TA	1 4 6	TAAGATGGCTATGTTTTTC TTCCCCAGTCT	3 6 4	UAAGAUGGCUAUGUUUUU CUUCCCCAGUCU
STMN2_ exon5	+	GT TT	1 4 7	TTCTTCCCCAGTCTCAGG AGGCCCAGGTGC	3 6 5	UUCUCCCCAGUCUCAGG AGGCCCAGGUGC
STMN2_ exon5	+	TT TT	1 4 8	TCTTCCCCAGTCTCAGGA GGCCCAGGTGCT	3 6 6	UCUCCCCAGUCUCAGGA GGCCCAGGUGCU
STMN2_ exon5	+	TT TT	1 4 9	CTTCCCCAGTCTCAGGAG GCCCAGGTGCTG	3 6 7	CUUCCCCAGUCUCAGGAG GCCCAGGUGCUG
STMN2_ exon5	+	TT TC	1 5 0	TTCCCCAGTCTCAGGAGG CCCAGGTGCTGA	3 6 8	UUCCCCAGUCUCAGGAGG CCCAGGUGCUGA
STMN2_ exon5	+	CT TC	1 5 1	CCCAGTCTCAGGAGGCC AGGTGCTGAAAC	3 6 9	CCCAGUCUCAGGAGGCC AGGUGCUGAAAC
STMN2_ exon5	+	AT TG	1 5 2	GCAGAGAAGAGGGAACA CGAGCGAGAAGTC	3 7 0	GCAGAGAAGAGGGAACAC GAGCGAGAAGUC
STMN2_ exon5	-	TT TG	1 5 3	TTCCATTTTCAGGATCAGC TTTTCTCCGC	3 7 1	UCCAUUUUCAGGAUCAG CUUUUCCUCCGC

STMN2_ exon5	+	GT TT	1 5 4	GGATAATTATAAGATGGC TATGTTTTTCTT	3 7 2	GGAUAAUUUAAGAUGGC UAUGUUUUUCUU
STMN2_ exon5	+	CT TT	1 5 5	GGAGGAGAACAACAACCTT CAGCAAGATGGC	3 7 3	GGAGGAGAACAACAACUU CAGCAAGAUGGC
STMN2_ exon5	+	CT TC	1 5 6	AGCAAGATGGCGGAGGA AAAGCTGATCCTG	3 7 4	AGCAAGAUGGCGGAGGAA AAGCUGAUCCUG
STMN2_ exon5	+	AT TA	1 5 7	AGGAAAACCGTGAGGCTA ATCTAGCTGCTA	3 7 5	AGGAAAACCGUGAGGCUA AUCUAGCUGCUA
STMN2_ exon5	+	AT TA	1 5 8	TTGAACGTCTGCAGGAAA AGGTAATCTCAG	3 7 6	UUGAACGUCUGCAGGAAA AGGUAAUCUCAG
STMN2_ exon5	-	AT TA	1 5 9	GCCTCACGGTTTTCTTA ATTTGTTCCATT	3 7 7	GCCUCACGGUUUUCUUA AUUUGUCCAUU
STMN2_ exon5	-	GT TT	1 6 0	TCCTTAATTTGTTCCATTT TCAGGATCAGC	3 7 8	UCCUUAUUUGUCCAUU UUCAGGAUCAGC
STMN2_ exon5	-	TT TT	1 6 1	CCTTAATTTGTTCCATTTT CAGGATCAGCT	3 7 9	CCUUAUUUGUCCAUUU UCAGGAUCAGCU
STMN2_ exon5	-	TT TC	1 6 2	CTTAATTTGTTCCATTTTC AGGATCAGCTT	3 8 0	CUUAAUUUGUCCAUUUU CAGGAUCAGCUU
STMN2_ exon5	-	CT TA	1 6 3	ATTTGTTCCATTTTCAGGA TCAGCTTTTCC	3 8 1	AUUUGUCCAUUUUCAGG AUCAGCUUUUCC
STMN2_ exon5	-	AT TT	1 6 4	GTTCCATTTTCAGGATCA GCTTTTCTCCG	3 8 2	GUUCCAUUUUCAGGAUCA GCUUUUCCUCCG
STMN2_ exon5	+	TT TG	1 6 5	GAGGAGAACAACAACCTTC AGCAAGATGGCG	3 8 3	GAGGAGAACAACAACUUC AGCAAGAUGGCG
STMN2_ exon5	+	TT TG	1 6 6	TGTTTGGATAATTATAAGA TGGCTATGTTT	3 8 4	UGUUUGGAUAAUUAUAAG AUGGCUAUGUUU
STMN2_ exon5	-	CT TA	1 6 7	TAATTATCCAAACACAAAC CTAG	3 8 5	UAAUUAUCCAAACACAAA CCUAG
STMN2_ exon6	-	GT TC	1 6 8	AGAAGAAATAAACTTGAC CAGCTATAAAGT	3 8 6	AGAAGAAAUAACUUGAC CAGCUAUAAGU
STMN2_ exon6	-	CT TA	1 6 9	TCGTTAAACTCTATTAATC TCAAGGAGTCT	3 8 7	UCGUUAAACUCUAUUAU CUCAAGGAGUCU
STMN2_ exon6	-	TT TA	1 7 0	GTTCAGAAGAAATAAACTT GACCAGCTATA	3 8 8	GUUCAGAAGAAUAAACU UGACCAGCUAUA
STMN2_ exon6	-	CT TG	1 7 1	ACCAGCTATAAAGTAAAA CTTATCGTTAAA	3 8 9	ACCAGCUAUAAGUAAAA CUUAUCGUUAAA

STMN2_ exon6	-	CT TT	1 7 2	TAGTTCAGAAGAAATAAAC TTGACCAGCTA	3 9 0	UAGUUCAGAAGAAAUAAA CUUGACCAGCUA
STMN2_ exon6	+	CT TG	1 7 3	AGATTAATAGAGTTTAACG ATAAGTTTTAC	3 9 1	AGAUUAAUAGAGUUUAAC GAUAAGUUUUAC
STMN2_ exon6	+	AT TA	1 7 4	ATAGAGTTTAACGATAAGT TTTACTTTATA	3 9 2	AUAGAGUUUAACGAUAAG UUUUACUUUAUA
STMN2_ exon6	+	GT TT	1 7 5	AACGATAAGTTTTACTTTA TAGCTGGTCAA	3 9 3	AACGAUAAGUUUUACUUU AUAGCUGGUCAA
STMN2_ exon6	+	TT TA	1 7 6	ACGATAAGTTTTACTTTAT AGCTGGTCAAG	3 9 4	ACGAUAAGUUUUACUUUA UAGCUGGUCAAG
STMN2_ exon6	+	GT TT	1 7 7	TACTTTATAGCTGGTCAAG TTTATTTCTTC	3 9 5	UACUUUAUAGCUGGUCAA GUUUUUUUCUUC
STMN2_ exon6	+	TT TT	1 7 8	ACTTTATAGCTGGTCAAGT TTATTTCTTCT	3 9 6	ACUUUAUAGCUGGUCAAG UUUAUUUCUUCU
STMN2_ exon6	+	TT TA	1 7 9	CTTTATAGCTGGTCAAGTT TATTTCTTCTG	3 9 7	CUUUUAUAGCUGGUCAAGU UUAUUUCUUCUG
STMN2_ exon6	+	CT TT	1 8 0	ATAGCTGGTCAAGTTTATT TCTTCTGAACT	3 9 8	AUAGCUGGUCAAGUUUAU UUCUUCUGAACU
STMN2_ exon6	+	TT TA	1 8 1	TAGCTGGTCAAGTTTATTT CTTCTGAACTA	3 9 9	UAGCUGGUCAAGUUUAUU UCUUCUGAACUA
STMN2_ exon6	+	GT TT	1 8 2	ATTTCTTCTGAACTAAAAG AATCTATAGAG	4 0 0	AUUUCUUCUGAACUAAAA GAAUCUAUAGAG
STMN2_ exon6	+	TT TA	1 8 3	TTTCTTCTGAACTAAAAGA ATCTATAGAGT	4 0 1	UUUCUUCUGAACUAAAAG AAUCUAUAGAGU
STMN2_ exon6	+	AT TT	1 8 4	CTTCTGAACTAAAAGAATC TATAGAGTCTC	4 0 2	CUUCUGAACUAAAAGAAU CUAUAGAGUCUC
STMN2_ exon6	+	TT TC	1 8 5	TTCTGAACTAAAAGAATCT ATAGAGTCTCA	4 0 3	UUCUGAACUAAAAGAAUC UAUAGAGUCUCA
STMN2_ exon6	+	CT TC	1 8 6	TGAACTAAAAGAATCTATA GAGTCTCAATT	4 0 4	UGAACUAAAAGAAUCUAU AGAGUCUCAAUU
STMN2_ exon6	+	AT TT	1 8 7	CTGGAGCTTCAGAGGGGAA GGAGAGAAGCAA	4 0 5	CUGGAGCUUCAGAGGGGAA GGAGAGAAGCAA
STMN2_ exon6	+	TT TC	1 8 8	TGGAGCTTCAGAGGGGAAG GAGAGAAGCAAT	4 0 6	UGGAGCUUCAGAGGGGAA GGAGAGAAGCAAU
STMN2_ exon6	+	CT TC	1 8 9	AGAGGGAAGGAGAGAAG CAATGTAAGCAAC	4 0 7	AGAGGGAAGGAGAGAAGC AAUGUAAGCAAC

STMN2_ exon6	-	AT TC	1 9 0	TTTTAGTTCAGAAGAAATA AACTTGACCAG	4 0 8	UUUUAGUUCAGAAGAAAU AAACUUGACCAG
STMN2_ exon6	-	AT TG	1 9 1	AGACTCTATAGATTCTTTT AGTTCAGAAGA	4 0 9	AGACUCUAUAGAUUCUUU UAGUUCAGAAGA
STMN2_ exon6	-	CT TC	1 9 2	CCTCTGAAGCTCCAGAAA TTGAGACTCTAT	4 1 0	CCUCUGAAGCUCCAGAAA UUGAGACUCUAU
STMN2_ exon6	-	CT TC	1 9 3	TCTCCTTCCCTCTGAAGC TCCAGAAATTGA	4 1 1	UCUCCUUCCCUCUGAAGC UCCAGAAAUUGA
STMN2_ exon6	-	AT TG	1 9 4	CTTCTCTCCTTCCCTCTGA AGCTCCAGAAA	4 1 2	CUUCUCUCCUCCCUCUG AAGCUCCAGAAA
STMN2_ exon6	-	CT TA	1 9 5	CATTGCTTCTCTCCTTCCC TCTGAAGCTCC	4 1 3	CAUUGCUUCUCUCCUCC CUCUGAAGCUCC
STMN2_ exon6	-	TT TT	1 9 6	AGTTCAGAAGAAATAAACT TGACCAGCTAT	4 1 4	AGUUCAGAAGAAAUAAC UUGACCAGCUAU
STMN2_ exon6	-	TT TC	1 9 7	TGTAGAATGTTGCTTACAT TGCTTCTCTCC	4 1 5	UGUAGAAUGUUGCUUACA UUGCUUCUCUCC
STMN2_ exon6	-	TT TA	1 9 8	TATTTCTGTAGAATGTTGC TTACATTGCTT	4 1 6	UAAUUCUGUAGAAUGUUG CUUACAUUGCUU
STMN2_ exon6	-	AT TT	1 9 9	ATATTTCTGTAGAATGTTG CTTACATTGCT	4 1 7	AUAUUUCUGUAGAAUGUU GCUUACAUUGCU
STMN2_ exon6	-	AT TA	2 0 0	TTTATATTTCTGTAGAATG TTGCTTACATT	4 1 8	UUUAUAUUUCUGUAGAAU GUUGCUUACAUU
STMN2_ exon6	-	AT TA	2 0 1	GTAGTATTATTTATATTTT TGTAGAATGTT	4 1 9	GUAGUAUUUUUAUUUUU CUGUAGAAUGUU
STMN2_ exon6	-	AT TA	2 0 2	TTAGTAGTATTATTTATATT TCTGTAGAAT	4 2 0	UUAGUAGUAUUUUUAUA UUUCUGUAGAAU
STMN2_ exon6	+	AT TC	2 0 3	TACAGAAATATAAATAATA CTACTAATAAT	4 2 1	UACAGAAAUAUAAUAUA CUACUAAUAU
STMN2_ exon6	-	AT TT	2 0 4	CTGTAGAATGTTGCTTACA TTGCTTCTCTC	4 2 2	CUGUAGAAUGUUGCUUAC AUUGCUUCUCUC
STMN2_ exon6	-	GT TG	2 0 5	CTTACATTGCTTCTCTCCT TCCCTCTGAAG	4 2 3	CUUACAUUGCUUCUCUCC UCCCCUCUGAAG
STMN2_ exon6	-	GT TA	2 0 6	AACTCTATTAATCTCAAGG AGTCTACA	4 2 4	AACUCUAUUAUCUCAAG GAGUCUACA
STMN2_ exon7	+	TT TT	2 0 7	GTGTTTTTTAGGAGAGGC ATGCTGCGGAGG	4 2 5	GUGUUUUUUAGGAGAGG CAUGCUGCGGAGG

STMN2_ exon7	+	TT TC	2 0 8	TTCTTCCTTTTGTGTTTTT AGGAGAGGCA	4 2 6	UUCUCCUUUUUGUGUUUU UUAGGAGAGGCA
STMN2_ exon7	+	TT TG	2 0 9	TGTTTTTTAGGAGAGGCA TGCTGCGGAGGT	4 2 7	UGUUUUUUAGGAGAGGCA UGCUGCGGAGGU
STMN2_ exon7	+	GT TT	2 1 0	TTTAGGAGAGGCATGCTG CGGAGGTGCGCA	4 2 8	UUUAGGAGAGGCAUGCU GCGGAGGUGCGCA
STMN2_ exon7	+	CT TC	2 1 1	CTTTTGTGTTTTTAGGAG AGGCATGCTGC	4 2 9	CUUUUGUGUUUUUUAGGA GAGGCAUGCUGC
STMN2_ exon7	+	TT TT	2 1 2	TAGGAGAGGCATGCTGCG GAGGTGCGCAGG	4 3 0	UAGGAGAGGCAUGCUGC GGAGGUGCGCAGG
STMN2_ exon7	+	TT TT	2 1 3	AGGAGAGGCATGCTGCG GAGGTGCGCAGGA	4 3 1	AGGAGAGGCAUGCUGC GAGGUGCGCAGGA
STMN2_ exon7	+	TT TA	2 1 4	GGAGAGGCATGCTGCGG AGGTGCGCAGGAA	4 3 2	GGAGAGGCAUGCUGC AGGUGCGCAGGAA
STMN2_ exon7	+	GT TG	2 1 5	AACGTGTCTGGCTGAAGCA AGGGAGGGTCTG	4 3 3	AACUGUCUGGCUGAAGCA AGGGAGGGUCUG
STMN2_ exon7	-	AT TT	2 1 6	ACTATTGGTGGGGCGTGC CAGACCCTCCCT	4 3 4	ACUUAUUGGUGGGGCGUG CCAGACCCUCCCU
STMN2_ exon7	+	AT TT	2 1 7	CTTCTTCCTTTTGTGTTTT TTAGGAGAGGC	4 3 5	CUUCUCCUUUUUGUGUUU UUUAGGAGAGGC
STMN2_ exon7	-	TT TA	2 1 8	CTATTGGTGGGGCGTGCC AGACCCTCCCTT	4 3 6	CUAUUGGUGGGGCGUGC CAGACCCUCCCUU
STMN2_ exon7	-	CT TG	2 1 9	CTTCAGCCAGACAGTTCA ACCTGGAGTTCC	4 3 7	CUUCAGCCAGACAGUUCA ACCUGGAGUUCC
STMN2_ exon7	-	CT TC	2 2 0	AGCCAGACAGTTCAACCT GGAGTTCCTGT	4 3 8	AGCCAGACAGUUCAACCU GGAGUCCUUGU
STMN2_ exon7	-	GT TC	2 2 1	AACCTGGAGTTCCTTGTT CCTGCGCACCTC	4 3 9	AACCUGGAGUCCUUGUU CCUGCGCACCTC
STMN2_ exon7	-	GT TC	2 2 2	CTTGTTCTGCGCACCTC CGCAGCATGCCT	4 4 0	CUUGUCCUGCGCACCTC CGCAGCAUGCCU
STMN2_ exon7	-	CT TG	2 2 3	TTCCTGCGCACCTCCGCA GCATGCCTCTCC	4 4 1	UCCUGCGCACCUCCGCA GCAUGCCUCUCC
STMN2_ exon7	-	GT TC	2 2 4	CTGCGCACCTCCGCAGCA TGCCTCTCCTAA	4 4 2	CUGCGCACCUCCGCAGCA UGCCUCUCCUAA
STMN2_ exon7	+	CT TT	2 2 5	TGTGTTTTTTAGGAGAGG CATGCTGCGGAG	4 4 3	UGUGUUUUUUAGGAGAG GCAUGCUGCGGAG

STMN2_ exon7	+	CT TC	2 2 6	TTCCTTTTGTGTTTTTAG GAGAGGCATGC	4 4 4	UCCCUUUUGUGUUUUUUA GGAGAGGCAUGC
STMN2_ exon7	-	AT TG	2 2 7	GTGGGGCGTGCCAGACC CTCCCTTGCTTCA	4 4 5	GUGGGGCGUGCCAGACC CUCCCUUGCUUCA
STMN2_ exon7	+	TT TT	2 2 8	TTAGGAGAGGCATGCTGC GGAGGTGCGCAG	4 4 6	UUAGGAGAGGCAUGCUG CGGAGGUGCGCAG

Table 5B. Target and Spacer Sequences – Intron

ref_id	str an d	PAM		target		spacer
STMN2_ intron1	+	GTT C	491	TCCGTCGGCTCTACCT GGAGCCCACCTCTC	249 7	UCCGUCGGCUCUACCU GGAGCCCACCUCUC
STMN2_ intron1	-	ATT T	492	GGAAGTATTTTCTCTT CAAGGTGAGTCTGT	249 8	GGAAGUAUUUUCUCUU CAAGGUGAGUCUGU
STMN2_ intron1	-	ATT A	493	AAACTAGGCATCAAT TTGGAAGTATTTTCT	249 9	AAACUAGGCAUCAAUU UGGAAGUAUUUUCU
STMN2_ intron1	-	TTT G	494	AATAAGCCCCAGGTA AGCTATTAAACTAG	250 0	AAUAAGCCCCAGGUAA GCUAUUAAAACUAG
STMN2_ intron1	-	ATT T	495	GAATAAGCCCCAGGT AAGCTATTAAACTA	250 1	GAAUAAGCCCCAGGUA AGCUAUUAAAACUA
STMN2_ intron1	-	ATT A	496	TTTGAATAAGCCCCAG GTAAGCTATTAAAA	250 2	UUUGAAUAAGCCCCAG GUAAGCUAUUAAAA
STMN2_ intron1	-	TTTC	497	TCCCAAAGCCTAAATC ATGGCAATTATTTG	250 3	UCCCAAAGCCUAAAUC AUGGCAAUAUUUG
STMN2_ intron1	-	CTTT	498	CTCCCAAAGCCTAAAT CATGGCAATTATTT	250 4	CUCCCAAAGCCUAAAU CAUGGCAUUUUUU
STMN2_ intron1	-	GTT A	499	CAACCCACACGGCCTC ATAGCTCTCTTTCT	250 5	CAACCCACACGGCCUC AUAGCUCUCUUUCU
STMN2_ intron1	-	GTT C	500	CCACCAGAAATCGAT GCTGTGCTGAGCCTG	250 6	CCACCAGAAUCCAUG CUGUGCUGAGCCUG
STMN2_ intron1	-	TTTC	501	TGGAAGTGGTCATCA GAGTGTGTTCCCACC	250 7	UGGAACUGGUCAUCAG AGUGUGUUCCCACC
STMN2_ intron1	-	ATT T	502	CTGGAAGTGGTCATCA GAGTGTGTTCCCAC	250 8	CUGGAACUGGUCAUCA GAGUGUGUUCCCAC
STMN2_ intron1	-	GTT A	503	TTTCTGGAAGTGGTCA TCAGAGTGTGTTCC	250 9	UUUCUGGAACUGGUCA UCAGAGUGUGUCC
STMN2_ intron1	-	ATT A	504	AGTCAATGTTATTTCT GGAAGTGGTCATCA	251 0	AGUCAAGUUAUUUCU GGAACUGGUCAUCA
STMN2_ intron1	-	TTT G	505	AAATGTGCTAACCAT GATGGGACTGAGGAG	251 1	AAAUGUGCUAACCAUG AUGGGACUGAGGAG

STMN2_ intron1	-	TTTT	506	GAAATGTGCTAACCA TGATGGGACTGAGGA	251 2	GAAAUGUGCUAACCAU GAUGGGACUGAGGA
STMN2_ intron1	-	ATT T	507	TGAAATGTGCTAACC ATGATGGGACTGAGG	251 3	UGAAAUGUGCUAACCA UGAUGGGACUGAGG
STMN2_ intron1	-	GTT A	508	AGGAGGCATTTTGAA ATGTGCTAACCATGA	251 4	AGGAGGCAUUUUGAAA UGUGCUAACCAUGA
STMN2_ intron1	-	GTT A	509	AAACTAAATATCTCTG GCCTATGGAAGTAG	251 5	AAACUAAAUUAUCUCUG GCCUAUGGAAGUAG
STMN2_ intron1	-	ATT C	510	AACAAAATGTTAAAA CTAAATATCTCTGGC	251 6	AACAAAUGUUAAAAAC UAAAUUAUCUCUGGC
STMN2_ intron1	-	TTT A	511	TTCAACAAAATGTTAA AACTAAATATCTCT	251 7	UUCAACAAAUGUUAA AACUAAAUUAUCUCU
STMN2_ intron1	-	TTTT	512	ATTCAACAAAATGTTA AACTAAATATCTC	251 8	AUUCAACAAAUGUUA AAACUAAAUUAUCUC
STMN2_ intron1	-	ATT T	513	TATTCAACAAAATGTT AAAATAAATATCT	251 9	UAUUCAACAAAUGUU AAAACUAAAUUAUCU
STMN2_ intron1	-	TTT A	514	TTTTATTCAACAAAAT GTTAAACTAAATA	252 0	UUUUUAUCAACAAA GUUAAAACUAAUA
STMN2_ intron1	-	ATT T	515	ATTTTATTCAACAAA TGTTAAACTAAAT	252 1	AUUUUUAUCAACAAA UGUUAAAACUAAAU
STMN2_ intron1	-	ATT A	516	AATGTGAATGTGTAA ATTTATTTTATTCAA	252 2	AAUGUGAAUGUGUAAA UUUAUUUUUAUUCAA
STMN2_ intron1	-	GTT A	517	TATTAAATGTGAATGT GTAAATTTATTTTA	252 3	UAUUAAAUGUGAAUGU GUAAAUUUAUUUUA
STMN2_ intron1	-	CTT G	518	AAATAACATCTAATA GTTATATTAAATGTG	252 4	AAAUAAACAUCAAUAG UUUAUUUAAAUGUG
STMN2_ intron1	-	TTT G	519	GAAGTATTTTCTCTTC AAGGTGAGTCTGTG	252 5	GAAGUAUUUUCUCUUC AAGGUGAGUCUGUG
STMN2_ intron1	-	TTT G	520	ATGGTAATATGAAGA GAATCTTGAAATAAC	252 6	AUGGUAAUAUGAAGAG AAUCUUGAAAUAAC
STMN2_ intron1	-	ATT T	521	TCTCTCAAGGTGAGT CTGTGATCAGAAAG	252 7	UCUCUUCAAGGUGAGU CUGUGAUCAGAAAG
STMN2_ intron1	-	TTTC	522	TCTTCAAGGTGAGTCT GTGATCAGAAAGGA	252 8	UCUUCAAGGUGAGUCU GUGAUCAGAAAGGA
STMN2_ intron1	-	ATT G	523	CGGGAAAATGTTTGA GTAAAGAAATAGGAA	252 9	CGGGAAAUGUUUGAG UAAAGAAAUAGGAA
STMN2_ intron1	-	GTT G	524	AAAGAAAGCACCATT GCGGGAAAATGTTTG	253 0	AAAGAAAGCACCAUUG CGGGAAAUGUUUG
STMN2_ intron1	-	TTT A	525	TGAATACACCAGAAA AACAGTTGAAAGAAA	253 1	UGAAUACACCAGAAAA ACAGUUGAAAGAAA
STMN2_ intron1	-	ATT T	526	ATGAATACACCAGAA AAACAGTTGAAAGAA	253 2	AUGAAUACACCAGAAA AACAGUUGAAAGAA
STMN2_ intron1	-	CTT C	527	CCATAGAGAATCTGG AATTTATGAATACAC	253 3	CCAUAGAGAAUCUGGA AUUUAUGAAUACAC

STMN2_ intron1	-	GTT A	528	CTTCCCATAGAGAATC TGGAATTTATGAAT	253 4	CUUCCCAUAGAGAAUC UGGAAUUAUGAAU
STMN2_ intron1	-	GTT A	529	AATCAATCAATAAAA GTTACTTCCCATAGA	253 5	AAUCAAUCAUAAAAAG UUACUCCCCAUAGA
STMN2_ intron1	-	GTT A	530	TATGTGCTATACAAGG GTTAAATCAATCAA	253 6	UAUGUGCUAUACAAGG GUUAAAUCAAUCAA
STMN2_ intron1	-	CTT G	531	CATGTTATATGTGCTA TACAAGGGTTAAAT	253 7	CAUGUUAUAUGUGCUA UACAAGGGUUAUU
STMN2_ intron1	-	CTT A	532	GAACAATGCCTTGCAT GTTATATGTGCTAT	253 8	GAACAAUGCCUUGCAU GUUAUAUGUGCUAU
STMN2_ intron1	-	GTT C	533	TTAGAACAATGCCTTG CATGTTATATGTGC	253 9	UUAGAACA AUGCCUUG CAUGUUAUAUGUGC
STMN2_ intron1	-	GTT A	534	ATATGTGGAAAGTTCT TAGAACAATGCCTT	254 0	AUAUGUGGAAAGUUCU UAGAACA AUGCCU
STMN2_ intron1	-	ATT A	535	ACACAGTTAATATGTG GAAAGTTCTTAGAA	254 1	ACACAGUUAUAUGUG GAAAGUUCUAGAA
STMN2_ intron1	-	ATT A	536	AGTGATTAACACAGTT AATATGTGGAAAGT	254 2	AGUGAUUAACACAGUU AAUAUGUGGAAAGU
STMN2_ intron1	-	ATT A	537	TTAAGTGATTAACACA GTTAATATGTGGAA	254 3	UUAAGUGAUUAACACA GUUAAUAUGUGGAA
STMN2_ intron1	-	CTT A	538	GGATTATTAAGTGATT AACACAGTTAATAT	254 4	GGAUUAUUAAGUGAUU AACACAGUUAUAU
STMN2_ intron1	-	TTTC	539	CATATCTGTAATAGAA CCTACTTAGGATTA	254 5	CAUAUCUGUAAUAGAA CCUACUUAGGAUUA
STMN2_ intron1	-	GTT T	540	CCATATCTGTAATAGA ACCTACTTAGGATT	254 6	CCAUAUCUGUAAUAGA ACCUACUUAGGAUU
STMN2_ intron1	-	TTTC	541	TGTGCCTCAGTTTCCA TATCTGTAATAGAA	254 7	UGUGCCUCAGUUUCCA UAUCUGUAAUAGAA
STMN2_ intron1	-	CTTT	542	CTGTGCCTCAGTTTCC ATATCTGTAATAGA	254 8	CUGUGCCUCAGUUUCC AUAUCUGUAAUAGA
STMN2_ intron1	-	CTT C	543	AACTTTCTGTGCCTCA GTTTCCATATCTGT	254 9	AACUUUCUGUGCCUCA GUUCCAUAUCUGU
STMN2_ intron1	-	CTT G	544	AGTAAGATACTTCAA CTTTCTGTGCCTCAG	255 0	AGUAAGAUACUUC AAC UUUCUGUGCCUCAG
STMN2_ intron1	-	ATT C	545	TGGATCTGACTAACTG TGTGACCTTGAGTA	255 1	UGGAUCUGACUAACUG UGUGACCUUGAGUA
STMN2_ intron1	-	ATT C	546	CGAAGCCAGATGGCC TGGGCCCAAATTCTG	255 2	CGAAGCCAGAUGGCCU GGGCCCAAUUCUG
STMN2_ intron1	-	TTT A	547	AATAAAATGGTGATA TCACAGGTGTGACCT	255 3	AAUAAA AUGGUGAU AU CACAGGUGUGACCU
STMN2_ intron1	-	GTT T	548	AAATAAAATGGTGAT ATCACAGGTGTGACC	255 4	AAAUAAA AUGGUGAU A UCACAGGUGUGACC
STMN2_ intron1	-	CTT C	549	AAGGTGAGTCTGTGA TCAGAAAGGAGAAGA	255 5	AAGGUGAGUCUGUGAU CAGAAAGGAGAAGA

STMN2_ intron1	-	TTTT	550	CTCTTCAAGGTGAGTC TGTGATCAGAAAGG	255 6	CUCUUCAAGGUGAGUC UGUGAUCAGAAAGG
STMN2_ intron1	-	CTTT	551	GATGGTAATATGAAG AGAATCTTGAAATAA	255 7	GAUGGUAAUAUGAAGA GAAUCUUGAAAUA
STMN2_ intron1	-	GTT C	552	TCTCCTGCCTGCCTGC CTGCTTTGATGGTA	255 8	UCUCCUGCCUGCCUGC CUGCUUUGAUGGUA
STMN2_ intron1	-	CTT C	553	CTACAGTTCTCTCCTG CCTGCCTGCCTGCT	255 9	CUACAGUUCUCUCCUG CCUGCCUGCCUGCU
STMN2_ intron1	-	ATT T	554	TTGTTATGGTTTTATA GTATAATATGTGGC	256 0	UUGUUAUGGUUUUAUA GUAUAAUAUGUGGC
STMN2_ intron1	-	CTT A	555	AAATATTTTTTGTATG GTTTTATAGTATAA	256 1	AAAUUUUUUGUUAUG GUUUUAUAGUAUA
STMN2_ intron1	-	TTT A	556	CTCTGGAGGTCAACA ACAAGTGAGAACAAA	256 2	CUCUGGAGGUCAACAA CAAGUGAGAACAAA
STMN2_ intron1	-	TTTT	557	ACTCTGGAGGTCAAC AACAAGTGAGAACAA	256 3	ACUCUGGAGGUCAACA ACAAGUGAGAACAA
STMN2_ intron1	-	ATT T	558	TACTCTGGAGGTCAAC AACAAGTGAGAACA	256 4	UACUCUGGAGGUCAAC AACAAGUGAGAACA
STMN2_ intron1	-	ATT A	559	AATATTTTACTCTGGA GGTCAACAACAAGT	256 5	AAUAUUUUACUCUGGA GGUCAACAACAAGU
STMN2_ intron1	-	TTTC	560	CAGAGTATTAAATATT TTACTCTGGAGGTC	256 6	CAGAGUAUUAAUAUU UUACUCUGGAGGUC
STMN2_ intron1	-	CTTT	561	CCAGAGTATTAAATAT TTACTCTGGAGGT	256 7	CCAGAGUAUUAAUAU UUUACUCUGGAGGU
STMN2_ intron1	-	TTT G	562	AAACCCATAACTTTCC AGAGTATTAAATAT	256 8	AAACCCAUAAACUUCC AGAGUAUUAAUAU
STMN2_ intron1	-	TTTT	563	GAAACCCATAACTTTC CAGAGTATTAAATA	256 9	GAAACCCAUAAACUUUC CAGAGUAUUAAUA
STMN2_ intron1	-	ATT T	564	TGAAACCCATAACTTT CCAGAGTATTAAAT	257 0	UGAAACCCAUAAACUUU CCAGAGUAUUAAUA
STMN2_ intron1	-	CTT G	565	CCATAAAATAAATTTT GAAACCCATAACTT	257 1	CCAUAAAAUAAAUUUU GAAACCCAUAAACUU
STMN2_ intron1	-	TTTC	566	TTGCCATAAAATAAAT TTTGAAACCCATAA	257 2	UUGCCAUAAAAUAAAU UUUGAAACCCAUAA
STMN2_ intron1	-	ATT T	567	CTTGCCATAAAATAA ATTTTGAAACCCATA	257 3	CUUGCCAUAAAAUAAA UUUUGAAACCCAUAA
STMN2_ intron1	-	ATT A	568	TCTATTTCTTGCCATA AAATAAATTTTGAA	257 4	UCUAUUUCUUGCCAUAA AAAUAAAUUUUGAA
STMN2_ intron1	-	TTT A	569	AATGTGCTCTATGAGA ACTGTAATTATCTA	257 5	AAUGUGCUCUAUGAGA ACUGUAAUUAUCUA
STMN2_ intron1	-	TTTT	570	AAATGTGCTCTATGAG AACTGTAATTATCT	257 6	AAAUGUGCUCUAUGAG AACUGUAAUUAUCU
STMN2_ intron1	-	ATT T	571	TAAATGTGCTCTATGA GAACTGTAATTATC	257 7	UAAAUGUGCUCUAUGA GAACUGUAAUUAUC

STMN2_ intron1	-	ATT A	572	TTTTAAATGTGCTCTA TGAGAACTGTAATT	257 8	UUUUAAAUGUGCUCUA UGAGAACUGUAAUU
STMN2_ intron1	-	TTT G	573	CCCTATAAAAAATAAA TTATTTTAAATGTGC	257 9	CCCUAUAAAAAUAAU UAUUUUAAAUGUGC
STMN2_ intron1	-	TTTT	574	GCCCTATAAAAAATAA ATTATTTTAAATGTG	258 0	GCCCUAUAAAAAUAAA UUUUUUAAAUGUG
STMN2_ intron1	-	TTTT	575	TGCCCTATAAAAAATA AATTATTTTAAATGT	258 1	UGCCCUAUAAAAAUAA AUUAUUUUAAAUGU
STMN2_ intron1	-	ATT T	576	TTGCCCTATAAAAAATA AATTATTTTAAATG	258 2	UUGCCCUAUAAAAAU AAUAUUUUAAAUG
STMN2_ intron1	-	ATT C	577	AGTCCTAGGCAATATT TTTGCCCTATAAAA	258 3	AGUCCUAGGCAUAU UUUGCCCUAUAAAA
STMN2_ intron1	-	TTT G	578	TAAAAAAAAAAAAAAT CATTGAGTCCTAGGC	258 4	UAAAAAAAAAAAAAUC AUUCAGUCCUAGGC
STMN2_ intron1	-	CTTT	579	GTAAAAAAAAAAAAAA TCATTGAGTCCTAGG	258 5	GUAAAAAAAAAAAAAU CAUUCAGUCCUAGG
STMN2_ intron1	-	TTT A	580	CAATCTTTGTAAAAAA AAAAAATCATTCA	258 6	CAUCUUUGUAAAAAA AAAAAAUCAUUC
STMN2_ intron1	-	TTTT	581	TGTTATGGTTTTATAG TATAATATGTGGCT	258 7	UGUUAUGGUUUUAUAG UAUAAUAUGUGGCU
STMN2_ intron1	-	TTTT	582	GTTATGGTTTTATAGT ATAATATGTGGCTC	258 8	GUUAUGGUUUUAUAGU AUAUAUGUGGCUC
STMN2_ intron1	-	TTT G	583	TTATGGTTTTATAGTA TAATATGTGGCTCC	258 9	UUAUGGUUUUAUAGUA UAAUAUGUGGCUC
STMN2_ intron1	-	GTT A	584	TGGTTTTATAGTATAA TATGTGGCTCCTAC	259 0	UGGUUUUAUAGUAUAA UAUGUGGCUCUAC
STMN2_ intron1	-	ATT C	585	AAAACCTTCCTACAGT TCTCTCCTGCCTGC	259 1	AAAACCUUCCUACAGU UCUCUCCUGCCUGC
STMN2_ intron1	-	TTTC	586	ACAAGGGATTCAAAA CCTTCCTACAGTTCT	259 2	ACAAGGGAUUCAAAA CUUCCUACAGUUCU
STMN2_ intron1	-	GTT T	587	CACAAGGGATTCAAAA ACCTTCCTACAGTTC	259 3	CACAAGGGAUUCAAAA CCUCCUACAGUUC
STMN2_ intron1	-	ATT A	588	AAAATGTTTCACAAG GGATTCAAAACCTTC	259 4	AAAUGUUUCACAAGG GAUUCAAAACCUUC
STMN2_ intron1	-	ATT A	589	AAAGATAATTAAAAA TGTTTCACAAGGGAT	259 5	AAAGAUAAUUAAAAAU GUUUCACAAGGGAU
STMN2_ intron1	-	TTT A	590	TTAAAAGATAATTAA AAATGTTTCACAAGG	259 6	UUAAAAGAUAAUUAAA AAUGUUUCACAAGG
STMN2_ intron1	-	CTTT	591	ATTAAGATAATTAA AAAATGTTTCACAAG	259 7	AUUAAGAUAAUUAA AAAUGUUUCACAAG
STMN2_ intron1	-	ATT C	592	CTTTATTAAAAGATAA TTAAAATGTTTCA	259 8	CUUUAUUAAAAGAUAA UUAAAAAUGUUUCA
STMN2_ intron1	-	CTT G	593	ACAAATGACAGGGCC TGATTCCTTTATTAA	259 9	ACAAUGACAGGGCCU GAUCCUUUAUUA

STMN2_ intron1	-	TTT A	594	CTACTGCAAATGTCTC CTTGACAAATGACA	260 0	CUACUGCAA AUGUCUC CUUGACAA AUGACA
STMN2_ intron1	-	CTTT	595	ACTACTGCAAATGTCT CCTTGACAAATGAC	260 1	ACUACUGCAA AUGUCU CCUUGACAA AUGAC
STMN2_ intron1	-	ATT A	596	TAAACACAAGCTTTAC TACTGCAAATGTCT	260 2	UAAACACAAGCUUAC UACUGCAA AUGUCU
STMN2_ intron1	-	TTT A	597	ATCATGACTAATAAA AATGGATATTATAAA	260 3	AUCAUGACUAAUAAAA AUGGAU AUUAUAAA
STMN2_ intron1	-	GTT T	598	GAGTAAAGAAATAGG AAGACTTATTGGCTC	260 4	GAGUAAAAGAAUAGGA AGACUUAUUGGCUC
STMN2_ intron1	-	CTTT	599	AATCATGACTAATAA AAATGGATATTATAA	260 5	AAUCAUGACUAAUAAA AAUGGAU AUUAUAA
STMN2_ intron1	-	TTT G	600	TGAGAACAAATGTAC ACAAATGTTATCTTT	260 6	UGAGAACAA AUGUACA CAA AUGUUAUCUUU
STMN2_ intron1	-	TTTT	601	GTGAGAACAAATGTA CACAAATGTTATCTT	260 7	GUGAGAACAA AUGUAC ACAA AUGUUAUCUU
STMN2_ intron1	-	GTT T	602	TGTGAGAACAAATGT ACACAAATGTTATCT	260 8	UGUGAGAACAA AUGUA CACAA AUGUUAUCU
STMN2_ intron1	-	TTT A	603	CACTCATATAAAAGT GTTTTGTGAGAACAA	260 9	CACUCAU AUAAAAGUG UUUUGUGAGAACAA
STMN2_ intron1	-	CTTT	604	ACACTCATATAAAAG TGTTTTGTGAGAACA	261 0	ACACUCAU AUAAAAGU GUUUUGUGAGAACA
STMN2_ intron1	-	ATT A	605	ACCTTTACTCATAT AAAAGTGTTTTGTG	261 1	ACCUUACACUCAU AU AAAAGUGUUUUGUG
STMN2_ intron1	-	ATT A	606	ATTAACCTTTACTCTC ATATAAAAGTGTTT	261 2	AUUAACCUUACACUC AU AUAAAAGUGUUU
STMN2_ intron1	-	TTTC	607	CACATGACCAGCAAA ATGATGGCTGAAATG	261 3	CACAUGACCAGCAAAA UGAUGGCUGAAAUG
STMN2_ intron1	-	ATT T	608	CCACATGACCAGCAA AATGATGGCTGAAAT	261 4	CCACAUGACCAGCAAA AUGAUGGCUGAAAU
STMN2_ intron1	-	ATT C	609	CTAAAGAAGCTATATT TCCACATGACCAGC	261 5	CUAAAGAAGCUAU AU UCCACAUGACCAGC
STMN2_ intron1	-	TTT A	610	TAGTATAATATGTGGC TCCTACTCTAAGTA	261 6	UAGUAUAAU AUGUGGC UCCUACUCUAAGUA
STMN2_ intron1	-	TTTT	611	ATAGTATAATATGTGG CTCCTACTCTAAGT	261 7	AUAGUAUAAU AUGUGG CUCCUACUCUAAGU
STMN2_ intron1	-	GTT T	612	TATAGTATAATATGTG GCTCCTACTCTAAG	261 8	UAUAGUAUAAU AUGUG GCUCCUACUCUAAG
STMN2_ intron1	-	GTT A	613	TCTTTAATCATGACTA ATAAAAATGGATAT	261 9	UCUUUAAU AUGACUA AUAAAA AUGGAU AU
STMN2_ intron1	-	TTT G	614	AGTAAAGAAATAGGA AGACTTATTGGCTCG	262 0	AGUAAAAGAAU AGGAA GACUUAUUGGCUCG
STMN2_ intron1	-	CTT A	615	TTGGCTCGAGGCCCTC AAGTTTAGATTTTT	262 1	UUGGCUCGAGGCCUC AAGUUUAGAUUUUU

STMN2_ intron1	-	ATT G	616	GCTCGAGGCCCTCAA GTTTAGATTTTGTGTC	262 2	GCUCGAGGCCCUCAAG UUUAGAUUUUUGUC
STMN2_ intron1	-	TTT G	617	TTTTAATTTCTTCAGT ATTGCTATTCATAA	262 3	UUUUAAUUUCUUCAGU AUUGCUAUUCAUAA
STMN2_ intron1	-	TTTT	618	GTTTTAATTTCTTCAG TATTGCTATTCATA	262 4	GUUUUAAUUUCUUCAG UAUUGCUAUUCAUAA
STMN2_ intron1	-	CTTT	619	TGTTTTAATTTCTTCA GTATTGCTATTCAT	262 5	UGUUUAAUUUCUUCU GUAUUGCUAUUCAU
STMN2_ intron1	-	ATT G	620	AGACAGCAATCTTTTG TTTTAATTTCTTCA	262 6	AGACAGCAAUCUUUUG UUUUAAUUUCUUCU
STMN2_ intron1	-	TTT G	621	GTAAATAATAAATAT AAGATATATTGAGAC	262 7	GUAAAUAUAAAUUAUA AGAUUAUUGAGAC
STMN2_ intron1	-	ATT T	622	GGTAAATAATAAATA TAAGATATATTGAGA	262 8	GGUAAAUAUAAAUUAU AAGAUUAUUGAGA
STMN2_ intron1	-	CTT A	623	GAATAATTTGGTAAAT AATAAATATAAGAT	262 9	GAAUAAUUUGGUAUAAU AAUAAAUAUAAGAU
STMN2_ intron1	-	ATT C	624	AGGAAGAAATACTCT TAGAATAATTTGGTA	263 0	AGGAAGAAUACUCU AGAAUAAUUUGGUA
STMN2_ intron1	-	TTTC	625	TCACATGGTATTCAGG AAGAAATACTCTTA	263 1	UCACAUGGUAUUCAGG AAGAAUACUCUUA
STMN2_ intron1	-	TTTT	626	CTCACATGGTATTCAG GAAGAAATACTCTT	263 2	CUCACAUGGUAUUCAG GAAGAAUACUCU
STMN2_ intron1	-	ATT T	627	TCTCACATGGTATTC GGAAGAAATACTCT	263 3	UCUCACAUGGUAUUC GGAAGAAUACUCU
STMN2_ intron1	-	CTT A	628	AGAATTTTCTCACATG GTATTCAGGAAGAA	263 4	AGAAUUUCUCACAUG GUAUUCAGGAAGAA
STMN2_ intron1	-	ATT C	629	TTAAGAATTTTCTCAC ATGGTATTCAGGAA	263 5	UUAAGAAUUUUCUCAC AUGGUAUUCAGGAA
STMN2_ intron1	-	TTTC	630	AAATATACAGTCATA CTCAATAAATTCTTA	263 6	AAAUUACAGUCAUAC UCAAUAAAUUCUUA
STMN2_ intron1	-	TTTT	631	CAAATATACAGTCAT ACTCAATAAATTCTT	263 7	CAAUAUACAGUCAUA CUCAAUAAAUUCU
STMN2_ intron1	-	CTTT	632	TCAAATATACAGTCAT ACTCAATAAATTCT	263 8	UCAAUAUACAGUCAU ACUCAUAAAUUCU
STMN2_ intron1	-	CTT A	633	GATAAGCAGAAGAAA ACACTCTTTTCAAAT	263 9	GAUAAGCAGAAGAAAA CACUCUUUUCAAAU
STMN2_ intron1	-	ATT G	634	GCTTAGATAAGCAGA AGAAAACACTCTTTT	264 0	GCUUAGAUAAAGCAGAA GAAAACACUCUUU
STMN2_ intron1	-	TTT A	635	TTGGCTTAGATAAGCA GAAGAAAACACTCT	264 1	UUGGCUUAGAUAAAGCA GAAGAAAACACUCU
STMN2_ intron1	-	CTTT	636	ATTGGCTTAGATAAGC AGAAGAAAACACTC	264 2	AUUGGCUUAGAUAAAGC AGAAGAAAACACUC
STMN2_ intron1	-	ATT G	637	AATAATGAAGATCCTT TATTGGCTTAGATA	264 3	AAUAAUGAAGAUCCU UAUUGGCUUAGAU

STMN2_ intron1	-	GTT A	638	GAATTGAATAATGAA GATCCTTTATTGGCT	264 4	GAAUUGAAUAAUGAAG AUCCUUUAUUGGCU
STMN2_ intron1	-	CTT A	639	GAAAGTTAGAATTGA ATAATGAAGATCCTT	264 5	GAAAGUUAGAAUUGAA UAAUGAAGAUCUU
STMN2_ intron1	-	CTT C	640	CTTAGAAAGTTAGAA TTGAATAATGAAGAT	264 6	CUUAGAAAGUUAGAAU UGAAUAAUGAAGAU
STMN2_ intron1	-	GTT G	641	ACTTCCTTAGAAAGTT AGAATTGAATAATG	264 7	ACUUCCUUAGAAAGUU AGAAUUGAAUAAUG
STMN2_ intron1	-	TTTC	642	TGATCTGTAGGTTGAC TTCCTTAGAAAGTT	264 8	UGAUCUGUAGGUUGAC UUCCUUAGAAAGUU
STMN2_ intron1	-	CTTT	643	CTGATCTGTAGGTTGA CTTCCTTAGAAAGT	264 9	CUGAUCUGUAGGUUGA CUUCCUUAGAAAGU
STMN2_ intron1	-	GTT T	644	TAATTTCTTCAGTATT GCTATTCATAAATG	265 0	UAAUUUCUUCAGUAUU GCUAUUCAUAAAUG
STMN2_ intron1	-	TTTT	645	AATTTCTTCAGTATTG CTATTCATAAATGA	265 1	AAUUUCUUCAGUAUUG CUAUUCAUAAAUGA
STMN2_ intron1	-	TTT A	646	ATTTCTTCAGTATTGC TATTCATAAATGAT	265 2	AUUUCUUCAGUAUUGC UAUUCAUAAAUGAU
STMN2_ intron1	-	ATT T	647	CTTCAGTATTGCTATT CATAAATGATAGTA	265 3	CUUCAGUAUUGCUAUU CAUAAAUGAUAGUA
STMN2_ intron1	-	ATT A	648	AGAGAGAGTGATGGG GCAGAACACATAATT	265 4	AGAGAGAGUGAUGGGG CAGAACACAUAAUU
STMN2_ intron1	-	TTT A	649	AAAATCCAATTAAGA GAGAGTGATGGGGCA	265 5	AAAAUCCAAUUAAGAG AGAGUGAUGGGGGCA
STMN2_ intron1	-	TTTT	650	AAAAATCCAATTAAG AGAGAGTGATGGGGC	265 6	AAAAAUCCAAUUAAGA GAGAGUGAUGGGGC
STMN2_ intron1	-	ATT T	651	TAAAAATCCAATTAA GAGAGAGTGATGGGG	265 7	UAAAAAUCCAAUUAAG AGAGAGUGAUGGGG
STMN2_ intron1	-	CTT C	652	TGCCGAGTCCTGCAAT ATGAATATAATTTT	265 8	UGCCGAGUCCUGCAAU AUGAAUAUAAUUUU
STMN2_ intron1	-	TTTC	653	TCTCGAAGGTCTTCTG CCGAGTCCTGCAAT	265 9	UCUCGAAGGUCUUCUG CCGAGUCCUGCAAU
STMN2_ intron1	-	CTTT	654	CTCTCGAAGGTCTTCT GCCGAGTCCTGCAA	266 0	CUCUCGAAGGUCUUCU GCCGAGUCCUGCAA
STMN2_ intron1	-	TTTC	655	TACCTTTCTCTCGAAG GTCTTCTGCCGAGT	266 1	UACCUUUCUCUCGAAG GUCUUCUGCCGAGU
STMN2_ intron1	-	TTTT	656	CTACCTTTCTCTCGAA GGTCTTCTGCCGAG	266 2	CUACCUUUCUCUCGAA GGUCUUCUGCCGAG
STMN2_ intron1	-	ATT T	657	TCTACCTTTCTCTCGA AGGTCTTCTGCCGA	266 3	UCUACCUUUCUCUCGA AGGUCUUCUGCCGA
STMN2_ intron1	-	CTT A	658	TTTTCTACCTTTCTCTC GAAGGTCTTCTGC	266 4	UUUUCUACCUUUCUCU CGAAGGUCUUCUGC
STMN2_ intron1	-	ATT C	659	TTATTTTCTACCTTTCT CTCGAAGGTCTTC	266 5	UUAUUUUCUACCUUUC UCUCGAAGGUCUUC

STMN2_ intron1	-	CTT A	660	GGCAGGCTGTCTGTCT CTCTCTCTCGCACA	266 6	GGCAGGCUGUCUGUCU CUCUCUCUCGCACA
STMN2_ intron1	-	CTT G	661	AAGATCCTCTTTCTGA TCTGTAGGTTGACT	266 7	AAGAUCUCUUUCUGA UCUGUAGGUUGACU
STMN2_ intron1	-	CTT C	662	TTAGGCAGGCTGTCTG TCTCTCTCTCTCGC	266 8	UUAGGCAGGCUGUCUG UCUCUCUCUCUCGC
STMN2_ intron1	-	ATT T	663	CTTCTTAGGCAGGCTG TCTGTCTCTCTCTC	266 9	CUUCUUAGGCAGGCUG UCUGUCUCUCUCUC
STMN2_ intron1	-	ATT C	664	ATTTCTTCTTAGGCAG GCTGTCTGTCTCTC	267 0	AUUUCUUUCUAGGCAG GCUGUCUGUCUCUC
STMN2_ intron1	-	ATT C	665	ACATTCATTTCTTCTT AGGCAGGCTGTCTG	267 1	ACAUUCAUUUCUUCUU AGGCAGGCUGUCUG
STMN2_ intron1	-	CTT G	666	TCAACTGTGCCACAAG CCGCATTACATTC	267 2	UCAACUGUGCCACAAG CCGCAUUCACAUC
STMN2_ intron1	-	TTT A	667	TCATCCTTGTCAACTG TGCCACAAGCCGCA	267 3	UCAUCCUUGUCAACUG UGCCACAAGCCGCA
STMN2_ intron1	-	ATT T	668	ATCATCCTTGTCAACT GTGCCACAAGCCGC	267 4	AUCAUCCUUGUCAACU GUGCCACAAGCCGC
STMN2_ intron1	-	ATT G	669	ATTTATCATCCTTGTC AACTGTGCCACAAG	267 5	AUUUAUCAUCCUUGUC AACUGUGCCACAAG
STMN2_ intron1	-	ATT A	670	TTGATTTATCATCCTT GTCAACTGTGCCAC	267 6	UUGAUUUUAUCAUCCU GUCAACUGUGCCAC
STMN2_ intron1	-	CTT G	671	CATTATTGATTTATCA TCCTTGTCAACTGT	267 7	CAUUUAUUGAUUUUAU UCCUUGUCAACUGU
STMN2_ intron1	-	ATT C	672	ATAAATGATAGTAAG CTTGCAATTATTGATT	267 8	AUAAAUGAUAGUAAGC UUGCAUUAUUGAUU
STMN2_ intron1	-	ATT G	673	CTATTCATAAATGATA GTAAGCTTGCATTA	267 9	CUAUUCAUAAAUGAUA GUAAGCUUGCAUUA
STMN2_ intron1	-	CTT C	674	AGTATTGCTATTCATA AATGATAGTAAGCT	268 0	AGUAUUGCUAUUCAUA AAUGAUAGUAAGCU
STMN2_ intron1	-	TTTC	675	TTCAGTATTGCTATTC ATAAATGATAGTAA	268 1	UUCAGUAUUGCUAUUC AUAAAUGAUAGUAA
STMN2_ intron1	-	TTTC	676	TTCTTAGGCAGGCTGT CTGTCTCTCTCTCT	268 2	UUCUUAGGCAGGCUGU CUGUCUCUCUCUCU
STMN2_ intron1	-	CTTT	677	ACAATCTTTGTAAAAA AAAAAAATCATTC	268 3	ACAAUCUUUGUAAAAA AAAAAAAUCAUUC
STMN2_ intron1	-	ATT C	678	CTTGAAGATCCTCTTT CTGATCTGTAGGTT	268 4	CUUGAAGAUCCUCUUU CUGAUCUGUAGGUU
STMN2_ intron1	-	CTTT	679	GATGCTATTCTTGAA GATCCTCTTTCTGA	268 5	GAUGCUAUUCCUUGAA GAUCCUCUUUCUGA
STMN2_ intron1	-	CTT A	680	GTCCAACCTTGTGTTG AGTAACAGTATATT	268 6	GUCCAACUUUGUGUUG AGUAACAGUAUAUU
STMN2_ intron1	-	TTT G	681	AGACTTAGTCCAACCT TGTGTTGAGTAACA	268 7	AGACUUAGUCCAACUU UGUGUUGAGUAACA

STMN2_ intron1	-	CTTT	682	GAGACTTAGTCCAAC TTGTGTTGAGTAAC	268 8	GAGACUAGUCCAACU UUGUGUUGAGUAAC
STMN2_ intron1	-	GTT A	683	ACAACAACGAATGG CTAACTTTGAGACTT	268 9	ACAACAACUGAAUGGC UAACUUUGAGACUU
STMN2_ intron1	-	CTT C	684	TGAGAGACCCTGAAA TGAACGTTAACAAC	269 0	UGAGAGACCCUGAAAU GAACUGUUAACAAC
STMN2_ intron1	-	TTTC	685	CCAGCTTCTGAGAGAC CCTGAAATGAACTG	269 1	CCAGCUUCUGAGAGAC CCUGAAAUGAACUG
STMN2_ intron1	-	GTT T	686	CCCAGCTTCTGAGAGA CCCTGAAATGAACT	269 2	CCCAGCUUCUGAGAGA CCCUGAAAUGAACU
STMN2_ intron1	-	ATT G	687	CAAAAATGGAAAGTT TCCCAGCTTCTGAGA	269 3	CAAAAUGGAAAGUUU CCCAGCUUCUGAGA
STMN2_ intron1	-	CTT C	688	AATGTACAAGAAATT GCAAAAATGGAAAGT	269 4	AAUGUACAAGAAAUUG CAAAAUGGAAAGU
STMN2_ intron1	-	TTTC	689	CTTCAATGTACAAGA AATTGCAAAAATGGA	269 5	CUUCAAUUGACAAGAA AUUGCAAAAUGGA
STMN2_ intron1	-	CTTT	690	CCTTCAATGTACAAGA AATTGCAAAAATGG	269 6	CCUUCAAUGUACAAGA AAUUGCAAAAUGG
STMN2_ intron1	-	CTT C	691	CTTTCCTTCAATGTAC AAGAAATTGCAAAA	269 7	CUUCCUUCUAAUGUAC AAGAAUUGCAAAA
STMN2_ intron1	-	CTT A	692	AGTGTGTCTTCCTTTC CTTCAATGTACAAG	269 8	AGUGUGUCUCCUUUC CUUCAAUUGACAAG
STMN2_ intron1	-	TTT G	693	TAATGCTGTCTTAAGT GTGTCTTCCTTTCC	269 9	UAAUGCUGUCUUAAGU GUGUCUCCUUUCC
STMN2_ intron1	-	TTTT	694	GTAATGCTGTCTTAAG TGTGTCTTCCTTTC	270 0	GUAAGCUGUCUUAAG UGUGUCUCCUUUC
STMN2_ intron1	-	CTTT	695	TGTAATGCTGTCTTAA GTGTGTCTTCCTTT	270 1	UGUAAUGCUGUCUUA GUGUGUCUCCUUU
STMN2_ intron1	-	ATT A	696	CTTTTGTAATGCTGTC TTAAGTGTGTCTTC	270 2	CUUUUGUAAUGCUGUC UUAAGUGUGUCUUC
STMN2_ intron1	-	TTT A	697	AAACATGAATTACTTT TGTAATGCTGTCTT	270 3	AAACAUGAAUUAUUU UGUAAUGCUGUCU
STMN2_ intron1	-	ATT T	698	AAAACATGAATTACTT TTGTAATGCTGTCT	270 4	AAAACAUGAAUUAUU UUGUAAUGCUGUCU
STMN2_ intron1	-	ATT A	699	AACATTTAAAACATG AATTACTTTTGTAAT	270 5	AACAUUUAAAACAUGA AUUACUUUUGUAAU
STMN2_ intron1	-	GTT A	700	TACAGAGAGCCCTGC CCGACTGCCAGAATT	270 6	UACAGAGAGCCCUGCC CGACUGCCAGAAUU
STMN2_ intron1	-	TTT G	701	TCATCTCCAAATGAGG TTATACAGAGAGCC	270 7	UCAUCUCCAAAUGAGG UUAUACAGAGAGCC
STMN2_ intron1	-	TTTT	702	GTCATCTCCAAATGAG GTTATACAGAGAGC	270 8	GUCAUCUCCAAAUGAG GUUAUACAGAGAGC
STMN2_ intron1	-	TTTT	703	TGTCATCTCCAAATGA GGTTATACAGAGAG	270 9	UGUCAUCUCCAAAUGA GGUUAUACAGAGAG

STMN2_ intron1	-	ATT T	704	TTGTCATCTCCAAATG AGGTTATACAGAGA	271 0	UUGUCAUCUCCAAAUG AGGUUAUACAGAGA
STMN2_ intron1	-	TTT A	705	GATTTTTGTCATCTCC AAATGAGGTTATAC	271 1	GAUUUUUGUCAUCUCC AAAUGAGGUUAUAC
STMN2_ intron1	-	GTT T	706	AGATTTTTGTCATCTC CAAATGAGGTTATA	271 2	AGAUUUUUGUCAUCUC CAAUGAGGUUAUA
STMN2_ intron1	-	CTTT	707	GTGTTGAGTAACAGT ATATTCTGCAAACCC	271 3	GUGUUGAGUAACAGUA UAUUCUGCAAACCC
STMN2_ intron1	-	TTT G	708	TGTTGAGTAACAGTAT ATTCTGCAAACCCCT	271 4	UGUUGAGUAACAGUAU AUUCUGCAAACCCU
STMN2_ intron1	-	GTT G	709	AGTAACAGTATATTCT GCAAACCCCTGAAGC	271 5	AGUAACAGUAUAUUCU GCAAACCCUGAAGC
STMN2_ intron1	-	ATT C	710	TGCAAACCCCTGAAGCT AGTTTTATTGGGA	271 6	UGCAAACCCUGAAGCU AGUUUUAUUUGGA
STMN2_ intron1	-	TTTC	711	CAGAAAGGTGGTAAT GGCTGCATGGTCAGC	271 7	CAGAAAGGUGGUAAUG GCUGCAUGGUCAGC
STMN2_ intron1	-	ATT T	712	CCAGAAAGGTGGTAA TGGCTGCATGGTCAG	271 8	CCAGAAAGGUGGUAAU GGCUGCAUGGUCAG
STMN2_ intron1	-	TTT G	713	CAGCATAATATTTCCA GAAAGGTGGTAATG	271 9	CAGCAUAAUAAUUCCA GAAAGGUGGUAAUG
STMN2_ intron1	-	TTTT	714	GCAGCATAATATTTCC AGAAAGGTGGTAAT	272 0	GCAGCAUAAUAAUUC AGAAAGGUGGUAAU
STMN2_ intron1	-	TTTT	715	TGCAGCATAATATTTT CAGAAAGGTGGTAA	272 1	UGCAGCAUAAUAAUUC CAGAAAGGUGGUAA
STMN2_ intron1	-	ATT T	716	TTGCAGCATAATATTT CCAGAAAGGTGGTA	272 2	UUGCAGCAUAAUAAU CCAGAAAGGUGGUAA
STMN2_ intron1	-	ATT G	717	TATCATTTTTGCAGCA TAATATTTCCAGAA	272 3	UAUCAUUUUUGCAGCA UAAUAAUUCAGAA
STMN2_ intron1	-	TTTC	718	GTGTATTGTATCATTT TTGCAGCATAATAT	272 4	GUGUAUUGUAUCAUU UUGCAGCAUAAUAAU
STMN2_ intron1	-	ATT T	719	CGTGTATTGTATCATT TTTGCAGCATAATA	272 5	CGUGUAUUGUAUCAU UUUGCAGCAUAAUA
STMN2_ intron1	-	TTT G	720	AGATATTTTCGTGTATT GTATCATTTTTGCA	272 6	AGAUAAUUCGUGUAU GUAUCAUUUUUGCA
STMN2_ intron1	-	ATT T	721	GAGATATTTTCGTGTAT TGTATCATTTTTGC	272 7	GAGAUAAUUCGUGUAU UGUAUCAUUUUUGC
STMN2_ intron1	-	TTT A	722	ATTTGAGATATTTTCGT GTATTGTATCATTT	272 8	AUUUGAGAUAAUUCGU GUAUUGUAUCAUUU
STMN2_ intron1	-	TTTT	723	AATTTGAGATATTTTCG TGTATTGTATCATT	272 9	AAUUUGAGAUAAUUCG UGUAUUGUAUCAUU
STMN2_ intron1	-	TTT G	724	ATGCTATTCCTTGAAG ATCCTCTTTCTGAT	273 0	AUGCUAAUCCUUGAAG AUCCUCUUUCUGAU
STMN2_ intron1	-	TTTT	725	TAATTTGAGATATTTT GTGTATTGTATCAT	273 1	UAAUUUGAGAUAAUUC GUGUAUUGUAUCAU

STMN2_ intron1	-	ATT T	726	TTTAATTTGAGATATT TCGTGTATTGTATC	273 2	UUUAAUUUGAGAUUU UCGUGUAUUGUAUC
STMN2_ intron1	-	GTT A	727	TATTTTTTAATTTGAG ATATTTTCGTGTATT	273 3	UAUUUUUUAAUUUGAG AUUUUUCGUGUAUU
STMN2_ intron1	-	TTT G	728	GGAAATGTTATATTTT TTAATTTGAGATAT	273 4	GGAAAUGUUUAUUUU UUAAUUUGAGAUUU
STMN2_ intron1	-	ATT T	729	GGGAAATGTTATATTT TTTAATTTGAGATA	273 5	GGGAAAUGUUUAUUUU UUUAAUUUGAGAUUU
STMN2_ intron1	-	TTT A	730	GTGCCCTATTTGGGAA ATGTTATATTTTTT	273 6	GUGCCCUAUUUGGGAA AUGUUUAUUUUUU
STMN2_ intron1	-	TTTT	731	AGTGCCCTATTTGGGA AATGTTATATTTTT	273 7	AGUGCCCUAUUUGGGA AAUGUUUAUUUUUU
STMN2_ intron1	-	TTTT	732	TAGTGCCCTATTTGGG AAATGTTATATTTTT	273 8	UAGUGCCCUAUUUGGG AAAUGUUUAUUUUUU
STMN2_ intron1	-	GTT T	733	TTAGTGCCCTATTTGG GAAATGTTATATTT	273 9	UUAGUGCCCUAUUUGG GAAAUGUUUAUUUU
STMN2_ intron1	-	TTT G	734	GGATCATGTTTTTAGT GCCCTATTTGGGAA	274 0	GGAUCAUGUUUUUAGU GCCCUAUUUGGGAA
STMN2_ intron1	-	ATT T	735	GGGATCATGTTTTTAG TGCCCTATTTGGGA	274 1	GGGAUCAUGUUUUUAG UGCCCUAUUUGGGA
STMN2_ intron1	-	TTT A	736	TTGGGATCATGTTTT TAGTGCCCTATTTG	274 2	UUUGGGAUCAUGUUUU UAGUGCCCUAUUUG
STMN2_ intron1	-	TTTT	737	ATTTGGGATCATGTTT TTAGTGCCCTATTT	274 3	AUUUGGGAUCAUGUUU UUAGUGCCCUAUUU
STMN2_ intron1	-	GTT T	738	TATTTGGGATCATGTT TTAGTGCCCTATT	274 4	UAUUUGGGAUCAUGUU UUUAGUGCCCUAUU
STMN2_ intron1	-	TTTT	739	TTAATTTGAGATATTT CGTGTATTGTATCA	274 5	UUAAUUUGAGAUUUUU CGUGUAUUGUAUCA
STMN2_ intron1	-	ATT C	740	CCAGAGTAATAAAAAT CCCCAGGTATATGAG	274 6	CCAGAGUAAUAAAAUC CCCAGGUUAUAUGAG
STMN2_ intron1	-	GTT G	741	CTTTACAATCTTTGTA AAAAAAAAAAAAATC	274 7	CUUUACAAUCUUUGUA AAAAAAAAAAAAAUC
STMN2_ intron1	-	ATT C	742	CAGAAGAATAACTGC TAAATGGGCACTCTT	274 8	CAGAAGAAUACUGCU AAUUGGGCACUCUU
STMN2_ intron1	-	TTTT	743	TATTTTTGTTCTCATA ATACCTGGCACAGG	274 9	UAUUUUUGUUCUCAUA AUACCUGGCACAGG
STMN2_ intron1	-	ATT T	744	TTATTTTTGTTCTCAT AATACCTGGCACAG	275 0	UUUUUUUGUUCUCAU AAUACCUGGCACAG
STMN2_ intron1	-	TTTC	745	TGCAAAAGACTAAAT CCACCAAGGGTGAGG	275 1	UGCAAAAGACUAAAUC CACCAAGGGUGAGG
STMN2_ intron1	-	TTTT	746	CTGCAAAAGACTAAA TCCACCAAGGGTGAG	275 2	CUGCAAAAGACUAAA CCACCAAGGGUGAG
STMN2_ intron1	-	TTTT	747	TCTGCAAAAGACTAA ATCCACCAAGGGTGA	275 3	UCUGCAAAAGACUAAA UCCACCAAGGGUGA

STMN2_ intron1	-	TTTT	748	TTCTGCAAAAGACTA AATCCACCAAGGGTG	275 4	UUCUGCAAAAGACUAA AUCCACCAAGGGUG
STMN2_ intron1	-	TTTT	749	TTTCTGCAAAAGACTA AATCCACCAAGGGT	275 5	UUUCUGCAAAAGACUA AAUCCACCAAGGGU
STMN2_ intron1	-	CTTT	750	TTTTCTGCAAAAGACT AAATCCACCAAGGG	275 6	UUUUCUGCAAAAGACU AAAUCCACCAAGGG
STMN2_ intron1	-	TTTC	751	TGACATGTACAGGAT CTTTTTTTCTGCAAA	275 7	UGACAUGUACAGGAUC UUUUUUUCUGCAAA
STMN2_ intron1	-	CTTT	752	CTGACATGTACAGGA TCTTTTTTTCTGCAA	275 8	CUGACAUGUACAGGAU CUUUUUUUCUGCAA
STMN2_ intron1	-	ATT G	753	AACTTTCTGACATGTA CAGGATCTTTTTTT	275 9	AACUUUCUGACAUGUA CAGGAUCUUUUUUU
STMN2_ intron1	-	ATT A	754	CTATTGAACTTTCTGA CATGTACAGGATCT	276 0	CUAUUGAACUUCUGA CAUGUACAGGAUCU
STMN2_ intron1	-	ATT A	755	TTACTATTGAACTTTC TGACATGTACAGGA	276 1	UUACUAUUGAACUUUC UGACAUGUACAGGA
STMN2_ intron1	-	ATT A	756	CCATTATTACTATTGA ACTTTCTGACATGT	276 2	CCAUUAUUACUAUUGA ACUUCUGACAUGU
STMN2_ intron1	-	GTT A	757	TAAATTACCATTATTA CTATTGAACTTTCT	276 3	UAAAUUACCAUUAUUA CUAUUGAACUUCU
STMN2_ intron1	-	TTT A	758	TAGTTATAAATTACCA TTATTACTATTGAA	276 4	UAGUUAUAAAUUACCA UUAUUACUAUUGAA
STMN2_ intron1	-	ATT T	759	ATAGTTATAAATTACC ATTATTACTATTGA	276 5	AUAGUUAUAAAUUACC AUUAUUACUAUUGA
STMN2_ intron1	-	CTT C	760	CATTTATAGTTATAAA TTACCATTATTACT	276 6	CAUUUAUAGUUAUAAA UUACCAUUAUUACU
STMN2_ intron1	-	ATT G	761	TGAGATGGTGACTTCC ATTTATAGTTATAA	276 7	UGAGAUGGUGACUCC AUUUAUAGUUAUAA
STMN2_ intron1	-	GTT A	762	AGATGGTGAAATTGT GAGATGGTGACTTCC	276 8	AGAUGGUGAAAUUGUG AGAUGGUGACUCC
STMN2_ intron1	-	ATT G	763	TTAAGATGGTGAAATT GTGAGATGGTGACT	276 9	UUAAGAUGGUGAAAUU GUGAGAUGGUGACU
STMN2_ intron1	-	TTT A	764	ACAAAATTGTTAAGA TGGTGAAATTGTGAG	277 0	ACAAAUUGUUAAGAU GGUGAAAUUGUGAG
STMN2_ intron1	-	GTT T	765	AACAAAATTGTTAAG ATGGTGAAATTGTGA	277 1	AACAAAUUGUUAAGA UGGUGAAAUUGUGA
STMN2_ intron1	-	ATT G	766	TAGGGCAGTTTAACA AAATTGTTAAGATGG	277 2	UAGGGCAGUUUAACAA AAUUGUUAAGAUGG
STMN2_ intron1	-	CTT G	767	TAATATTGTAGGGCA GTTTAACAAAATTGT	277 3	UAAUAUUGUAGGGCAG UUUAACAAAUUGU
STMN2_ intron1	-	ATT A	768	TGTACTATCTTGTAAT ATTGTAGGGCAGTT	277 4	UGUACUAUCUUGUAAU AUUGUAGGGCAGUU
STMN2_ intron1	-	GTT A	769	CTAGTGTATCATTATG TACTATCTTGTAAT	277 5	CUAGUGUAUCAUUAUG UACUAUCUUGUAAU

STMN2_ intron1	-	TTTT	770	ATTTTTGTTCTCATAA TACCTGGCACAGGC	277 6	AUUUUUGUUCUCAUAA UACCUGGCACAGGC
STMN2_ intron1	-	GTT G	771	ATGTTACTAGTGTATC ATTATGTACTATCT	277 7	AUGUUACUAGUGUAUC AUUAUGUACUAUCU
STMN2_ intron1	-	TTT A	772	TTTTTGTTCTCATAAT ACCTGGCACAGGCT	277 8	UUUUUGUUCUCAUAAU ACCUGGCACAGGCU
STMN2_ intron1	-	TTTT	773	TGTTCTCATAATACCT GGCACAGGCTTCAG	277 9	UGUUCUCAUAAUACCU GGCACAGGCUUCAG
STMN2_ intron1	-	TTTT	774	GATAGGTAAATAATA TACACAACCTTTATTA	278 0	GAUAGGUAAAUAUAAU ACACAACUUUAUUA
STMN2_ intron1	-	ATT T	775	TGATAGGTAAATAAT ATACACAACCTTTATT	278 1	UGAUAGGUAAAUAUAA UACACAACUUUAUU
STMN2_ intron1	-	ATT A	776	CATATAAATATTTTGA TAGGTAAATAATAT	278 2	CAUAUAAAUUUUUGA UAGGUAAAUAUAAU
STMN2_ intron1	-	TTT A	777	TATATTACATATAAAT ATTTTGATAGGTAA	278 3	UAUAUUACAUAUAAA AUUUUGAUAGGUAA
STMN2_ intron1	-	ATT T	778	ATATATTACATATAAA TATTTTGATAGGTA	278 4	AUAUAUUACAUAUAAA UAUUUUGAUAGGUAA
STMN2_ intron1	-	TTT G	779	CATGAATGTGTATATA TGTATGAAATAGGC	278 5	CAUGAAUGUGUAUAUA UGUAUGAAAUAGGC
STMN2_ intron1	-	TTTT	780	GCATGAATGTGTATAT ATGTATGAAATAGG	278 6	GCAUGAAUGUGUAUAU AUGUAUGAAAUAGG
STMN2_ intron1	-	ATT T	781	TGCATGAATGTGTATA TATGTATGAAATAG	278 7	UGCAUGAAUGUGUAUA UAUGUAUGAAAUAG
STMN2_ intron1	-	CTT A	782	TTTTGCATGAATGTGT ATATATGTATGAAA	278 8	UUUUGCAUGAAUGUGU AUUAUUGUAUGAAA
STMN2_ intron1	-	ATT A	783	CAGGACAGTGGAGGG AGTGCTAAACCTTAT	278 9	CAGGACAGUGGAGGGA GUGCUAAACCUAUU
STMN2_ intron1	-	TTT A	784	TTACAGGACAGTGGA GGGAGTGCTAAACCT	279 0	UUACAGGACAGUGGAG GGAGUGCUAAACCU
STMN2_ intron1	-	TTTT	785	ATTACAGGACAGTGG AGGGAGTGCTAAACC	279 1	AUUACAGGACAGUGGA GGGAGUGCUAAACC
STMN2_ intron1	-	GTT T	786	TATTACAGGACAGTG GAGGGAGTGCTAAAC	279 2	UAUUACAGGACAGUGG AGGGAGUGCUAAAC
STMN2_ intron1	-	ATT C	787	TCACTGTGCATGTTTT ATTACAGGACAGTG	279 3	UCACUGUGCAUGUUUU AUUACAGGACAGUG
STMN2_ intron1	-	TTT A	788	AACTGAAGACAAATA TGCCCTCGTGTATGAC	279 4	AACUGAAGACAAAUAA GCCUCGUGUAUGAC
STMN2_ intron1	-	CTTT	789	AACTGAAGACAAAT ATGCCTCGTGTATGA	279 5	AAACUGAAGACAAAUAA UGCCUCGUGUAUGA
STMN2_ intron1	-	GTT A	790	GTGACACTGACTATCA ATGACTTTAACTG	279 6	GUGACACUGACUAUCA AUGACUUAAACUG
STMN2_ intron1	-	TTT A	791	GTTAGTGACACTGACT ATCAATGACTTTAA	279 7	GUUAGUGACACUGACU AUCAAUGACUUUAA

STMN2_ intron1	-	CTTT	792	AGTTAGTGACACTGA CTATCAATGACTTTA	279 8	AGUUAGUGACACUGAC UAUCAAUGACUUUA
STMN2_ intron1	-	TTT A	793	CTTTAGTTAGTGACAC TGACTATCAATGAC	279 9	CUUUAGUUAGUGACAC UGACUAUCAAUGAC
STMN2_ intron1	-	TTTT	794	ACTTTAGTTAGTGACA CTGACTATCAATGA	280 0	ACUUUAGUUAGUGACA CUGACUAUCAAUGA
STMN2_ intron1	-	ATT T	795	TACTTTAGTTAGTGAC ACTGACTATCAATG	280 1	UACUUUAGUUAGUGAC ACUGACUAUCAAUG
STMN2_ intron1	-	GTT G	796	GTGCTCCAATCTATTT TACTTTAGTTAGTG	280 2	GUGCUCCAAUCUAUUU UACUUUAGUUAGUG
STMN2_ intron1	-	CTT C	797	AGAACAAAGTTGGTG CTCCAATCTATTTTA	280 3	AGAACAAAGUUGGUGC UCCAAUCUAUUUUA
STMN2_ intron1	-	GTT C	798	TCATAATACCTGGCAC AGGCTTCAGAACAA	280 4	UCAUAAUACCUGGCAC AGGCUUCAGAACAA
STMN2_ intron1	-	TTT G	799	TTCTCATAATACCTGG CACAGGCTTCAGAA	280 5	UUCUCAUAAUACCUGG CACAGGCUUCAGAA
STMN2_ intron1	-	TTTT	800	GTTCTCATAATACCTG GCACAGGCTTCAGA	280 6	GUUCUCAUAAUACCUG GCACAGGCUUCAGA
STMN2_ intron1	-	ATT T	801	TTGTTCTCATAATACC TGGCACAGGCTTCA	280 7	UUGUUCUCAUAAUACC UGGCACAGGCUUCA
STMN2_ intron1	-	CTT C	802	CTAGTTGATGTTACTA GTGTATCATTATGT	280 8	CUAGUUGAUGUUACUA GUGUAUCAUUAUGU
STMN2_ intron1	-	CTT G	803	GTACTTCCTAGTTGAT GTTACTAGTGTATC	280 9	GUACUCCUAGUUGAU GUUACUAGUGUAUC
STMN2_ intron1	-	TTT G	804	GTGGATCTTGGTACTT CCTAGTTGATGTTA	281 0	GUGGAUCUUGGUACUU CCUAGUUGAUGUUA
STMN2_ intron1	+	TTTT	805	ACTGAGAATCAGCAG CGTTTGAGGAGCTAG	281 1	ACUGAGAAUCAGCAGC GUUUGAGGAGCUAG
STMN2_ intron1	+	ATT T	806	TACTGAGAATCAGCA GCGTTTGAGGAGCTA	281 2	UACUGAGAAUCAGCAG CGUUUGAGGAGCUA
STMN2_ intron1	+	CTT C	807	CCAAATTTTACTGAGA ATCAGCAGCGTTTG	281 3	CCAAAUUUUACUGAGA AUCAGCAGCGUUUG
STMN2_ intron1	+	ATT A	808	AAATGCTTCCCAAATT TACTGAGAATCAG	281 4	AAUUGCUUCCCAAUU UUACUGAGAAUCAG
STMN2_ intron1	+	TTT A	809	ATTAAAATGCTTCCCA AATTTTACTGAGAA	281 5	AUUAAAAUGCUUCCCA AAUUUUACUGAGAA
STMN2_ intron1	+	CTTT	810	AATTAAAATGCTTCCC AAATTTTACTGAGA	281 6	AAUUAAAAUGCUUCCC AAUUUUUACUGAGA
STMN2_ intron1	+	ATT C	811	TTTAATTAAAATGCTT CCCAAATTTTACTG	281 7	UUUAAUUAAAAUGCUU CCCAAUUUUACUG
STMN2_ intron1	+	TTT A	812	ATGAGTCCATCAACCA ATCTGGCCAGAGAA	281 8	AUGAGUCCAUCAACCA AUCUGGCCAGAGAA
STMN2_ intron1	+	ATT T	813	AATGAGTCCATCAACC AATCTGGCCAGAGA	281 9	AAUGAGUCCAUCAACC AAUCUGGCCAGAGA

STMN2_ intron1	+	TTT A	814	AATATTTAATGAGTCC ATCAACCAATCTGG	282 0	AAUAUUUAAUGAGUCC AUCAACCAAUCUGG
STMN2_ intron1	+	ATT T	815	AAATATTTAATGAGTC CATCAACCAATCTG	282 1	AAAUAUUUAAUGAGUC CAUCAACCAAUCUG
STMN2_ intron1	+	ATT A	816	CAAGATAGTACATAA TGATACACTAGTAAC	282 2	CAAGAUAGUACAUAUU GAUACACUAGUAAC
STMN2_ intron1	+	GTT A	817	AACTGCCCTACAATAT TACAAGATAGTACA	282 3	AACUGCCCUACAAUAU UACAAGAUAGUACA
STMN2_ intron1	+	TTT G	818	TTAAACTGCCCTACAA TATTACAAGATAGT	282 4	UUAACUGCCCUACAA UAUUACAAGAUAGU
STMN2_ intron1	+	TTTT	819	GTAAACTGCCCTACA ATATTACAAGATAG	282 5	GUUAAACUGCCCUACA AUUUACAAGAUAG
STMN2_ intron1	+	ATT T	820	TGTTAAACTGCCCTAC AATATTACAAGATA	282 6	UGUAAACUGCCCUAC AAUAUUACAAGUA
STMN2_ intron1	+	CTT A	821	ACAATTTTGTTAAACT GCCCTACAATATTA	282 7	ACAAUUUUGUAAACU GCCCUACAUAUUA
STMN2_ intron1	+	TTTC	822	ACCATCTTAACAATTT TGTTAAACTGCCCT	282 8	ACCAUCUUAACAAUUU UGUAAACUGCCCU
STMN2_ intron1	+	ATT T	823	CACCATCTTAACAATT TTGTTAAACTGCC	282 9	CACCAUCUUAACAAUU UUGUAAACUGCCC
STMN2_ intron1	+	TTT A	824	TAACTATAAATGGAA GTCACCATCTCACAA	283 0	UAACUAUAAAUGGAAG UCACCAUCUCACAA
STMN2_ intron1	+	ATT T	825	ATAACTATAAATGGA AGTCACCATCTCACA	283 1	AUAACUAUAAAUGGAA GUCACCAUCUCACA
STMN2_ intron1	+	GTT C	826	AATAGTAATAATGGT AATTTATAACTATAA	283 2	AAUAGUAAUAAUGGUA AUUUUAACUAUAA
STMN2_ intron1	+	TTT G	827	CAGAAAAAAAGATCC TGTACATGTCAGAAA	283 3	CAGAAAAAAAGAUCCU GUACAUGUCAGAAA
STMN2_ intron1	+	TTTT	828	GCAGAAAAAAAGATC CTGTACATGTCAGAA	283 4	GCAGAAAAAAAGAUCC UGUACAUGUCAGAA
STMN2_ intron1	+	CTTT	829	TGCAGAAAAAAAGAT CCTGTACATGTCAGA	283 5	UGCAGAAAAAAAGAUCC CUGUACAUGUCAGA
STMN2_ intron1	+	TTT A	830	GTCTTTTGCAGAAAA AAGATCCTGTACAT	283 6	GUCUUUUGCAGAAAA AAGAUCCUGUACAU
STMN2_ intron1	+	ATT T	831	AGTCTTTTGCAGAAAA AAAGATCCTGTACA	283 7	AGUCUUUUGCAGAAAA AAAGAUCCUGUACA
STMN2_ intron1	+	TTT A	832	CTGAGAATCAGCAGC GTTTGAGGAGCTAGC	283 8	CUGAGAAUCAGCAGCG UUUGAGGAGCUAGC
STMN2_ intron1	+	GTT T	833	GAGGAGCTAGCCTCC ACCCCAGAGGTTCT	283 9	GAGGAGCUAGCCUCCA CCCCCAGAGGUUCU
STMN2_ intron1	+	TTT G	834	AGGAGCTAGCCTCCA CCCCCAGAGGTTCTC	284 0	AGGAGCUAGCCUCCAC CCCCCAGAGGUUCUC
STMN2_ intron1	+	GTT C	835	TCACTCTATTAGGTCT GAAGCAGGTCCCAT	284 1	UCACUCUAUUAGGUCU GAAGCAGGUCCCAU

STMN2_ intron1	-	TTTT	836	GGTGGATCTTGGTACT TCCTAGTTGATGTT	284 2	GGUGGAUCUUGGUACU UCCUAGUUGAUGUU
STMN2_ intron1	-	CTTT	837	TGGTGGATCTTGGTAC TTCCTAGTTGATGT	284 3	UGGUGGAUCUUGGUAC UCCUAGUUGAUGU
STMN2_ intron1	-	TTTC	838	AGCCTTTTGGTGGATC TTGGTACTTCCTAG	284 4	AGCCUUUUGGUGGAUC UUGGUACUCCUAG
STMN2_ intron1	-	TTTT	839	CAGCCTTTTGGTGGAT CTTGGTACTTCCTA	284 5	CAGCCUUUUGGUGGAU CUUGGUACUCCUA
STMN2_ intron1	-	TTTT	840	TCAGCCTTTTGGTGGA TCTTGGTACTTCCT	284 6	UCAGCCUUUUGGUGGA UCUUGGUACUCCU
STMN2_ intron1	-	ATT T	841	TTCAGCCTTTTGGTGG ATCTTGGTACTTCC	284 7	UUCAGCCUUUUGGUGG AUCUUGGUACUCC
STMN2_ intron1	-	TTT A	842	AATTTTTCAGCCTTTT GGTGGATCTTGGTA	284 8	AAUUUUUCAGCCUUU GGUGGAUCUUGGUA
STMN2_ intron1	-	ATT T	843	AAATTTTTCAGCCTTT TGGTGGATCTTGGT	284 9	AAUUUUUCAGCCUU UGGUGGAUCUUGGU
STMN2_ intron1	-	ATT A	844	AATATTTAAATTTTTC AGCCTTTTGGTGGA	285 0	AAUAAUUAAAUUUUC AGCCUUUUGGUGGA
STMN2_ intron1	-	GTT G	845	ATGGACTCATTAATA TTTAAATTTTTCAG	285 1	AUGGACUCAUAAAUA UUUAAAUUUUCAG
STMN2_ intron1	-	ATT G	846	GTTGATGGACTCATTA AATATTTAAATTTT	285 2	GUUGAUGGACUCAUA AAUAAUUAAAUUU
STMN2_ intron1	-	ATT C	847	TCTGGCCAGATTGGTT GATGGACTCATTA	285 3	UCUGGCCAGAUUGGU GAUGGACUCAUAA
STMN2_ intron1	-	ATT A	848	AAGAATTCTCTGGCCA GATTGGTTGATGGA	285 4	AAGAAUUCUCUGGCCA GAUUGGUUGAUGGA
STMN2_ intron1	-	TTT G	849	ATAGGTAAATAATAT ACACAACCTTTATTAT	285 5	AUAGGUAAAUAUAUA CACAACUUUAUAU
STMN2_ intron1	-	TTT A	850	ATTAAAGAATTCTCTG GCCAGATTGGTTGA	285 6	AUUAAGAAUUCUCUG GCCAGAUUGGUUGA
STMN2_ intron1	-	ATT T	851	TAATTAAAGAATTCTC TGGCCAGATTGGTT	285 7	UAAUUAAGAAUUCUC UGGCCAGAUUGGUU
STMN2_ intron1	-	TTT G	852	GGAAGCATTTTAATTA AAGAATTCTCTGGC	285 8	GGAAGCAUUUUAUAUA AAGAAUUCUCUGGC
STMN2_ intron1	-	ATT T	853	GGGAAGCATTTTAATT AAAGAATTCTCTGG	285 9	GGGAAGCAUUUUAUAU AAAGAAUUCUCUGG
STMN2_ intron1	-	ATT C	854	TCAGTAAAATTTGGG AAGCATTTTAATTAA	286 0	UCAGUAAAUAUUGGGA AGCAUUUUAUAUA
STMN2_ intron1	-	CTT C	855	AGACCTAATAGAGTG AGAACCTCTGGGGT	286 1	AGACCUAUAGAGUGA GAACCUCUGGGGU
STMN2_ intron1	-	GTT A	856	GAAATGCAAATCCAT GGGACCTGCTCAGA	286 2	GAAAUGCAAUCCAUG GGACCUGCUUCAGA
STMN2_ intron1	-	CTT G	857	TTAGAAATGCAAATC CATGGGACCTGCTTC	286 3	UUAGAAAUGCAAUCC AUGGGACCUGCUUC

STMN2_ intron1	-	GTT C	858	TGAATCAGCCTCATCA GCACCACCTGGGAG	286 4	UGAAUCAGCCUCAUCA GCACCACCUGGGAG
STMN2_ intron1	+	TTTC	859	TAACAAGCTCCCAGGT GGTGCTGATGAGGC	286 5	UAACAAGCUCCCAGGU GGUGCUGAUGAGGC
STMN2_ intron1	+	ATT T	860	CTAACAAGCTCCCAG GTGGTGCTGATGAGG	286 6	CUAACAAGCUCCCAGG UGGUGCUGAUGAGG
STMN2_ intron1	+	TTT G	861	CATTTCTAACAAGCTC CCAGGTGGTGCTGA	286 7	CAUUUCUAACAAGCUC CCAGGUGGUGCUGA
STMN2_ intron1	+	ATT T	862	GCATTTCTAACAAGCT CCCAGGTGGTGCTG	286 8	GCAUUUCUAACAAGCU CCCAGGUGGUGCUG
STMN2_ intron1	+	ATT A	863	GGTCTGAAGCAGGTC CCATGGATTTGCATT	286 9	GGUCUGAAGCAGGUCC CAUGGAUUUGCAUU
STMN2_ intron1	-	TTTT	864	AATTAAAGAATTCTCT GGCCAGATTGGTTG	287 0	AAUUAAGAAUUCUCU GGCCAGAUUGGUUG
STMN2_ intron1	-	CTTT	865	ATTATATGTAATATAT ATATTATATGTTAT	287 1	AUUUAUGUAAUUAU AUAUUUAUGUUAU
STMN2_ intron1	-	TTT A	866	TTATATGTAATATATA TATTATATGTTATA	287 2	UUUAUUGUAAUUAUA UAUUAUUGUUAUA
STMN2_ intron1	-	ATT A	867	TATGTAATATATATAT TATATGTTATAATA	287 3	UAUGUAAUUAUUAU UAUUAUGUUAUAAUA
STMN2_ intron1	-	TTT G	868	TTAATGGAAGTTAAA CTTTATGGCTGCATT	287 4	UUAUUGGAAGUUAAC UUUAUGGCUGCAUU
STMN2_ intron1	-	CTTT	869	GTTAATGGAAGTTAA ACTTTATGGCTGCAT	287 5	GUUAAUGGAAGUUA CUUUAUGGCUGCAU
STMN2_ intron1	-	TTT A	870	CTGTGAGCAGCTTTGT TAATGGAAGTTAAA	287 6	CUGUGAGCAGCUUUGU UAAUGGAAGUUA
STMN2_ intron1	-	GTT T	871	ACTGTGAGCAGCTTTG TTAATGGAAGTTAA	287 7	ACUGUGAGCAGCUUUG UUAUUGGAAGUUA
STMN2_ intron1	-	ATT A	872	TAATAGGTTTACTGTG AGCAGCTTTGTAA	287 8	UAAUAGGUUACUGUG AGCAGCUUUGUUA
STMN2_ intron1	-	ATT A	873	TTATAATAGGTTTACT GTGAGCAGCTTTGT	287 9	UUUAUAGGUUUACU GUGAGCAGCUUUGU
STMN2_ intron1	-	GTT G	874	CTCCTCACTAGGAAGC CCAAACTGGGAAAC	288 0	CUCCUCACUAGGAAGC CCAAACUGGGAAAC
STMN2_ intron1	-	GTT A	875	GGTTGCTCCTCACTAG GAAGCCCAAACCTGG	288 1	GGUUGCUCCUCACUAG GAAGCCCAAACUGG
STMN2_ intron1	-	TTTC	876	GTGTGAGTTAGGTTGC TCCTCACTAGGAAG	288 2	GUGUGAGUUAGGUUGC UCCUCACUAGGAAG
STMN2_ intron1	-	GTT T	877	CGTGTGAGTTAGGTTG CTCCTCACTAGGAA	288 3	CGUGUGAGUUAGGUUG CUCCUCACUAGGAA
STMN2_ intron1	-	GTT G	878	TTTCGTGTGAGTTAGG TTGCTCCTCACTAG	288 4	UUUCGUGUGAGUUAGG UUGCUCUCACUAG
STMN2_ intron1	-	GTT G	879	GGGTTGTTTCGTGTGA GTTAGGTTGCTCCT	288 5	GGGUUGUUUCGUGUGA GUUAGGUUGCUCU

STMN2_ intron1	-	ATT A	880	TAAGTTGGGGTTGTTT CGTGTGAGTTAGGT	288 6	UAAGUUGGGGUUGUUU CGUGUGAGUUAGGU
STMN2_ intron1	-	TTT G	881	TAACAGTCAATATATT ATAAGTTGGGGTTG	288 7	UAAACAGUCAAUUAUUAU AUAAGUUGGGGUUG
STMN2_ intron1	-	TTTT	882	GTAACAGTCAATATAT TATAAGTTGGGGTT	288 8	GUAACAGUCAAUUAUUAU UAUAAGUUGGGGUU
STMN2_ intron1	-	GTT T	883	TGTAACAGTCAATATA TTATAAGTTGGGGT	288 9	UGUAACAGUCAAUUAUA UUAUAAGUUGGGGU
STMN2_ intron1	-	TTTC	884	TGGTCTCAGTTTTGTA ACAGTCAATATATT	289 0	UGGUCUCAGUUUUGUA ACAGUCAAUUAUUAU
STMN2_ intron1	-	TTTT	885	CTGGTCTCAGTTTTGT AACAGTCAATATAT	289 1	CUGGUCUCAGUUUUGU AACAGUCAAUUAUUAU
STMN2_ intron1	-	ATT T	886	TCTGGTCTCAGTTTTG TAACAGTCAATATA	289 2	UCUGGUCUCAGUUUUG UAAACAGUCAAUUAUA
STMN2_ intron1	-	CTT G	887	ATGGGATTTTCTGGTC TCAGTTTTGTAACA	289 3	AUGGGAUUUCUGGUC UCAGUUUUGUAACA
STMN2_ intron1	-	CTT C	888	CCGAGAGTCTGGA TGATAACAGTACCAT	289 4	CCGAGAGUCUGGAAAU GAUAACAGUACCAU
STMN2_ intron1	-	GTT C	889	TTCCCGAGAGTCTGGA AATGATAACAGTAC	289 5	UUCCCGAGAGUCUGGA AAUGAUAAACAGUAC
STMN2_ intron1	-	ATT A	890	ATGTTCTTCCCGAGAG TCTGGAAATGATAA	289 6	AUGUUCUCCCCGAGAG UCUGGAAAUGAUAA
STMN2_ intron1	-	GTT C	891	CCAGGGAGGCTGCAA TAAGTCTATCCTAAA	289 7	CCAGGGAGGCUGCAAU AAGUCUAUCCUAAA
STMN2_ intron1	-	GTT C	892	TGAAGCAGAGTTCCC AGGGAGGCTGCAATA	289 8	UGAAGCAGAGUCCCCA GGGAGGCUGCAAUA
STMN2_ intron1	-	ATT A	893	TGTTCTGAAGCAGAGT TCCCAGGGAGGCTG	289 9	UGUUCUGAAGCAGAGU UCCCAGGGAGGCUG
STMN2_ intron1	-	ATT A	894	ATAAAAATAATTATGT TCTGAAGCAGAGTT	290 0	AUAAAAAUAAUUAUGU UCUGAAGCAGAGUU
STMN2_ intron1	-	GTT A	895	ATGGAAGTTAACTTT ATGGCTGCATTTCA	290 1	AUGGAAGUAAACUUU AUGGCUGCAUUUCA
STMN2_ intron1	-	GTT A	896	AACTTTATGGCTGCAT TTCATAAGGAAAAA	290 2	AACUUUAUGGCUGCAU UUCAUAAGGAAAAA
STMN2_ intron1	-	CTTT	897	ATGGCTGCATTTTCATA AGGAAAAAAAAACTT	290 3	AUGGCUGCAUUUCAUA AGGAAAAAAAAACUU
STMN2_ intron1	-	TTT A	898	TGGCTGCATTTTCATA GGAAAAAAAAACTTC	290 4	UGGCUGCAUUUCAUAA GGAAAAAAAAACUUC
STMN2_ intron1	-	ATT A	899	TTCCAGAAGAATAAC TGCTAAATGGGCACT	290 5	UUCCAGAAGAAUAAACU GCUAAAUGGGCACU
STMN2_ intron1	-	GTT A	900	ATGTGCGAACTCCAAC ATCCAAAATACAAT	290 6	AUGUGCGAACUCCAAC AUCCAAAUAACAAU
STMN2_ intron1	-	CTT G	901	TACTAATGGTTAATGT GCGAACTCCAACAT	290 7	UACUAAUGGUUAAUGU GCGAACUCCAACAU

STMN2_ intron1	-	ATT G	902	GGTACTTGTACTAATG GTTAATGTGCGAAC	290 8	GGUACUUGUACUAAUG GUUAAUGUGCGAAC
STMN2_ intron1	-	GTT A	903	TATTGGGTTACTTGTAC TAATGGTTAATGTG	290 9	UAUUGGGUACUUGUAC UAAUGGUUAAUGUG
STMN2_ intron1	-	ATT G	904	TTATATTGGGTACTTG TACTAATGGTTAAT	291 0	UUAUUAUUGGGUACUUG UACUAAUGGUUAAU
STMN2_ intron1	-	ATT A	905	TCCTGATGATCTATTG TTATATTGGGTACT	291 1	UCCUGAUGAUCUAAUG UUAUUAUUGGGUACU
STMN2_ intron1	-	TTT A	906	TTATCCTGATGATCTA TTGTTATATTGGGT	291 2	UUAUCCUGAUGAUCUA UUGUUAUUAUUGGGU
STMN2_ intron1	-	ATT T	907	ATTATCCTGATGATCT ATTGTTATATTGGG	291 3	AUUAUCCUGAUGAUCU AUUGUUAUUAUUGGG
STMN2_ intron1	-	TTT A	908	TCCTGATATAAAAGAC ATACAATAAAAGAT	291 4	UCCUGAUUAAAAGACA UACAACUAAAAGAU
STMN2_ intron1	-	CTTT	909	ATCCTGATATAAAGA CATACAATAAAGA	291 5	AUCCUGAUUAAAAGAC AUACAACUAAAAGA
STMN2_ intron1	-	ATT C	910	TCTTTATCCTGATATA AAGACATACAACTA	291 6	UCUUUAUCCUGAUUA AAGACAUACAACUA
STMN2_ intron1	-	TTTC	911	ACTCAATTCTCTTTAT CCTGATATAAAAGAC	291 7	ACUCAAUUCUCUUUAU CCUGAUUAAAAGAC
STMN2_ intron1	-	GTT G	912	GAAATAAAAAGTAAC TCTGCATTAATAAAA	291 8	GAAAUAAAAGUAAACU CUGCAUUAUAAAA
STMN2_ intron1	-	ATT T	913	CACTCAATTCTCTTTA TCCTGATATAAAGA	291 9	CACUCAAUUCUCUUUA UCCUGAUUAAAAGA
STMN2_ intron1	-	GTT T	914	AGATAAATTTCACTCA ATTCTCTTTATCCT	292 0	AGAUAAAUUUCACUCA AUUCUCUUUAUCCU
STMN2_ intron1	-	TTT G	915	TGGGACTAGGTTTAG ATAAATTTCACTCAA	292 1	UGGGACUAGGUUUAGA UAAAUUUCACUCAA
STMN2_ intron1	-	ATT T	916	GTGGGACTAGGTTTA GATAAATTTCACTCA	292 2	GUGGGACUAGGUUUAG AUAAAUUUCACUCA
STMN2_ intron1	-	CTT G	917	TAAAAGTATTTGTGGG ACTAGGTTTAGATA	292 3	UAAAAGUAUUUGUGGG ACUAGGUUUAGUA
STMN2_ intron1	-	TTT A	918	ACATGCTCTCTTGTA AAGTATTTGTGGGA	292 4	ACAUGCUCUCUUGUAA AAGUAUUUGUGGGA
STMN2_ intron1	-	CTTT	919	AACATGCTCTCTTGTA AAAGTATTTGTGGG	292 5	AACAUGCUCUCUUGUA AAAGUAUUUGUGGG
STMN2_ intron1	-	TTT A	920	CACTTTAACATGCTCT CTTGTAAGTATT	292 6	CACUUAAACAUGCUCU CUUGUAAAAGUAUU
STMN2_ intron1	-	ATT T	921	ACACTTTAACATGCTC TCTTGTAAGTAT	292 7	ACACUUAAACAUGCUC UCUUGUAAAAGUAU
STMN2_ intron1	-	TTT A	922	ATTTACACTTTAACAT GCTCTCTTGTAAGT	292 8	AUUUACACUUUAAACAU GCUCUCUUGUAAAA
STMN2_ intron1	-	ATT T	923	AATTTACACTTTAACA TGCTCTCTTGTAAGT	292 9	AAUUUACACUUUAAACA UGCUCUCUUGUAAA

STMN2_ intron1	-	CTT C	924	CAAAGACAGAGTAGA ATGCTAATAAAAAATT	293 0	CAAAGACAGAGUAGAA UGC UAAUAAAAAUU
STMN2_ intron1	-	TTTC	925	ATAAGGAAAAAAAAAC TTCCAAAGACAGAGT	293 1	AUAAGGAAAAAAAAACU UCCAAAGACAGAGU
STMN2_ intron1	-	ATT T	926	CATAAGGAAAAAAAAA CTTCCAAAGACAGAG	293 2	CAUAAGGAAAAAAAAAC UUCCAAAGACAGAG
STMN2_ intron1	-	TTT A	927	GATAAATTTCACTCAA TTCTCTTTATCCTG	293 3	GAUAAAUUUCACUCAA UUCUCUUUAUCCUG
STMN2_ intron1	-	CTT G	928	CAGGCGTTGCTTTACA ATCTTTGTAAAAAA	293 4	CAGGCGUUGCUUUACA AUCUUUGUAAAAAA
STMN2_ intron1	-	TTT G	929	TTGGAAATAAAAAAGT AACTCTGCATTAATA	293 5	UUGGAAAUAAAAAGUA ACUCUGCAUUAUA
STMN2_ intron1	-	TTTT	930	TGTTGGAAATAAAAA GTAACCTCTGCATTAA	293 6	UGUUGGAAAUAAAAAG UAAUCUCUGCAUUA
STMN2_ intron1	-	TTTT	931	GAACATTTTTTAGTCT TCTATGCTTGCTG	293 7	GAACAUUUUUUAGUCU UCUAUGCUUGCCUG
STMN2_ intron1	-	CTTT	932	TGAACATTTTTTAGTC TTCTATGCTTGCTT	293 8	UGAACAUUUUUUAGUC UUCUAUGCUUGCCU
STMN2_ intron1	-	TTTC	933	TTTTGAACATTTTTTA GTCTTCTATGCTTG	293 9	UUUUGAACAUUUUUUA GUCUUCUAUGCUUG
STMN2_ intron1	-	TTTT	934	CTTTTGAACATTTTTT AGTCTTCTATGCTT	294 0	CUUUUGAACAUUUUUU AGUCUUCUAUGCUU
STMN2_ intron1	-	TTTT	935	TCTTTTGAACATTTTT TAGTCTTCTATGCT	294 1	UCUUUUGAACAUUUUU UAGUCUUCUAUGCU
STMN2_ intron1	-	ATT T	936	TTCTTTTGAACATTTT TtagTCTTCTATGC	294 2	UUCUUUUGAACAUUUU UUAGUCUUCUAUGC
STMN2_ intron1	-	TTT A	937	ATTTTTCTTTTGAACA TTTTTTAGTCTTCT	294 3	AUUUUUCUUUUGAACA UUUUUUAGUCUUCU
STMN2_ intron1	-	ATT T	938	AATTTTTCTTTTGAAC ATTTTTTAGTCTTC	294 4	AAUUUUUCUUUUGAAC AUUUUUUAGUCUUC
STMN2_ intron1	-	TTTC	939	TAAAAATGACAAGGT CCCATATAGATAGAT	294 5	UAAAAUGACAAGGUC CCAUAUAGAUAGAU
STMN2_ intron1	-	TTTT	940	CTAAAAATGACAAGG TCCCATATAGATAGA	294 6	CUAAAAUGACAAGGU CCCAUAUAGAUAGA
STMN2_ intron1	-	GTT T	941	TCTAAAAATGACAAG GTCCCATATAGATAG	294 7	UCUAAAAUGACAAGG UCCCAUAUAGAUAG
STMN2_ intron1	-	ATT C	942	AAAAGGATGAAGCAG GTGAATGTTTTCTAA	294 8	AAAAGGAUGAAGCAGG UGAAUGUUUUCUAA
STMN2_ intron1	-	ATT A	943	TATGAAGATTCAAAA GGATGAAGCAGGTGA	294 9	UAUGAAGAUUCAAAAG GAUGAAGCAGGUGA
STMN2_ intron1	-	CTT G	944	TATAGTATGCCCATCT CAGAGGGATTATAT	295 0	UAUAGUAUGCCCAUCU CAGAGGGAUUAUAU
STMN2_ intron1	-	TTT A	945	AATAAGACAACCTTGT ATAGTATGCCCATCT	295 1	AAUAAGACAACUUGUA UAGUAUGCCCAUCU

STMN2_ intron1	-	CTTT	946	AAATAAGACAACCTTG TATAGTATGCCCATC	295 2	AAAUAAAGACAACUUGU AUAGUAUGCCCAUC
STMN2_ intron1	-	TTT A	947	CCAATCTTTAAATAAG ACAACTTGTATAGT	295 3	CCAAUCUUUAAAUAAG ACAACUUGUAUAGU
STMN2_ intron1	-	ATT T	948	ACCAATCTTTAAATAA GACAACCTTGTATAG	295 4	ACCAAUCUUUAAAUA GACAACUUGUAUAG
STMN2_ intron1	-	CTT A	949	AATTTACCAATCTTTA AATAAGACAACCTTG	295 5	AAUUUACCAAUCUUUA AAUAAGACAACUUG
STMN2_ intron1	-	TTT G	950	AGCTTAAATTTACCAA TCTTTAAATAAGAC	295 6	AGCUUAAAUUUACCAA UCUUUAAAUAAGAC
STMN2_ intron1	-	ATT T	951	GAGCTTAAATTTACCA ATCTTTAAATAAGA	295 7	GAGCUUAAAUUUACCA AUCUUUAAAUAAGA
STMN2_ intron1	-	ATT A	952	TTTGAGCTTAAATTTA CCAATCTTTAAATA	295 8	UUUGAGCUUAAAUUUA CCAAUCUUUAAAUA
STMN2_ intron1	-	CTT G	953	CCACTGAATAAATTAT TTGAGCTTAAATTT	295 9	CCACUGAAUAAAUAU UUGAGCUUAAAUUU
STMN2_ intron1	-	GTT C	954	CGAGTCTGCCTCTGAG GCTTGCCACTGAAT	296 0	CGAGUCUGCCUCUGAG GCUUGCCACUGAAU
STMN2_ intron1	-	ATT A	955	GACCTGTGTTCCGAGT CTGCCTCTGAGGCT	296 1	GACCUGUGUCCGAGU CUGCCUCUGAGGCU
STMN2_ intron1	-	GTT A	956	TAATATATATATAATA TATATTAGACCTGT	296 2	UAAUAUAUAUAUAUA UAUAUUAGACCUGU
STMN2_ intron1	-	ATT A	957	TATGTTATAATATATA TATAATATATATTA	296 3	UAUGUUAAUAUAUAUA UAUAAUAUAUAUA
STMN2_ intron1	-	TTT G	958	AACATTTTTTAGTCTT CTATGCTTGCCCTGC	296 4	AACAUUUUUAGUCUU CUAUGCUUGCCUGC
STMN2_ intron1	-	ATT T	959	TTAGTCTTCTATGCT TGCCTGCTCCTTTT	296 5	UUUAGUCUUCUAUGCU UGCCUGCUCCUUUU
STMN2_ intron1	-	TTTT	960	TTAGTCTTCTATGCTT GCCTGCTCCTTTTA	296 6	UUAGUCUUCUAUGCUU GCCUGCUCCUUUUA
STMN2_ intron1	-	TTTT	961	TAGTCTTCTATGCTTG CCTGCTCCTTTTAA	296 7	UAGUCUUCUAUGCUUG CCUGCUCCUUUUA
STMN2_ intron1	-	ATT T	962	TTGTTGGAAATAAAA AGTAACTCTGCATTA	296 8	UUGUUGGAAAUAAAAA GUAACUCUGCAUUA
STMN2_ intron1	-	CTT A	963	AATAATAACAATAGA TATTTTTGTTGGAAA	296 9	AAUAAUAACAAUAGAU AUUUUUGUUGGAAA
STMN2_ intron1	-	TTTC	964	TCAGATAAAGCTGTA AGACTTAAATAATAA	297 0	UCAGAUAAAGCUGUAA GACUAAAUAUAUA
STMN2_ intron1	-	ATT T	965	CTCAGATAAAGCTGT AAGACTTAAATAATA	297 1	CUCAGAUAAAGCUGUA AGACUAAAUAUAUA
STMN2_ intron1	-	ATT G	966	GAATTTCTCAGATAAA GCTGTAAGACTTAA	297 2	GAAUUUCUCAGAUAAA GCUGUAAGACUUA
STMN2_ intron1	-	ATT A	967	TGAGAAGGGTGCTAA TTGGAATTTCTCAGA	297 3	UGAGAAGGGUGCUAAU UGGAAUUUCUCAGA

STMN2_ intron1	-	TTT A	968	TTATGAGAAGGGTGC TAATTGGAATTTCTC	297 4	UUAUGAGAAGGGUGCU AAUUGGAAUUCUC
STMN2_ intron1	-	ATT T	969	ATTATGAGAAGGGTG CTAATTGGAATTTCT	297 5	AUUAUGAGAAGGGUGC UAAUUGGAAUUCU
STMN2_ intron1	-	TTT G	970	AATATTTATTATGAGA AGGGTGCTAATTGG	297 6	AAUAUUUAUUAUGAGA AGGGUGCUAAUUGG
STMN2_ intron1	-	GTT T	971	GAATATTTATTATGAG AAGGGTGCTAATTG	297 7	GAAUAUUUAUUAUGAG AAGGGUGCUAAUUG
STMN2_ intron1	-	TTTC	972	ATGTGTTTGAATATTT ATTATGAGAAGGGT	297 8	AUGUGUUUGAAUUAUU AUUAUGAGAAGGGU
STMN2_ intron1	-	TTTT	973	CATGTGTTTGAATATT TATTATGAGAAGGG	297 9	CAUGUGUUUGAAUUAU UAUUAUGAGAAGGG
STMN2_ intron1	-	TTTT	974	TCATGTGTTTGAATAT TTATTATGAGAAGG	298 0	UCAUGUGUUUGAAUAU UUAUUAUGAGAAGG
STMN2_ intron1	-	TTTT	975	GTTGGAAATAAAAAG TAACTCTGCATTAAT	298 1	GUUGGAAAUAAAAAGU AACUCUGCAUUAUU
STMN2_ intron1	-	ATT T	976	TTCATGTGTTTGAATA TTTATTATGAGAAG	298 2	UUCAUGUGUUUGAAUA UUUAUUAUGAGAAG
STMN2_ intron1	-	CTTT	977	GGTAATTTTTCATGTG TTTGAATATTTATT	298 3	GGUAAUUUUUCAUGUG UUUGAAUUAUUUU
STMN2_ intron1	-	ATT A	978	AAAGACTAGAACAAC TTTGGTAATTTTCA	298 4	AAAGACUAGAACAACU UUGGUAAUUUUUCA
STMN2_ intron1	-	TTT A	979	AAGTGACAAGAGTGC AGGATCATGTAATAT	298 5	AAGUGACAAGAGUGCA GGAUCAUGUAAUAU
STMN2_ intron1	-	TTTT	980	AAAGTGACAAGAGTG CAGGATCATGTAATA	298 6	AAAGUGACAAGAGUGC AGGAUCAUGUAAUA
STMN2_ intron1	-	TTTT	981	TAAAGTGACAAGAGT GCAGGATCATGTAAT	298 7	UAAAGUGACAAGAGUG CAGGAUCAUGUAAU
STMN2_ intron1	-	ATT T	982	TTAAAGTGACAAGAG TGCAGGATCATGTAA	298 8	UUAAGUGACAAGAGU GCAGGAUCAUGUAA
STMN2_ intron1	-	TTT A	983	AAAAACTATATAAGA AAAAAATCATCAGAA	298 9	AAAAACUAUAUAAGAA AAAAAUCAUCAGAA
STMN2_ intron1	-	TTTT	984	AAAAAACTATATAAG AAAAAAATCATCAGA	299 0	AAAAAACUAUAUAAGA AAAAAAUCAUCAGA
STMN2_ intron1	-	CTTT	985	TAAAAAACTATATAA GAAAAAAATCATCAG	299 1	UAAAAAACUAUAUAAG AAAAAAUCAUCAG
STMN2_ intron1	-	CTT G	986	CCTGCTCCTTTTAAAA AACTATATAAGAAA	299 2	CCUGCUCCUUUUAAAA AACUAUAUAAGAAA
STMN2_ intron1	-	CTT C	987	TATGCTTGCTGCTCC TTTTAAAAAACTAT	299 3	UAUGCUUGCCUGCUCC UUUUAAAAAACUAU
STMN2_ intron1	-	TTT A	988	GTCTTCTATGCTTGCC TGCTCCTTTTAAAA	299 4	GUCUUCUAUGCUUGCC UGCUCUUUUAAAA
STMN2_ intron1	-	TTTT	989	AGTCTTCTATGCTTGC CTGCTCCTTTTAAA	299 5	AGUCUUCUAUGCUUGC CUGCUCCUUUUAAA

STMN2_ intron1	-	TTT G	990	GTAATTTTTCATGTGT TTGAATATTTATTA	299 6	GUAAUUUUUCAUGUGU UUGAAUAUUUAUUA
STMN2_ intron1	+	CTT G	991	GTGGATTTAGTCTTTT GCAGAAAAAAGAT	299 7	GUGGAUUUAGUCUUUU GCAGAAAAAAGAU
STMN2_ intron1	-	GTT C	992	GGAAGTAAAATATTTT GTAAAGATTACCAT	299 8	GGAAGUAAAAUAUUUU GUAAAGAUUACCAU
STMN2_ intron1	-	TTTT	993	GTAAAGATTACCATA GATTTAAAAATGTTA	299 9	GUAAAGAUUACCAUAG AUUUAAAAAUGUUA
STMN2_ intron1	-	TTT A	994	CCTTTTGTGGGGGAA AGGGATGAGGGCAA	300 0	CCUUUUUGUGGGGGAA AGGGAUGAGGGCAA
STMN2_ intron1	-	ATT T	995	ACCTTTTGTGGGGGA AAGGGATGAGGGCA	300 1	ACCUUUUUGUGGGGGA AAGGGAUGAGGGCA
STMN2_ intron1	-	CTT A	996	AAATGAACAACCTGGA GACAAATTTACCTTT	300 2	AAAUGAACAACUGGAG ACAAAUUUACCUUU
STMN2_ intron1	-	TTT A	997	TAACCTAAAATGAAC AACTGGAGACAAATT	300 3	UAACUUAAAAUGAACA ACUGGAGACAAAUU
STMN2_ intron1	-	CTTT	998	ATAACTTAAAATGAA CAACTGGAGACAAAT	300 4	AUAACUUAAAAUGAAC AACUGGAGACAAAU
STMN2_ intron1	-	TTT G	999	CTTTATAACTTAAAAT GAACAACTGGAGAC	300 5	CUUUAUAACUUAAAAU GAACAACUGGAGAC
STMN2_ intron1	-	ATT T	100 0	GCTTTATAACTTAAAA TGAACAACCTGGAGA	300 6	GCUUUAUAACUUAAAA UGAACAACUGGAGA
STMN2_ intron1	-	CTT A	100 1	GCCACATGAACATAC ATAATCCTGGCAGGA	300 7	GCCACAUGAACAUACA UAAUCCUGGCAGGA
STMN2_ intron1	-	CTT G	100 2	CACATGTATCTTAGCC ACATGAACATACAT	300 8	CACAUGUAUCUUAGCC ACAUGAACAUACAU
STMN2_ intron1	-	CTT A	100 3	GCAAGCACTTGCACAT GTATCTTAGCCACA	300 9	GCAAGCACUUGCACAU GUAUCUUAGCCACA
STMN2_ intron1	-	GTT G	100 4	GCACACAAACCCTGCT CTTAGCAAGCACTT	301 0	GCACACAAACCUGCU CUUAGCAAGCACUU
STMN2_ intron1	-	TTTC	100 5	CAGCAATCGTTGGCAC ACAAACCCTGCTCT	301 1	CAGCAAUCGUUGGCAC ACAAACCUGCUCU
STMN2_ intron1	-	TTTT	100 6	CCAGCAATCGTTGGCA CACAAACCCTGCTC	301 2	CCAGCAAUCGUUGGCA CACAAACCUGCUC
STMN2_ intron1	-	ATT T	100 7	TCCAGCAATCGTTGGC ACACAAACCCTGCT	301 3	UCCAGCAAUCGUUGGC ACACAAACCUGCU
STMN2_ intron1	-	TTT G	100 8	CAGAGAATTTCCAGC AATCGTTGGCACAC	301 4	CAGAGAAUUUCCAGC AAUCGUUGGCACAC
STMN2_ intron1	-	CTTT	100 9	GCAGAGAATTTCCA GCAATCGTTGGCACA	301 5	GCAGAGAAUUUCCAG CAAUCGUUGGCACA
STMN2_ intron1	-	ATT C	101 0	TTTGCAGAGAATTTTC CAGCAATCGTTGGC	301 6	UUUGCAGAGAAUUUUC CAGCAAUCGUUGGC
STMN2_ intron1	-	ATT G	101 1	CAGCCACAAACAATT CTTGCAGAGAATTT	301 7	CAGCCACAAACA AUUC UUUGCAGAGAAUUU

STMN2_ intron1	-	ATT C	101 2	TCACCCATTGCAGCCA CAAACAATTCTTTG	301 8	UCACCCAUUGCAGCCA CAAACAAUUCUUUG
STMN2_ intron1	-	ATT A	101 3	TATATGTGTATTCTCA CCCATTGCAGCCAC	301 9	UAUAUGUGUAUUCUCA CCCAUUGCAGCCAC
STMN2_ intron1	-	GTT G	101 4	AAGATCATCTCAATTA TATATGTGTATTCT	302 0	AAGAUCAUCUCAUUA UAUAUGUGUAUUCU
STMN2_ intron1	-	CTT A	101 5	TGTTGAAGATCATCTC AATTATATATGTGT	302 1	UGUUGAAGAUAUCUC AAUUAUAUUGUGU
STMN2_ intron1	-	TTT A	101 6	TAGATATAACCTTATG TTGAAGATCATCTC	302 2	UAGAUUAACCUUAUG UUGAAGAUAUCUC
STMN2_ intron1	-	ATT T	101 7	ATAGATATAACCTTAT GTTGAAGATCATCT	302 3	AUAGAUUAACCUUAU GUUGAAGAUAUCU
STMN2_ intron1	-	TTT A	101 8	TATATTTATAGATATA ACCTTATGTTGAAG	302 4	UAUAUUUAUAGAUUA ACCUUAUGUUGAAG
STMN2_ intron1	-	ATT T	101 9	ATATATTTATAGATAT AACCTTATGTTGAA	302 5	AUAUAUUUAUAGAUU AACCUUAUGUUGAA
STMN2_ intron1	-	TTT G	102 0	TGCATAAACTATATTT ATATATTTATAGAT	302 6	UGCAUAAAACUAUAUU AUAUAUUUAUAGAU
STMN2_ intron1	-	CTTT	102 1	TTGTGGGGGAAAGGG ATGAGGGCAATTAGG	302 7	UUGUGGGGGAAAGGGA UGAGGGCAAUUAGG
STMN2_ intron1	-	TTTT	102 2	GTGCATAAACTATATT TATATATTTATAGA	302 8	GUGCAUAAAACUAUAU UAUAUAUUUAUAGA
STMN2_ intron1	-	TTTT	102 3	TGTGGGGGAAAGGGA TGAGGGCAATTAGGA	302 9	UGUGGGGGAAAGGGAU GAGGGCAAUUAGGA
STMN2_ intron1	-	TTT G	102 4	TGGGGGAAAGGGATG AGGGCAATTAGGAGG	303 0	UGGGGGAAAGGGAUGA GGGCAAUUAGGAGG
STMN2_ intron1	-	GTT G	102 5	TGGACTGCGGGGCTG AAAAAAGAGGTTCCA	303 1	UGGACUGCGGGGCUGA AAAAAGAGGUUCCA
STMN2_ intron1	-	CTT G	102 6	GCTGGGAGGGGCTCG GTGCTGGGGCTGAGA	303 2	GCUGGGAGGGGCUCGG UGCUGGGGCUGAGA
STMN2_ intron1	-	TTTC	102 7	TGCAGAGCCACCCGCT TGGCTGGGAGGGGC	303 3	UGCAGAGCCACCCGCU UGGCUGGGAGGGGC
STMN2_ intron1	-	TTTT	102 8	CTGCAGAGCCACCCG CTTGGCTGGGAGGGG	303 4	CUGCAGAGCCACCCGC UUGGCUGGGAGGGG
STMN2_ intron1	-	CTTT	102 9	TCTGCAGAGCCACCCG CTTGGCTGGGAGGG	303 5	UCUGCAGAGCCACCCG CUUGGCUGGGAGGG
STMN2_ intron1	-	TTT G	103 0	TGTGGCCGGGCGGGG CTCGAGCCAGCTTTT	303 6	UGUGGCCGGGCGGGGC UCGAGCCAGCUUUU
STMN2_ intron1	-	CTTT	103 1	GTGTGGCCGGGCGGG GCTCGAGCCAGCTTT	303 7	GUGUGGCCGGGCGGGG CUCGAGCCAGCUUU
STMN2_ intron1	-	CTT G	103 2	GGCTGGGGGAAAAAA AGCCCCGAGCTCCGC	303 8	GGCUGGGGGAAAAAAA GCCCCGAGCUCCGC
STMN2_ intron1	-	ATT C	103 3	TGGAATAATCATAGAG AACAGAGGGTGGGCG	303 9	UGGAAAAUCAUAGAGA ACAGAGGGUGGGCG

STMN2_ intron1	-	CTT A	103 4	GAGAAGCCCCTCGCG GGGTCTCCATTCTGG	304 0	GAGAAGCCCCUCGCGG GGUCUCCAUUCUGG
STMN2_ intron1	-	ATT G	103 5	TGGAAAGCGGGGGTA GCTCAGGACACTGCG	304 1	UGGAAAGCGGGGGUAG CUCAGGACACUGCG
STMN2_ intron1	-	TTTC	103 6	TGGACGTGCGAGTGA ACTGCGAATTGTGGA	304 2	UGGACGUGCGAGUGAA CUGCGAAUUGUGGA
STMN2_ intron1	-	CTTT	103 7	CTGGACGTGCGAGTG AACTGCGAATTGTGG	304 3	CUGGACGUGCGAGUGA ACUGCGAAUUGUGG
STMN2_ intron1	-	ATT C	103 8	TCAGAACCTTTCTGGA CGTGCGAGTGA	304 4	UCAGAACCUUUCUGGA CGUGCGAGUGAACU
STMN2_ intron1	-	TTTC	103 9	TGAGGGGTGCAGAAA GCGAGGCGAGATCGC	304 5	UGAGGGGUGCAGAAAG CGAGGCGAGAU
STMN2_ intron1	-	CTTT	104 0	CTGAGGGGTGCAGAA AGCGAGGCGAGATCG	304 6	CUGAGGGGUGCAGAAA GCGAGGCGAGAU
STMN2_ intron1	-	TTT G	104 1	CAGCCACTAGCCTGCA GCGGAAACCTTTCT	304 7	CAGCCACUAGCCUGCA GCGGAAACCUUUCU
STMN2_ intron1	-	GTT T	104 2	GCAGCCACTAGCCTGC AGCGGAAACCTTTC	304 8	GCAGCCACUAGCCUGC AGCGGAAACCUUUC
STMN2_ intron1	-	TTT G	104 3	AAATGATAATAATAC TGATGATGACGATGA	304 9	AAAUGAUAAUAAUACU GAUGAUGACGAUGA
STMN2_ intron1	-	ATT T	104 4	GAAATGATAATAATA CTGATGATGACGATG	305 0	GAAAUGAUAAUAAUAC UGAUGAUGACGAUG
STMN2_ intron1	-	ATT A	104 5	AATAATAACAACGAT TTGAAATGATAATAA	305 1	AAUAAUAAACAACGAUU UGAAAUGAUAAUAA
STMN2_ intron1	-	TTT G	104 6	AACAAATGAGAACAA ACAAGGCTACTGAAT	305 2	AACAAAUGAGAACAAA CAAGGCUACUGAAU
STMN2_ intron1	-	TTTT	104 7	GAACAAATGAGAACAA AACAAGGCTACTGAA	305 3	GAACAAAUGAGAACAA ACAAGGCUACUGAA
STMN2_ intron1	-	CTTT	104 8	TGAACAAATGAGAAC AAACAAGGCTACTGA	305 4	UGAACAAAUGAGAACAA AACAAGGCUACUGA
STMN2_ intron1	-	CTT A	104 9	ACCAAGAGCAATCCA CGTCCCTTTTGAACA	305 5	ACCAAGAGCAAUCCAC GUCCCUUUGAACA
STMN2_ intron1	-	GTT A	105 0	ATCCTTAACCAAGAGC AATCCACGTCCCTT	305 6	AUCCUUAACCAAGAGC AAUCCACGUCCCUU
STMN2_ intron1	-	ATT A	105 1	GGAGGAAGCAAAGCG AACGCAACAAGGGTT	305 7	GGAGGAAGCAAAGCGA ACGCAACAAGGGUU
STMN2_ intron1	-	TTTT	105 2	GTGGGGGAAAGGGAT GAGGGCAATTAGGAG	305 8	GUGGGGGAAAGGGAUG AGGGCAAUAGGAG
STMN2_ intron1	-	ATT T	105 3	TGTGCATAAACTATAT TTATATATTTATAG	305 9	UGUGCAUAAACUAUUAU UUAUAUAUUUAUAG
STMN2_ intron1	-	CTT A	105 4	AAATTTTGTGCATAAA CTATATTTATATAT	306 0	AAUUUUUGUGCAUAAA CUAUUUUAUAUAU
STMN2_ intron1	-	TTTC	105 5	AGGGGAAAAAACTTA AAATTTTGTGCATAA	306 1	AGGGGAAAAAAACUAAA AAUUUUUGUGCAUAA

STMN2_ intron1	-	ATT A	105 6	ATTTCAAAATCTATTA TTTTAATACTGCAG	306 2	AUUUCAAAAUCUAUUA UUUUAAUACUGCAG
STMN2_ intron1	-	ATT G	105 7	GAATTAATTTCAAAAT CTATTATTTTAATA	306 3	GAAUUAUUUCAAUUA CUAUUAUUUUAAUA
STMN2_ intron1	-	TTT G	105 8	AAATTGGAATTAATTT CAAAATCTATTATT	306 4	AAAUUGGAAUUAUUU CAAAAUCUAUUAAU
STMN2_ intron1	-	CTTT	105 9	GAAATTGGAATTAATT TCAAAATCTATTAT	306 5	GAAAUUGGAAUUAUU UCAAAAUCUAUUUAU
STMN2_ intron1	-	ATT A	106 0	TCTTTGAAATTGGAAT TAATTTCAAAATCT	306 6	UCUUUGAAAUUGGAAU UAAUUUCAAAAUCU
STMN2_ intron1	-	ATT A	106 1	ATTATCTTTGAAATTG GAATTAATTTCAAA	306 7	AUUAUCUUUGAAAUG GAAUUAUUUCAAA
STMN2_ intron1	-	TTT A	106 2	ATGAATCAGGAAAAA AGCACTCGCCCTGAT	306 8	AUGAAUCAGGAAAAA GCACUCGCCCUGAU
STMN2_ intron1	-	GTT T	106 3	AATGAATCAGGAAAA AAGCACTCGCCCTGA	306 9	AAUGAAUCAGGAAAA AGCACUCGCCCUGA
STMN2_ intron1	-	ATT G	106 4	TTTAATGAATCAGGA AAAAAGCACTCGCCC	307 0	UUUAAUGAAUCAGGAA AAAAGCACUCGCCC
STMN2_ intron1	-	CTT A	106 5	CAATCATGCTGAATAC ATAATTGTTTAATG	307 1	CAAUCAUGCUGAAUAC AUAAUUGUUUAAUG
STMN2_ intron1	-	ATT A	106 6	TATGCACCTCTTACAA TCATGCTGAATACA	307 2	UAUGCACCUCUACAA UCAUGCUGAAUACA
STMN2_ intron1	-	ATT A	106 7	GAAAAGATAATGGGG AATATTATATGCACC	307 3	GAAAAGAUAAUGGGGA AUUUUAUUAUGCACC
STMN2_ intron1	-	CTT C	106 8	ATTAGAAAAGATAAT GGGGAATATTATATG	307 4	AUUAGAAAAGAUAAUG GGGAUUAUUUAUUG
STMN2_ intron1	-	ATT C	106 9	AGAAGGTGCCCACTTC ATTAGAAAAGATAA	307 5	AGAAGGUGCCCAUUC AUUAGAAAAGAUAA
STMN2_ intron1	-	CTT A	107 0	TATATCCATTGAGAAG GTGCCCACTTCATT	307 6	UAUAUCCAUCAGAAG GUGCCCAUUCUUAU
STMN2_ intron1	-	GTT A	107 1	CTTATATATCCATTCA GAAGGTGCCCACTT	307 7	CUUAUUAUCCAUCUA GAAGGUGCCCAUUC
STMN2_ intron1	-	TTTC	107 2	TAGTTACTTATATATC CATTGAGAAGGTGC	307 8	UAGUUACUUAUUAUUC CAUUCAGAAGGUGC
STMN2_ intron1	-	ATT T	107 3	CTAGTTACTTATATAT CCATTGAGAAGGTG	307 9	CUAGUUACUUAUUAU CCAUUCAGAAGGUG
STMN2_ intron1	-	TTTC	107 4	ATTTCTAGTTACTTAT ATATCCATTGAGAA	308 0	AUUUCUAGUUACUUAU AUAUCCAUCAGAA
STMN2_ intron1	-	TTTT	107 5	CATTTCTAGTTACTTA TATATCCATTGAGA	308 1	CAUUUCUAGUUACUUA UAUAUCCAUCAGAA
STMN2_ intron1	-	CTTT	107 6	TCATTTCTAGTTACTT ATATATCCATTGAG	308 2	UCAUUUCUAGUUACU AUAUAUCCAUCAG
STMN2_ intron1	-	ATT C	107 7	TGACCAAATCCTCAGC TTTTCATTCTAGT	308 3	UGACCAAAUCCUCAGC UUUUCAUUUCUAGU

STMN2_ intron1	-	TTT A	107 8	TCCTGAAATTCTGACC AAATCCTCAGCTTT	308 4	UCCUGAAAUUCUGACC AAAUCCUCAGCUUU
STMN2_ intron1	-	TTTT	107 9	ATCCTGAAATTCTGAC CAAATCCTCAGCTT	308 5	AUCCUGAAAUUCUGAC CAAAUCCUCAGCUU
STMN2_ intron1	-	GTT T	108 0	TATCCTGAAATTCTGA CCAAATCCTCAGCT	308 6	UAUCCUGAAAUUCUGA CCAAAUCCUCAGCU
STMN2_ intron1	-	TTTC	108 1	AGTTTTATCCTGAAAT TCTGACCAAATCCT	308 7	AGUUUUAUCCUGAAAU UCUGACCAAUCCU
STMN2_ intron1	-	CTTT	108 2	CAGTTTTATCCTGAAA TTCTGACCAAATCC	308 8	CAGUUUUAUCCUGAAA UUCUGACCAAUCC
STMN2_ intron1	-	ATT T	108 3	CAAAATCTATTATTTT AATACTGCAGAAGT	308 9	CAAAAUUCUAUUAUUU AAUACUGCAGAAGU
STMN2_ intron1	-	TTTC	108 4	AAAATCTATTATTTTA ATACTGCAGAAGTA	309 0	AAAUCUAUUAUUUUA AUACUGCAGAAGUA
STMN2_ intron1	-	ATT A	108 5	TTTTAATACTGCAGAA GTAGTGTTTTTTTC	309 1	UUUUAUACUGCAGAA GUAGUGUUUUUUC
STMN2_ intron1	-	ATT T	108 6	TAATACTGCAGAAGT AGTGTTTTTTTCATG	309 2	UAAUACUGCAGAAGUA GUGUUUUUUUCAUG
STMN2_ intron1	-	GTT T	108 7	CAGGGGAAAAAACTT AAAATTTTGTGCATA	309 3	CAGGGGAAAAAACUUA AAAUUUUGUGCAUA
STMN2_ intron1	-	GTT G	108 8	GAAGAACAGTTTCAG GGGAAAAAACTTAAA	309 4	GAAGAACAGUUCAGG GGAAAAAACUUAAA
STMN2_ intron1	-	ATT G	108 9	AGGCTGTATCAAGAA TCAGCAGTTGGAAGA	309 5	AGGCUGUAUCAAGAAU CAGCAGUUGGAAGA
STMN2_ intron1	-	TTTC	109 0	ACGATCCATGTATCTG TGTAGGATTGAGGC	309 6	ACGAUCCAUGUAUCUG UGUAGGAUUGAGGC
STMN2_ intron1	-	ATT T	109 1	CACGATCCATGTATCT GTGTAGGATTGAGG	309 7	CACGAUCCAUGUAUCU GUGUAGGAUUGAGG
STMN2_ intron1	-	TTT G	109 2	GATGGCGGCTACCATT TCACGATCCATGTA	309 8	GAUGGCGGCUACCAU UCACGAUCCAUGUA
STMN2_ intron1	-	ATT T	109 3	GGATGGCGGCTACCA TTTCACGATCCATGT	309 9	GGAUGGCGGCUACCAU UUCACGAUCCAUGU
STMN2_ intron1	-	TTT A	109 4	TTTGGATGGCGGCTAC CATTTACGATCCA	310 0	UUUGGAUGGCGGCUAC CAUUUCACGAUCCA
STMN2_ intron1	-	TTTT	109 5	ATTTGGATGGCGGCTA CCATTTACGATCC	310 1	AUUUGGAUGGCGGCUA CCAUUUCACGAUCC
STMN2_ intron1	-	TTTT	109 6	TATTTGGATGGCGGCT ACCATTTACGATC	310 2	UAUUUGGAUGGCGGCU ACCAUUUCACGAUC
STMN2_ intron1	-	ATT T	109 7	TTATTTGGATGGCGGC TACCATTTACGAT	310 3	UUAUUUGGAUGGCGGC UACCAUUUCACGAU
STMN2_ intron1	-	TTT G	109 8	GGGTGGGATTTTATT TGGATGGCGGCTAC	310 4	GGGUGGGAUUUUUAU UGGAUGGCGGCUAC
STMN2_ intron1	-	ATT T	109 9	GGGGTGGGATTTTAT TTGGATGGCGGCTA	310 5	GGGGUGGGAUUUUUAU UUGGAUGGCGGCUA

STMN2_ intron1	-	GTT C	110 0	CAGGACTGCATACAG CTCAACTGCCCCCTCC	310 6	CAGGACUGCAUACAGC UCAACUGCCCCUCC
STMN2_ intron1	-	TTT G	110 1	TCATATTTGGGGTGGG ATTTTTATTGGAT	310 7	UCAUAUUUGGGGUGGG AUUUUUUUUUGGAU
STMN2_ intron1	-	CTT G	110 2	CGTTTGTTCATATTGG GGTGGGATTTTTAT	310 8	CGUUUGUCAUAUUUGG GGUGGGAUUUUUUAU
STMN2_ intron1	-	ATT A	110 3	TGGCCAGAAAGGATG CTTGCGTTTGTTCATA	310 9	UGGCCAGAAAGGAUGC UUGCGUUUGUCAUA
STMN2_ intron1	-	GTT A	110 4	AATTATGGCCAGAAA GGATGCTTGCGTTTG	311 0	AAUUAUGGCCAGAAAG GAUGCUUGCGUUUG
STMN2_ intron1	-	TTT G	110 5	CAAATGCAGTTAAATT ATGGCCAGAAAGGA	311 1	CAAUUGCAGUUAUUU AUGGCCAGAAAGGA
STMN2_ intron1	-	ATT T	110 6	GCAAATGCAGTTAAA TTATGGCCAGAAAGG	311 2	GCAAUUGCAGUUAUU UAUGGCCAGAAAGG
STMN2_ intron1	-	TTTC	110 7	ATGATTTGCAAATGCA GTTAAATTATGGCC	311 3	AUGAUUUGCAAUUGCA GUUAAAUAUUGGCC
STMN2_ intron1	-	TTTT	110 8	CATGATTTGCAAATGC AGTTAAATTATGGC	311 4	CAUGAUUUGCAAUUGC AGUAAAUAUUGGCC
STMN2_ intron1	-	TTTT	110 9	TCATGATTTGCAAATG CAGTTAAATTATGG	311 5	UCAUGAUUUGCAAUUG CAGUAAAUAUUGG
STMN2_ intron1	-	TTTT	111 0	TTCATGATTTGCAAAT GCAGTTAAATTATG	311 6	UUCAUGAUUUGCAAU GCAGUAAAUAUUG
STMN2_ intron1	-	TTTT	111 1	TTTCATGATTTGCAAA TGCAGTTAAATTAT	311 7	UUUCAUGAUUUGCAAA UGCAGUAAAUAU
STMN2_ intron1	-	GTT T	111 2	TTTTCATGATTTGCAA ATGCAGTTAAATTA	311 8	UUUCAUGAUUUGCAA AUGCAGUAAAUA
STMN2_ intron1	-	TTT A	111 3	ATACTGCAGAAGTAG TGTTTTTTTCATGAT	311 9	AUACUGCAGAAGUAGU GUUUUUUUUCAUGAU
STMN2_ intron1	-	TTTT	111 4	AATACTGCAGAAGTA GTGTTTTTTTCATGA	312 0	AAUACUGCAGAAGUAG UGUUUUUUUCAUGA
STMN2_ intron1	-	GTT T	111 5	GTCATATTTGGGGTGG GATTTTTATTTGGA	312 1	GUCAUAUUUGGGGUGG GAUUUUUAUUUGGA
STMN2_ intron1	-	ATT C	111 6	CTCTTCCCCGCCAGTC TCGGAGCCTGAGGT	312 2	CUCUCCCCGCCAGUC UCGGAGCCUGAGGU
STMN2_ intron1	-	CTT C	111 7	CCCGCCAGTCTCGGAG CCTGAGGTCTCCCC	312 3	CCCGCCAGUCUCGGAG CCUGAGGUCUCCCC
STMN2_ intron1	-	CTTT	111 8	CGGCAGCTTCCCTGT CTCCGCATCCTGCA	312 4	CGGCAGCUUCCUGU CUCCGCAUCCUGCA
STMN2_ intron1	-	TTTC	111 9	CAAAATGTCCCTTAAG CCCATTAAAGGCAA	312 5	CAAAAUGUCCCUUAAG CCCAUUUAAGGCAA
STMN2_ intron1	-	CTTT	112 0	CAAAAATGTCCCTTAA GCCCATTTAAGGCA	312 6	CAAAAUGUCCCUUAA GCCCAUUUAAGGCA
STMN2_ intron1	-	GTT A	112 1	TAAAGCACTTTCCAAA ATGTCCCTTAAGCC	312 7	UAAAGCACUUCCAAA AUGUCCCUUAAGCC

STMN2_ intron1	-	CTT A	112 2	AACTAGAGAAGAAAT AAAAAAAAAAAAAGGT	312 8	AACUAGAGAAGAAUA AAAAAAAAAAAAAGGU
STMN2_ intron1	-	CTT C	112 3	TTAAACTAGAGAAGA AATAAAAAAAAAAAAA	312 9	UUAACUAGAGAAGAA AUAAAAAAAAAAAA
STMN2_ intron1	-	TTTC	112 4	TTCTTAACTAGAGAA GAAATAAAAAAAAA	313 0	UUCUUAACUAGAGAA GAAAUAAAAAAAA
STMN2_ intron1	-	TTTT	112 5	CTTCTTAACTAGAGA AGAAATAAAAAAAAA	313 1	CUUCUUAACUAGAGA AGAAAUAAAAAAAA
STMN2_ intron1	-	ATT T	112 6	TCTTCTTAACTAGAG AAGAAATAAAAAAAAA	313 2	UCUUCUUAACUAGAG AAGAAAUAAAAAAAA
STMN2_ intron1	-	TTTC	112 7	CTATTTTCTTCTTAAA CTAGAGAAGAAATA	313 3	CUAUUUUCUUCUAAA CUAGAGAAGAAUA
STMN2_ intron1	-	CTTT	112 8	CCTATTTTCTTCTTAA ACTAGAGAAGAAAT	313 4	CCUAUUUCUUCUAAA ACUAGAGAAGAAAU
STMN2_ intron1	-	TTT A	112 9	CCCCTTTCCTATTTCT TCTTAACTAGAG	313 5	CCCCUUCCUAUUUUC UUCUUAACUAGAG
STMN2_ intron1	-	CTTT	113 0	ACCCCTTTCCTATTTT CTTCTTAACTAGA	313 6	ACCCCUUCCUAUUUU CUUCUUAACUAGA
STMN2_ intron1	-	CTT C	113 1	CCTTTACCCCTTTCCT ATTTTCTTCTTAAA	313 7	CCUUUACCCCUUCCU AUUUUCUUCUAAA
STMN2_ intron1	-	TTTC	113 2	TCCCACCTTCCCTTFA CCCCTTTCCTATTT	313 8	UCCCACCUUCCCUUA CCCCUUCCUAUUU
STMN2_ intron1	-	CTTT	113 3	CTCCCACCTTCCCTTT ACCCCTTTCCTATT	313 9	CUCCCACCUUCCCUU ACCCCUUCCUAUU
STMN2_ intron1	-	TTTC	113 4	CTTTCTCCCACCTTCC CTTTACCCCTTTC	314 0	CUUCUCCCACCUCC CUUUACCCCUUCC
STMN2_ intron1	-	TTTT	113 5	CCTTTCTCCCACCTTC CCTTTACCCCTTTC	314 1	CCUUCUCCCACCUUC CCUUUACCCCUUUC
STMN2_ intron1	-	TTTT	113 6	TCCTTTCTCCCACCTT CCCTTTACCCCTTT	314 2	UCCUUCUCCCACCUU CCCUUUACCCCUU
STMN2_ intron1	-	CTTT	113 7	TTCCTTTCTCCCACCTT CCCTTTACCCCTT	314 3	UCCCUUCUCCCACCU UCCCUUUACCCCU
STMN2_ intron1	-	TTTC	113 8	TTTTCTCTTCTCCAC CTTCCCTTACCC	314 4	UUUUUCCUUCUCCCA CCUCCCUUUACCC
STMN2_ intron1	-	TTTT	113 9	CTTTTCTCTTCTCCCA CCTTCCCTTACC	314 5	CUUUUCCUUCUCCC ACCUUCCCUUUACC
STMN2_ intron1	-	ATT T	114 0	TCTTTTCTTCTCTCC ACCTTCCCTTAC	314 6	UCUUUCCUUCUCC CACCUUCCCUUAC
STMN2_ intron1	-	TTT G	114 1	CAATTTCTTTTTCTT TCTCCACCTTCC	314 7	CAAUUUUCUUUUCCU UUCUCCACCUCC
STMN2_ intron1	-	CTTT	114 2	GCAATTTCTTTTTCT TTTCTCCACCTTC	314 8	GCAAUUUUCUUUUCC UUUCUCCACCUUC
STMN2_ intron1	-	TTT G	114 3	ACTTTGCAATTTCTT TTCTCTTCTCCCA	314 9	ACUUUGCAAUUUUCU UUUCCUUCUCCCA

STMN2_ intron1	-	CTTT	114 4	GACTTTGCAATTTTCT TTTTCCTTCTCCC	315 0	GACUUUGCAAUUUUCU UUUUCUUUCUCCC
STMN2_ intron1	-	TTTC	114 5	AAACAGCGGGATGGG ACCGCTTTGACTTTG	315 1	AAACAGCGGGAUGGGA CCGCUUUGACUUUG
STMN2_ intron1	-	CTT A	114 6	AGCCCATTTAAGGCA AACAGTTAAGGTAGC	315 2	AGCCCAUUUAAGGCAA ACAGUUAAGGUAGC
STMN2_ intron1	-	ATT T	114 7	AAGGCAAACAGTTAA GGTAGCTTCTCCCC	315 3	AAGGCAAACAGUUAAG GUAGCUUCCUCCCC
STMN2_ intron1	-	TTT A	114 8	AGGCAAACAGTTAAG GTAGCTTCTCTCCCCT	315 4	AGGCAAACAGUUAAGG UAGCUUCCUCCCCU
STMN2_ intron1	-	GTT A	114 9	AGGTAGCTTCTCCCC TCACGATTGAGTCC	315 5	AGGUAGCUUCCUCCCC UCACGAUUGAGUCC
STMN2_ intron1	-	CTT C	115 0	TAGAGCTCAAGAGAG GAGGTGAGAGGTGGG	315 6	UAGAGCUCAAGAGAGG AGGUGAGAGGUGGG
STMN2_ intron1	-	TTT A	115 1	TAAATATCTCTGAAT GCTTCTAGAGCTCA	315 7	UAAAAUAUCUCUGAAU GCUUCUAGAGCUCA
STMN2_ intron1	-	CTTT	115 2	ATAAAATATCTCTGAA TGCTTCTAGAGCTC	315 8	AUAAAAUAUCUCUGAA UGCUUCUAGAGCUC
STMN2_ intron1	-	TTTC	115 3	TTTATAAAATATCTCT GAATGCTTCTAGAG	315 9	UUUAUAAAAUAUCUCU GAAUGCUUCUAGAG
STMN2_ intron1	-	TTTT	115 4	CTTTATAAAATATCTC TGAATGCTTCTAGA	316 0	CUUUAUAAAAUAUCUC UGAAUGCUUCUAGA
STMN2_ intron1	-	TTTT	115 5	TCTTTATAAAATATCT CTGAATGCTTCTAG	316 1	UCUUUAUAAAAUAUCU CUGAAUGCUUCUAG
STMN2_ intron1	-	CTTT	115 6	TTCTTTATAAAATATC TCTGAATGCTTCTA	316 2	UUCUUUAUAAAAUAUC UCUGAAUGCUUCUA
STMN2_ intron1	-	ATT A	115 7	ACATCTTTTTCTTTAT AAAATATCTCTGAA	316 3	ACAUCUUUUUCUUUAU AAAAUAUCUCUGAA
STMN2_ intron1	-	GTT A	115 8	CCATTAACATCTTTTT CTTTATAAAATATC	316 4	CCAUUAACAUCUUUUU CUUUAUAAAAUAUC
STMN2_ intron1	-	CTT C	115 9	CTGGTCTGTGTTACC ATTAACATCTTTTT	316 5	CUGGUCCUGUGUACC AUUAACAUCUUUUU
STMN2_ intron1	-	CTT C	116 0	TCTGCCCTCCACCTC CCCCAGAACTGCCC	316 6	UCUGCCCUCACCUC CCCAGAACUGCCC
STMN2_ intron1	-	TTTC	116 1	CATAGACCTCTTCTCT GCCCTCCACCTCC	316 7	CAUAGACCUCUUCUCU GCCCUCCACCUC
STMN2_ intron1	-	ATT T	116 2	CCATAGACCTCTTCTC TGCCCTCCACCTC	316 8	CCAUAGACCUCUUCUC UGCCCUCCACCUC
STMN2_ intron1	-	CTTT	116 3	CAAACAGCGGGATGG GACCGCTTTGACTTT	316 9	CAAACAGCGGGAUGGG ACCGCUUUGACUUU
STMN2_ intron1	-	TTT A	116 4	GATTTCCATAGACCTC TTCTCTGCCCTCCC	317 0	GAUUUCCAUAGACCUC UUCUCUGCCCUC
STMN2_ intron1	-	CTT C	116 5	GCTTTAGATTTCCATA GACCTCTTCTCTGC	317 1	GCUUUAGAUAUCCAUA GACCUCUUCUCUGC

STMN2_ intron1	-	ATT C	116 6	TTCGCTTTAGATTTC ATAGACCTCTTCTC	317 2	UUCGCUUUAGAUUCC AUAGACCUCUUCUC
STMN2_ intron1	-	TTT A	116 7	AAAGAAATTCTTCGCT TTAGATTTCATAG	317 3	AAAGAAAUUCUUCGU UUAGAUUCCAUAG
STMN2_ intron1	-	TTTT	116 8	AAAAGAAATTCTTCG CTTTAGATTTCATA	317 4	AAAAGAAAUUCUUCGC UUUAGAUUCCAU
STMN2_ intron1	-	CTTT	116 9	TAAAAGAAATTCTTCG CTTTAGATTTCAT	317 5	UAAAAGAAAUUCUUCG CUUUAGAUUCCAU
STMN2_ intron1	-	CTT C	117 0	TACCTTTTAAAAGAAA TTCTTCGCTTTAGA	317 6	UACCUUUAAAAGAAA UUCUUCGCUUUAGA
STMN2_ intron1	-	CTT A	117 1	CCCGCTTCTACCTTTT AAAAGAAATTCTTC	317 7	CCCGCUUCUACCUUU AAAAGAAAUUCUUC
STMN2_ intron1	-	ATT C	117 2	TCTACCCATAGGAGG GCAACTTACCCGCTT	317 8	UCUACCCAUAGGAGGG CAACUACCCGCUU
STMN2_ intron1	-	TTT A	117 3	AATATGGAAACAGAA TAAATTCTCTACCCA	317 9	AAUAUGGAAACAGAAU AAAUUCUCUACCCA
STMN2_ intron1	-	TTTT	117 4	AAATATGGAAACAGA ATAAATTCTCTACCC	318 0	AAUAUGGAAACAGAA UAAAUUCUCUACCC
STMN2_ intron1	-	ATT T	117 5	TAAATATGGAAACAG AATAAATTCTCTACC	318 1	UAAAUUGGAAACAGA AUAAAUUCUCUACC
STMN2_ intron1	-	ATT G	117 6	AGTCCTAATTTTAAAT ATGGAACAGAAATA	318 2	AGUCCUAAUUUAAA AUGGAAACAGAAUA
STMN2_ intron1	-	CTT C	117 7	CTCCCCTCACGATTGA GTCCTAATTTTAAA	318 3	CUCCCCUCACGAUUGA GUCCUAAUUUAAA
STMN2_ intron1	-	CTTT	117 8	AGATTTCATAGACCT CTTCTCTGCCCTCC	318 4	AGAUUCCAUAGACCU CUUCUCUGCCCUC
STMN2_ intron1	-	TTTC	117 9	TTTCAGTTTATCCTG AAATTCTGACCAA	318 5	UUUCAGUUUUAUCCUG AAAUUCUGACCAA
STMN2_ intron1	-	GTT C	118 0	TCTCCATCCCCTCCCC CCGTCTCCACCCAT	318 6	UCUCCAUCUCCCCC CGUCUCCACCAU
STMN2_ intron1	-	TTTC	118 1	TTCGACGAGACAATA CCGTAAAATGTGCCC	318 7	UUCGACGAGACAAUAC CGUAAAUGUGCCC
STMN2_ intron1	-	TTT A	118 2	TATACGATTTTATGTC ATCTCTATTATTAT	318 8	UAUACGAUUUCAUGUC AUCUCUAUUUAU
STMN2_ intron1	-	CTTT	118 3	ATATACGATTTTATGT CATCTCTATTATTA	318 9	AUAUACGAUUUCAUGU CAUCUCUAUUUAU
STMN2_ intron1	-	TTT G	118 4	CTTTATATACGATTTT ATGTCATCTCTATT	319 0	CUUUAUUAACGAUUUC AUGUCAUCUCUAU
STMN2_ intron1	-	TTTT	118 5	GCTTTATATACGATTT CATGTCATCTCTAT	319 1	GCUUUAUUAACGAUUU CAUGUCAUCUCUAU
STMN2_ intron1	-	CTTT	118 6	TGCTTTATATACGATT TCATGTCATCTCTA	319 2	UGCUUUAUUAACGAUU UCAUGUCAUCUCUA
STMN2_ intron1	-	TTT G	118 7	ACCTCTTTTGCTTTAT ATACGATTTTATGT	319 3	ACCUCUUUUGCUUUAU AUACGAUUUCAUGU

STMN2_ intron1	-	CTTT	118 8	GACCTCTTTTGCTTTA TATACGATTTTCATG	319 4	GACCUCUUUUGCUUUA UAUACGAUUUCAUG
STMN2_ intron1	-	CTT A	118 9	AGACTTTGACCTCTTT TGCTTTATATACGA	319 5	AGACUUUGACCUCUUU UGCUUUUAUUAACGA
STMN2_ intron1	-	CTT A	119 0	ACTTAAGACTTTGACC TCTTTTGCTTTATA	319 6	ACUUAAGACUUUGACC UCUUUUGCUUUUAUA
STMN2_ intron1	-	TTTC	119 1	GCGTGGCTTAACCTAA GACTTTGACCTCTT	319 7	GCGUGGCUUAACUUA GACUUUGACCUCUU
STMN2_ intron1	-	ATT T	119 2	CGCGTGGCTTAACCTA AGACTTTGACCTCT	319 8	CGCGUGGCUUAACUUA AGACUUUGACCUCU
STMN2_ intron1	-	TTT G	119 3	GCACTGTCTGACCCAC AAAACGGAAATTTT	319 9	GCACUGUCUGACCCAC AAAACGGAAAUUUC
STMN2_ intron1	-	ATT T	119 4	GGCACTGTCTGACCCA CAAAACGGAAATTT	320 0	GGCACUGUCUGACCCA CAAAACGGAAAUUU
STMN2_ intron1	-	ATT G	119 5	CCGATATTTGGCACTG TCTGACCCACAAAA	320 1	CCGAUAUUUGGCACUG UCUGACCCACAAAA
STMN2_ intron1	-	CTT A	119 6	TGAAATTGCCGATATT TGGCACTGTCTGAC	320 2	UGAAAUUGCCGAUAUU UGGCACUGUCUGAC
STMN2_ intron1	-	CTT G	119 7	TCTCTCTGAGCTTATG AAATTGCCGATATT	320 3	UCUCUCUGAGCUUAUG AAAUUGCCGAUAUU
STMN2_ intron1	-	TTTC	119 8	CGGTCATCCTGTGTCT CCACTGTCTTGTCT	320 4	CGGUCAUCCUGUGUCU CCACUGUCUUGUCU
STMN2_ intron1	-	TTTT	119 9	CCGGTCATCCTGTGTC TCCACTGTCTTGTC	320 5	CCGGUCAUCCUGUGUC UCCACUGUCUUGUC
STMN2_ intron1	-	CTTT	120 0	TCCGGTCATCCTGTGT CTCCACTGTCTTGT	320 6	UCCGGUCAUCCUGUGU CUCCACUGUCUUGU
STMN2_ intron1	-	ATT G	120 1	CGGATGAAGGCCCTG AATCCAGAATCTTTT	320 7	CGGAUGAAGGCCCUGA AUCCAGAAUCUUUU
STMN2_ intron1	-	TTTC	120 2	ACCCCGGGGGCCACTG AGCGCCAGAACCGTG	320 8	ACCCCGGGGGCCACUGA GCGCCAGAACCGUG
STMN2_ intron1	-	TTTT	120 3	CACCCCGGGGGCCACT GAGCGCCAGAACCGT	320 9	CACCCCGGGGGCCACUG AGCGCCAGAACCGU
STMN2_ intron1	-	CTTT	120 4	TCACCCCGGGGGCCACT GAGCGCCAGAACCG	321 0	UCACCCCGGGGGCCACU GAGCGCCAGAACCG
STMN2_ intron1	-	CTT C	120 5	CAGCTGCCACAGGAC CCCAGGCCCCACCCT	321 1	CAGCUGCCACAGGACC CCAGGCCCCACCCU
STMN2_ intron1	-	TTTC	120 6	CCTGTCTCCGCATCCT GCAACCAAGTCCCG	321 2	CCUGUCUCCGCAUCCU GCAACCAAGUCCCG
STMN2_ intron1	-	CTTT	120 7	CCCTGTCTCCGCATCC TGCAACCAAGTCCC	321 3	CCCUGUCUCCGCAUCC UGCAACCAAGUCCC
STMN2_ intron1	-	TTTC	120 8	GGCAGCTTTCCCTGTC TCCGCATCCTGCAA	321 4	GGCAGCUUCCCUGUC UCCGCAUCCUGCAA
STMN2_ intron1	-	ATT T	120 9	CATGTCATCTCTATTA TTATACATACACAT	321 5	CAUGUCAUCUCUAUUA UUAUACAUACACAU

STMN2_ intron1	-	TTTC	121 0	ATGTCATCTCTATTAT TATACATACACATG	321 6	AUGUCAUCUCUAAUUAU UAUACAUACACAUG
STMN2_ intron1	-	ATT A	121 1	TTATACATACACATGT CTAGGTTCTAGAAG	321 7	UUAUACAUACACAUGU CUAGGUUCUAGAAG
STMN2_ intron1	-	ATT A	121 2	TACATACACATGTCTA GGTTCTAGAAGCTT	321 8	UACAUACACAUGUCUA GGUUCUAGAAGCUU
STMN2_ intron1	-	GTT T	121 3	CTTCGACGAGACAAT ACCGTAAAATGTGCC	321 9	CUUCGACGAGACAAUA CCGUAAAAUGUGCC
STMN2_ intron1	-	CTT A	121 4	CCTCCCTGCACCGCAC CCCAGGACTAGCGG	322 0	CCUCCCUGCACCGCACC CCAGGACUAGCGG
STMN2_ intron1	-	CTT G	121 5	CCCTAAAACAAAGGA GCGGAGGTCCTACCC	322 1	CCCUAAAACAAAGGAG CGGAGGUCCUACCC
STMN2_ intron1	-	CTT C	121 6	CCCTCCCTTGCCCTAA AACAAAGGAGCGGA	322 2	CCCUCCCUGCCCUAA AACAAAGGAGCGGA
STMN2_ intron1	-	CTT C	121 7	CTCTCTCTTCCCCTC CCTTGCCCTAAAAC	322 3	CUCUCUCCUUCCCCUCC CUUGCCCUAAAAC
STMN2_ intron1	-	CTT C	121 8	CCCGCCCCTGCAGCTG CCCACCCGCGCCCT	322 4	CCCGCCCCUGCAGCUGC CCACCCGCGCCCU
STMN2_ intron1	-	CTT C	121 9	GAAGCCGCTGTCCCTC CACCCCTCCCTGCC	322 5	GAAGCCGCUGUCCUC CACCCUCCUCCUGCC
STMN2_ intron1	-	ATT G	122 0	TGCGCCCAGCGCTGCA GGTGCCTCCCCCG	322 6	UGCGCCCAGCGCUGCA GGUGCCUCCCCCG
STMN2_ intron1	-	GTT C	122 1	CGCACTGGGTGGGGC TGTCCGCATTGTGCG	322 7	CGCACUGGGUGGGGCU GUCCGCAUUGUGCG
STMN2_ intron1	-	TTTC	122 2	GAATGAAGATGCAGC ACCGGGCGGGGGGGC	322 8	GAAUGAAGAUGCAGCA CCGGGGCGGGGGGGC
STMN2_ intron1	-	CTTT	122 3	CGAATGAAGATGCAG CACCGGGCGGGGGGG	322 9	CGAUGAAGAUGCAGC ACCGGGCGGGGGGG
STMN2_ intron1	-	GTT G	122 4	GGCTCCTGGGTGTCAC GCTGCGCTCCCCAC	323 0	GGCUCCUGGGUGUCAC GCUGCGCUCCCCAC
STMN2_ intron1	-	CTT G	122 5	GAAGCCGCGGCGGGG AGTCGGGAGCGGGGA	323 1	GAAGCCGCGGCGGGGA GUCGGGAGCGGGGA
STMN2_ intron1	-	CTT C	122 6	GACGAGACAATACCG TAAATGTGCCAGT	323 2	GACGAGACAAUACCGU AAAUGUGCCCAGU
STMN2_ intron1	-	CTT A	122 7	AAAGCAGAACAATGA GGCCAGCGTGGGGAG	323 3	AAAGCAGAACAUGAG GCCAGCGUGGGGAG
STMN2_ intron1	-	TTTT	122 8	CCCATCTCTCTTAAAA GCAGAACAATGAGG	323 4	CCCAUCUCUCUAAAA GCAGAACAUGAGG
STMN2_ intron1	-	CTTT	122 9	TCCCATCTCTCTTAAA AGCAGAACAATGAG	323 5	UCCCAUCUCUCUAAA AGCAGAACAUGAG
STMN2_ intron1	-	GTT A	123 0	ACCCACTTTTCCCATC TCTCTTAAAAGCAG	323 6	ACCCACUUUCCCAUC UCUCUAAAAGCAG
STMN2_ intron1	-	CTT C	123 1	CGAAAAGAAAAATGT TAACCCACTTTTCCC	323 7	CGAAAAGAAAAAUGUU AACCACUUUCCCC

STMN2_ intron1	-	TTT G	123 2	CTTCCGAAAAGAAAA ATGTTAACCCACTTT	323 8	CUUCCGAAAAGAAAA UGUUAACCCACUUU
STMN2_ intron1	-	ATT T	123 3	GCTTCCGAAAAGAAA AATGTTAACCCACTT	323 9	GCUUCCGAAAAGAAAA AUGUUAACCCACUU
STMN2_ intron1	-	TTT A	123 4	TCTGTGTCTATGTCTA AACACTCTATGTAA	324 0	UCUGUGUCUAUGUCUA AACACUCUAUGUAA
STMN2_ intron1	-	CTTT	123 5	ATCTGTGTCTATGTCT AAACACTCTATGTA	324 1	AUCUGUGUCUAUGUCU AAACACUCUAUGUA
STMN2_ intron1	-	CTT C	123 6	AAAGAACCCTTTATCT GTGTCTATGTCTAA	324 2	AAAGAACCCUUUAUCU GUGUCUAUGUCUAA
STMN2_ intron1	-	TTTC	123 7	CCGCAAACGATCAAA GGTCTTCAAAGAACC	324 3	CCGCAAACGAUCAAG GUCUUCAAAGAACC
STMN2_ intron1	-	TTTT	123 8	CCCGCAAACGATCAA AGGTCTTCAAAGAAC	324 4	CCCGCAAACGAUCAA GGUCUUCAAAGAAC
STMN2_ intron1	-	CTTT	123 9	TCCCGCAAACGATCA AAGGTCTTCAAAGAA	324 5	UCCCGCAAACGAUCAA AGGUCUUCAAAGAA
STMN2_ intron1	-	GTT C	124 0	TAGAAGCTTTTCCCGC AAACGATCAAAGGT	324 6	UAGAAGCUUUUCCCGC AAACGAUCAAGGU
STMN2_ intron1	-	TTTC	124 1	CCATCTCTCTTAAAAG CAGAACAATGAGGC	324 7	CCAUCUCUCUAAAAG CAGAACAUGAGGC
STMN2_ intron1	-	ATT T	124 2	TGTAAAGATTACCATA GATTTAAAAATGTT	324 8	UGUAAAGAUUACCAUA GAUUUAAAAAUGUU
STMN2_ intron1	-	ATT T	124 3	CTTTCAGTTTTATCCT GAAATTCTGACCAA	324 9	CUUUCAGUUUUAUCCU GAAAUUCUGACCAA
STMN2_ intron1	-	ATT A	124 4	ATTGATAAACTACTGC CATTTCTTTCAGTT	325 0	AUUGAUAAACUACUGC CAUUUCUUUCAGUU
STMN2_ intron1	-	TTTC	124 5	TACTATTTATCCACTA CAAAATCTCAGAAG	325 1	UACUAUUUAUCCACUA CAAAAUCUCAGAAG
STMN2_ intron1	-	TTTT	124 6	CTACTATTTATCCACT ACAAAATCTCAGAA	325 2	CUACUAUUUAUCCACU ACAAAUCUCAGAA
STMN2_ intron1	-	TTTT	124 7	TCTACTATTTATCCAC TACAAAATCTCAGA	325 3	UCUACUAUUUAUCCAC UACAAAUCUCAGA
STMN2_ intron1	-	ATT T	124 8	TTCTACTATTTATCCA CTACAAAATCTCAG	325 4	UUCUACUAUUUAUCCA CUACAAAUCUCAG
STMN2_ intron1	-	ATT A	124 9	CTACTGACATTTTCT ACTATTTATCCACT	325 5	CUACUGACAUUUUUCU ACUAUUUAUCCACU
STMN2_ intron1	-	TTT G	125 0	CTATTACTACTGACAT TTTTCTACTATTTA	325 6	CUAUUACUACUGACAU UUUUCUACUAUUUA
STMN2_ intron1	-	CTTT	125 1	GCTATTACTACTGACA TTTTTCTACTATTT	325 7	GCUAUUACUACUGACA UUUUUCUACUAUUU
STMN2_ intron1	-	ATT C	125 2	GGCTGCTAAATAACTT TGCTATTACTACTG	325 8	GGCUGCUAAAUAACUU UGCUAUUACUACUG
STMN2_ intron1	-	ATT A	125 3	AAATATTGGGCTGCTA AATAACTTTGCTAT	325 9	AAUAUUCGGCUGCUA AAUAACUUUGCUAU

STMN2_ intron1	-	TTT A	125 4	AGCATTAAAAATATTCG GCTGCTAAATAACT	326 0	AGCAUUAUUAUUCG GCUGCUAAAUAACU
STMN2_ intron1	-	TTTT	125 5	AAGCATTAAAAATATTC GGCTGCTAAATAAC	326 1	AAGCAUUAUUAUUC GGCUGCUAAAUAAC
STMN2_ intron1	-	TTTT	125 6	TAAGCATTAAAAATATT CGGCTGCTAAATAA	326 2	UAAGCAUUAUUAUUC CGGCUGCUAAAUA
STMN2_ intron1	-	ATT T	125 7	TTAAGCATTAAAAATAT TCGGCTGCTAAATA	326 3	UUAAGCAUUAUUAUUC UCGGCUGCUAAAUA
STMN2_ intron1	-	TTT A	125 8	TTTTTAAGCATTAAAA TATTCGGCTGCTAA	326 4	UUUUUAAGCAUUAUUA UAUUCGGCUGCUAA
STMN2_ intron1	-	CTTT	125 9	ATTTTAAAGCATTAAAA ATATTCGGCTGCTA	326 5	AUUUUUAAGCAUUAUUA AUUUCGGCUGCUAA
STMN2_ intron1	-	ATT C	126 0	CTTTATTTTAAAGCAT TAAAAATATTCGGCT	326 6	CUUUAUUUUUAAGCAU UAAAAUAUUCGGCU
STMN2_ intron1	-	TTT A	126 1	TTCCTTTATTTTAAAG CATTAAAAATATTCG	326 7	UCCUUUAUUUUUAAG CAUUAUUAUUCG
STMN2_ intron1	-	ATT T	126 2	ATTCCTTTATTTTAA GCATTAAAAATATTC	326 8	AUCCUUUAUUUUUAUUA GCAUUAUUAUUC
STMN2_ intron1	-	TTT A	126 3	ATTTATTCCTTTATTTT TAAGCATTAAAAAT	326 9	AUUUAUCCUUUAUUU UUAAGCAUUAUUAU
STMN2_ intron1	-	CTTT	126 4	AATTTATTCCTTTATT TTTAAGCATTAAAA	327 0	AAUUUAUCCUUUAUU UUUAAGCAUUAUUA
STMN2_ intron1	-	TTTC	126 5	TTTAATTTATTCCTTT ATTTTAAAGCATTAA	327 1	UUUAAUUUAUCCUUU AUUUUUAAGCAUUA
STMN2_ intron1	-	TTTT	126 6	CTTTAATTTATTCCTTT ATTTTAAAGCATT	327 2	CUUUAUUUAUCCUUU UAUUUUUAAGCAUU
STMN2_ intron1	-	ATT T	126 7	TCTTTAATTTATTCCTT TATTTTAAAGCAT	327 3	UCUUUAUUUAUCCUU UUAUUUUUAAGCAU
STMN2_ intron1	-	ATT T	126 8	CAATCGATGAAGAAG TAAACAATGATTTTC	327 4	CAAUCGAUGAAGAAGU AAACAAUGAUUUUC
STMN2_ intron1	-	ATT C	126 9	AGATGTGCTCTGAAC AGGGGGCACATTTCA	327 5	AGAUGUGCUCUGAACA GGGGGCACAUUUA
STMN2_ intron1	-	GTT C	127 0	TCTGCAGGTGGAGAC TCTGATATTCAGATG	327 6	UCUGCAGGUGGAGACU CUGAUUUCAGAUUG
STMN2_ intron1	-	TTT A	127 1	CTCGCTAAGCTGCATG TTCTCTGCAGGTGG	327 7	CUCGCUAAGCUGCAUG UUCUCUGCAGGUGG
STMN2_ intron1	-	ATT T	127 2	ATCCACTACAAAATCT CAGAAGTAACATAA	327 8	AUCCACUACAAAUCU CAGAAGUAACAUAA
STMN2_ intron1	-	TTTT	127 3	ACTCGCTAAGCTGCAT GTTCTCTGCAGGTG	327 9	ACUCGCUAAGCUGCAU GUUCUCUGCAGGUG
STMN2_ intron1	-	TTT A	127 4	TCCACTACAAAATCTC AGAAGTAACATAAA	328 0	UCCACUACAAAUCUC AGAAGUAACAUAAA
STMN2_ intron1	-	ATT A	127 5	ACCAGGGCGTGTATCT ACTTTCAGATTATG	328 1	ACCAGGGCGUGUAUCU ACUUUCAGAUUAUG

STMN2_ intron1	-	ATT G	127 6	CCCTCTAGTGTGGTGA AAAGTTAATGCAGA	328 2	CCCUCUAGUGUGGUGA AAAGUUA AUGCAGA
STMN2_ intron1	-	TTT A	127 7	GAGAACATGATTGCC CTCTAGTGTGGTGAA	328 3	GAGAACAU GAUUGCCC UCUAGUGUGGUGAA
STMN2_ intron1	-	TTTT	127 8	AGAGAACATGATTGC CCTCTAGTGTGGTGA	328 4	AGAGAACAU GAUUGCC CUCUAGUGUGGUGA
STMN2_ intron1	-	TTTT	127 9	TAGAGAACATGATTG CCCTCTAGTGTGGTG	328 5	UAGAGAACAU GAUUGC CCUCUAGUGUGGUG
STMN2_ intron1	-	TTTT	128 0	TTAGAGAACATGATT GCCCTCTAGTGTGGT	328 6	UUAGAGAACAU GAUUG CCCUCUAGUGUGGU
STMN2_ intron1	-	CTTT	128 1	TTTAGAGAACATGATT GCCCTCTAGTGTGG	328 7	UUUAGAGAACAU GAU GCCCUCUAGUGUGG
STMN2_ intron1	-	TTT A	128 2	CATCAATCATCTGCTT TTTTAGAGAACATG	328 8	CAUCAUCAUCUGCUU UUUUAGAGAACAU
STMN2_ intron1	-	GTT T	128 3	ACATCAATCATCTGCT TTTTTAGAGAACAT	328 9	ACAUCAUCAUCUGCU UUUUUAGAGAACAU
STMN2_ intron1	-	TTT G	128 4	GAAGTAGGTTTACATC AATCATCTGCTTTT	329 0	GAACUAGGUUUACAUC AAUCAUCUGCUUUU
STMN2_ intron1	-	ATT T	128 5	GGAAGTAGGTTTACAT CAATCATCTGCTTT	329 1	GGAACUAGGUUUACAU CAAUCAUCUGCUUU
STMN2_ intron1	-	GTT A	128 6	ATATTTGGAAGTAGGT TTACATCAATCATC	329 2	AUAUUUGGAACUAGGU UUACAUCAAUCAUC
STMN2_ intron1	-	ATT A	128 7	AACAGTTAATATTTGG AACTAGGTTTACAT	329 3	AACAGUUAAUUAUUUGG AACUAGGUUUACAU
STMN2_ intron1	-	TTT A	128 8	TTAAACAGTTAATATT TGGAAGTAGGTTTA	329 4	UUAAACAGUUAAUAUU UGGAACUAGGUUA
STMN2_ intron1	-	TTTT	128 9	ATTAAACAGTTAATAT TTGGAAGTAGGTTT	329 5	AUUAACAGUUAAUAU UUGGAACUAGGUUU
STMN2_ intron1	-	ATT T	129 0	TATTAAACAGTTAATA TTGGAAGTAGGTT	329 6	UAUUAACAGUUAAUA UUUGGAACUAGGUU
STMN2_ intron1	-	GTT C	129 1	CTGGTAAAAGAAAAG ATTTTATTAAACAGT	329 7	CUGGUAAAAGAAAAGA UUUUAUUAAACAGU
STMN2_ intron1	-	CTT G	129 2	AATGTTCTGTTAAAA GAAAAGATTTTATT	329 8	AAUGUCCUGGUAAAA GAAAAGAUUUUAUU
STMN2_ intron1	-	ATT G	129 3	AATAAACACTTGAAT GTTCTGTTAAAAGA	329 9	AAUAAACACUUGAAUG UCCUGGUAAAAGA
STMN2_ intron1	-	CTT A	129 4	TTGAATAAACACTTGA ATGTTCTGTTAAA	330 0	UUGAAUAAACACUUGA AUGUCCUGGUAAA
STMN2_ intron1	-	GTT C	129 5	ATCCACTAGGGTAAA GCATGGCATCAGCTT	330 1	AUCCACUAGGGUAAAG CAUGGCAUCAGCUU
STMN2_ intron1	-	ATT G	129 6	TACAAGCTCTGTTCAT CCACTAGGGTAAAG	330 2	UACAAGCUCUGUUCAU CCACUAGGGUAAAG
STMN2_ intron1	-	CTT G	129 7	AAAATTGTACAAGCT CTGTTTATCCACTAG	330 3	AAAUUGUACAAGCUC UGUUCAUCCACUAG

STMN2_ intron1	-	TTTC	129 8	ATCCTGTCTCCTTGAA AATTGTACAAGCTC	330 4	AUCCUGUCUCCUUGAA AAUUGUACAAGCUC
STMN2_ intron1	-	ATT T	129 9	CATCCTGTCTCCTTGA AAATTGTACAAGCT	330 5	CAUCCUGUCUCCUUGA AAAUUGUACAAGCU
STMN2_ intron1	-	ATT A	130 0	TGACCACTCATTTTCAT CCTGTCTCCTTGAA	330 6	UGACCACUCAUUUCAU CCUGUCUCCUUGAA
STMN2_ intron1	-	TTTC	130 1	AGATTATGACCACTCA TTTCATCCTGTCTC	330 7	AGAUUAUGACCACUCA UUUCAUCCUGUCUC
STMN2_ intron1	-	CTTT	130 2	CAGATTATGACCACTC ATTTTCATCCTGTCT	330 8	CAGAUUAUGACCACUC AUUUCAUCCUGUCU
STMN2_ intron1	-	ATT A	130 3	TAATAACAATGTAAT AAAACCTGAGAAGTAA	330 9	UAAUAACAAUGUAAUA AAACUGAGAAGUAA
STMN2_ intron1	-	GTT T	130 4	TACTCGCTAAGCTGCA TGTTCTCTGCAGGT	331 0	UACUCGCUAAGCUGCA UGUUCUCUGCAGGU
STMN2_ intron1	-	TTT G	130 5	GTACACCTCCTCAGTA TCACATACCTGCCT	331 1	GUACACCUCCUCAGUA UCACAUACCUGCCU
STMN2_ intron1	-	TTTT	130 6	GGTACACCTCCTCAGT ATCACATACCTGCC	331 2	GGUACACCUCCUCAGU AUCACAUACCUGCC
STMN2_ intron1	-	ATT A	130 7	CATAAAATGTAATCA AAAAATAATTCTATC	331 3	CAUAAAAUGUAAUCAA AAAAUAAUUCUAUC
STMN2_ intron1	-	ATT A	130 8	GAATTACATAAAATG TAATCAAAAAATAAT	331 4	GAAUUACAUAAAAUGU AAUCAAAAAAUAAU
STMN2_ intron1	-	TTT A	130 9	TAGCTGGATTAGAATT ACATAAAATGTAAT	331 5	UAGCUGGAUUAGAAUU ACAUAAAAUGUAAU
STMN2_ intron1	-	TTTT	131 0	ATAGCTGGATTAGAA TTACATAAAATGTAA	331 6	AUAGCUGGAUUAGAAU UACAUAAAAUGUAA
STMN2_ intron1	-	ATT T	131 1	TATAGCTGGATTAGA ATTACATAAAATGTA	331 7	UAUAGCUGGAUUAGAA UUACAUAAAAUGUA
STMN2_ intron1	-	ATT A	131 2	AATATTTTATAGCTGG ATTAGAATTACATA	331 8	AAUAUUUUUUAUAGCUGG AUUAGAAUUACAU
STMN2_ intron1	-	TTT G	131 3	AGGAACACAGTAATA TGACACTATTAAATA	331 9	AGGAACACAGUAAUUAU GACACUAUUAAAUA
STMN2_ intron1	-	GTT T	131 4	GAGGAACACAGTAAT ATGACACTATTAAAT	332 0	GAGGAACACAGUAAUA UGACACUAUUAAAUA
STMN2_ intron1	-	ATT C	131 5	ATATGCACATCAAAG TTTGAGGAACACAGT	332 1	AUAUGCACAUCAAAGU UUGAGGAACACAGU
STMN2_ intron1	-	TTT A	131 6	ATGAAAATCAAAGGT AATTCATATGCACAT	332 2	AUGAAAAUCAAGGUA AUUCAUAUGCACAU
STMN2_ intron1	-	TTTT	131 7	AATGAAAATCAAAGG TAATTCATATGCACA	332 3	AAUGAAAAUCAAGGU AAUUCAUAUGCACA
STMN2_ intron1	-	ATT T	131 8	TAATGAAAATCAAAG GTAATTCATATGCAC	332 4	UAAUGAAAAUCAAGG UAAUUCAUAUGCAC
STMN2_ intron1	-	TTT G	131 9	CATTTTAATGAAAATC AAAGGTAATTTCATA	332 5	CAUUUUAAUGAAAUC AAAGGUAAUUCAUA

STMN2_ intron1	-	ATT T	132 0	GCATTTTAATGAAAAT CAAAGGTAATTCAT	332 6	GCAUUUUAAUGAAAAU CAAAGGUAAUUCAU
STMN2_ intron1	-	ATT G	132 1	AATCAGAATTTGCATT TTAATGAAAATCAA	332 7	AAUCAGAAUUUGCAUU UUAUUGAAAAUCA
STMN2_ intron1	-	GTT C	132 2	GGAAGACAGAATGTC TGCCTCAAGCCAGAT	332 8	GGAAGACAGAAUGUCU GCCUCAAGCCAGAU
STMN2_ intron1	-	CTT G	132 3	TTCGGAAGACAGAAT GTCTGCCTCAAGCCA	332 9	UUCGGAAGACAGAAUG UCUGCCUCAAGCCA
STMN2_ intron1	-	TTT A	132 4	GTGGTCAGAATCAGC ATCATCTGGGAGCTT	333 0	GUGGUCAGAAUCAGCA UCAUCUGGGAGCUU
STMN2_ intron1	-	GTT T	132 5	AGTGGTCAGAATCAG CATCATCTGGGAGCT	333 1	AGUGGUCAGAAUCAGC AUCAUCUGGGAGCU
STMN2_ intron1	-	GTT A	132 6	ATATCCCTAAAACTGA TGTGTTTAGTGGTC	333 2	AUAUCCCUAAAACUGA UGUGUUUAGUGGUC
STMN2_ intron1	-	ATT A	132 7	CAAGTTAATATCCCTA AAACTGATGTGTTT	333 3	CAAGUUAAUAUCCCUA AAACUGAUGUGUUU
STMN2_ intron1	-	CTT A	132 8	CCAGGAGGGATACCT GTATATTACAAGTTA	333 4	CCAGGAGGGAUACCUG UAUAUUACAAGUUA
STMN2_ intron1	-	GTT A	132 9	AGACATAATACCAGA GCTTACCAGGAGGGA	333 5	AGACAUAAUACCAGAG CUUACCAGGAGGGA
STMN2_ intron1	-	TTT A	133 0	AAAATGTTAAGACAT AATACCAGAGCTTAC	333 6	AAAUGUUAAAGACAU AUACCAGAGCUUAC
STMN2_ intron1	-	ATT T	133 1	AAAAATGTTAAGACA TAATACCAGAGCTTA	333 7	AAAAAUGUUAAAGACAU AAUACCAGAGCUUA
STMN2_ intron1	-	ATT A	133 2	CCATAGATTTAAAAAT GTTAAGACATAATA	333 8	CCAUAGAUUUAAAAAU GUUAAGACAUAAUA
STMN2_ intron1	-	TTT G	133 3	TAAAGATTACCATAG ATTTAAAAATGTAA	333 9	UAAAGAUUACCAUAGA UUUAAAAAUGUUAA
STMN2_ intron1	-	ATT C	133 4	TATCAATGCATATTTA AAAAATCCACTTTT	334 0	UAUCAAUUGCAUAUUUA AAAAAUCCACUUUU
STMN2_ intron1	-	ATT T	133 5	AAAAATCCACTTTTG ATGATACCCAAAAT	334 1	AAAAAUCCACUUUUG AUGAUACCCAAAAU
STMN2_ intron1	-	TTT A	133 6	AAAAATCCACTTTTGA TGATACCCAAAATT	334 2	AAAAAUCCACUUUUGA UGAUACCCAAAUAU
STMN2_ intron1	-	CTTT	133 7	TGATGATACCCAAAA TTAGTTTATACTTAT	334 3	UGAUGAUACCCAAAAU UAGUUUAUACUUAU
STMN2_ intron1	-	TTTT	133 8	TGGTACACCTCCTCAG TATCACATACCTGC	334 4	UGGUACACCUCCUCAG UAUCACAUACCGC
STMN2_ intron1	-	GTT T	133 9	TTGGTACACCTCCTCA GTATCACATACCTG	334 5	UUGGUACACCUCCUCA GUAUCACAUACCG
STMN2_ intron1	-	CTT A	134 0	GAAGATGGGAAAAAT AACAGCAGTCAGTTT	334 6	GAAGAUGGGAAAAUA ACAGCAGUCAGUUU
STMN2_ intron1	-	TTT A	134 1	AATGGAAAAGAAAGA CAGACTTAGAAGATG	334 7	AAUGGAAAAGAAAGAC AGACUUAGAAGAUG

STMN2_ intron1	-	CTTT	134 2	AAATGGAAAAGAAAG ACAGACTTAGAAGAT	334 8	AAAUGGAAAAGAAAGA CAGACUUAGAAGAU
STMN2_ intron1	-	TTT A	134 3	AAAAGGTATCTTTAA ATGGAAAAGAAAGAC	334 9	AAAAGGUAUCUUUAAA UGGAAAAGAAAGAC
STMN2_ intron1	-	ATT T	134 4	AAAAAGGTATCTTTA AATGGAAAAGAAAGA	335 0	AAAAAGGUAUCUUUAA AUGGAAAAGAAAGA
STMN2_ intron1	-	ATT A	134 5	GATTTAAAAAGGTAT CTTTAAATGGAAAAG	335 1	GAUUUAAAAAGGUAUC UUUAAAUGGAAAAG
STMN2_ intron1	-	ATT G	134 6	GATTAGATTTAAAAA GGTATCTTTAAATGG	335 2	GAUUAGAUUUAAAAAG GUAUCUUUAAAUGG
STMN2_ intron1	-	ATT G	134 7	AAATCACATTGGATTA GATTTAAAAAGGTA	335 3	AAAUACAUAUGGAUUA GAUUUAAAAAGGUA
STMN2_ intron1	-	GTT G	134 8	AAATCTGATAAAACT AGATTGAAATCACAT	335 4	AAAUUGAUUAAAACUA GAUUGAAAUCACAU
STMN2_ intron1	-	ATT G	134 9	TTGAAATCTGATAAA ACTAGATTGAAATCA	335 5	UUGAAAUCUGAUAAAA CUAGAUUGAAAUCA
STMN2_ intron1	-	TTTC	135 0	TAATAAACAGAAAAC CACTACAAGGAGATG	335 6	UAAUAAACAGAAAACC ACUACAAGGAGAUG
STMN2_ intron1	-	GTT A	135 1	ATGCAGACACCGAGG TTTTCCAATGGACAG	335 7	AUGCAGACACCGAGGU UUUCCAAUGGACAG
STMN2_ intron1	-	TTTT	135 2	CTAATAAACAGAAAA CCACTACAAGGAGAT	335 8	CUAAUAAACAGAAAAC CACUACAAGGAGAU
STMN2_ intron1	-	ATT A	135 3	ACATCGATTTTCTAAT AAACAGAAAACCAC	335 9	ACAUCGAUUUUCUAAU AAACAGAAAACCAC
STMN2_ intron1	-	GTT A	135 4	AAATTAACATCGATTT TCTAATAAACAGAA	336 0	AAAUUACAUCGAUUU UCUAAUAAACAGAA
STMN2_ intron1	-	CTT C	135 5	GTAAAAATTAACATCG ATTTTCTAATAAAC	336 1	GUUAAAAUUAACAUCG AUUUUCUAAUAAAC
STMN2_ intron1	-	CTT A	135 6	CTTCGTAAAAATTAAC ATCGATTTTCTAAT	336 2	CUUCGUUAAAAUUAAC AUCGAUUUUCUAAU
STMN2_ intron1	-	CTT C	135 7	TTACTTCGTAAAAATT AACATCGATTTTCT	336 3	UUACUUCGUUAAAAU ACAUCGAUUUUCU
STMN2_ intron1	-	TTTC	135 8	TTCTTACTTCGTAAAA ATTAACATCGATTT	336 4	UUCUUACUUCGUUAAA AUUAACAUCGAUUU
STMN2_ intron1	-	ATT T	135 9	CTTCTTACTTCGTAA AATTAACATCGATT	336 5	CUUCUUACUUCGUUAA AAUUAACAUCGAUU
STMN2_ intron1	-	CTT A	136 0	TATATTTCTTCTTACTT CGTTAAAATTAAC	336 6	UAUAUUUCUUCUUAUCU UCGUUAAAAUUAAC
STMN2_ intron1	-	TTT A	136 1	TACTTATATATTCTT CTTACTTCGTAAAA	336 7	UACUUAUAUAUUUCUU CUUACUUCGUUAAA
STMN2_ intron1	-	GTT T	136 2	ATACTTATATATTCT TCTTACTTCGTAA	336 8	AUACUUAUAUAUUUCU UCUACUUCGUUAA
STMN2_ intron1	-	ATT A	136 3	GTTTATACTTATATAT TTCTTCTTACTTCG	336 9	GUUUAUACUUAUAUAU UUCUUCUACUUCG

STMN2_ intron1	-	TTT G	136 4	ATGATACCCAAAATT AGTTTATACTTATAT	337 0	AUGAUACCCAAAAUUA GUUUUAUCUUUAUUAU
STMN2_ intron1	-	TTTT	136 5	GATGATACCCAAAAT TAGTTTATACTTATA	337 1	GAUGAUACCCAAAAUU AGUUUAUACUUUAUA
STMN2_ intron1	-	ATT T	136 6	TCTAATAAACAGAAA ACCACTACAAGGAGA	337 2	UCUAAUAAACAGAAAA CCACUACAAGGAGA
STMN2_ intron1	-	GTT T	136 7	TCCAATGGACAGAAC CAGTCTAGGTTCTGA	337 3	UCCAAUGGACAGAACC AGUCUAGGUUCUGA
STMN2_ intron1	-	TTTT	136 8	CCAATGGACAGAACC AGTCTAGGTTCTGAA	337 4	CCAAUGGACAGAACCA GUCUAGGUUCUGAA
STMN2_ intron1	-	TTTC	136 9	CAATGGACAGAACCA GTCTAGGTTCTGAAA	337 5	CAAUGGACAGAACCAG UCUAGGUUCUGAAA
STMN2_ intron1	-	TTTT	137 0	AGAATAGAATAATTT ACTACAAATCTGTAA	337 6	AGAAUAGAAUAAUUA CUACAAAUCUGUAA
STMN2_ intron1	-	CTTT	137 1	TAGAATAGAATAATTT ACTACAAATCTGTA	337 7	UAGAAUAGAAUAAUUU ACUACAAAUCUGUA
STMN2_ intron1	-	TTTC	137 2	TCTTTTAGAATAGAAT AATTTACTACAAAT	337 8	UCUUUUAGAAUAGAAU AAUUUACUACAAAU
STMN2_ intron1	-	ATT T	137 3	CTCTTTTAGAATAGAA TAATTTACTACAAA	337 9	CUCUUUUAGAAUAGAA UAAUUUACUACAAA
STMN2_ intron1	-	ATT A	137 4	ATGAGGTAATAGCTG TAACAATAAAAACAC	338 0	AUGAGGUAAUAGCUGU AACAAUAAAACAC
STMN2_ intron1	-	TTT G	137 5	CTAAAAATATTAATG AGGTAATAGCTGTAA	338 1	CUAAAAAUUUAAUGA GGUAAUAGCUGUAA
STMN2_ intron1	-	GTT T	137 6	GCTAAAAATATTAAT GAGGTAATAGCTGTA	338 2	GCUAAAAAUUUAAUG AGGUAAUAGCUGUA
STMN2_ intron1	-	TTTC	137 7	AATGCAACAAATAAA AGTTTGCTAAAAATA	338 3	AAUGCAACAAAUAAAA GUUUGCUAAAAUA
STMN2_ intron1	-	CTTT	137 8	CAATGCAACAAATAA AAGTTTGCTAAAAAT	338 4	CAAUGCAACAAAUAAA AGUUUGCUAAAAAU
STMN2_ intron1	-	ATT A	137 9	AACTGCTTTCAATGC AACAAATAAAAGTT	338 5	AAACUGCUUUCAAUGC AACAAAUAAAAGUU
STMN2_ intron1	-	TTT G	138 0	AAAAATAAAAACCCA AAGTAATTAAAACCTG	338 6	AAAAAUAAAACCCAA AGUAAUUAAAACUG
STMN2_ intron1	-	ATT T	138 1	GAAAAATAAAAACCC AAAGTAATTAAAACCT	338 7	GAAAAAUAAAACCCA AAGUAAUUAAAACU
STMN2_ intron1	-	ATT A	138 2	GTAATTTGAAAAATA AAAACCCAAAGTAAT	338 8	GUAAUUUGAAAAAUAA AAACCCAAAGUAAU
STMN2_ intron1	-	ATT C	138 3	CACCATCTATCCATTA GTAATTTGAAAAAT	338 9	CACCAUCUAUCCAUA GUAAUUUGAAAAAU
STMN2_ intron1	-	CTT A	138 4	TTCCACCATCTATCCA TTAGTAATTTGAAA	339 0	UCCACCAUCUAUCCA UUAGUAAUUUGAAA
STMN2_ intron1	-	ATT A	138 5	AATGCTTATTCCACCA TCTATCCATTAGTA	339 1	AAUGCUUAUCCACCA UCUAUCCAUAUAGUA

STMN2_ intron1	-	ATT G	138 6	TGCCAAATGATTAAAT GCTTATTCCACCAT	339 2	UGCCAAAUGAUUAAA GCUUAUUCCACCAU
STMN2_ intron1	-	TTT G	138 7	ATGGAAGTCATATTGT GCCAAATGATTAAA	339 3	AUGGAAGUCAUAAUGU GCCAAAUGAUUAAA
STMN2_ intron1	-	ATT T	138 8	GATGGAAGTCATATT GTGCCAAATGATTAA	339 4	GAUGGAAGUCAUAAUG UGCCAAAUGAUUAA
STMN2_ intron1	-	TTT A	138 9	ATCACTGAGAATGAG CTATTTGATGGAAGT	339 5	AUCACUGAGAAUGAGC UAUUUGAUGGAAGU
STMN2_ intron1	-	TTTT	139 0	AATCACTGAGAATGA GCTATTTGATGGAAG	339 6	AAUCACUGAGAAUGAG CUAUUUGAUGGAAG
STMN2_ intron1	-	TTTT	139 1	TAATCACTGAGAATG AGCTATTTGATGGAA	339 7	UAAUCACUGAGAAUGA GCUAUUUGAUGGAA
STMN2_ intron1	-	TTTT	139 2	TTAATCACTGAGAATG AGCTATTTGATGGA	339 8	UUAUCACUGAGAAUG AGCUAUUUGAUGGA
STMN2_ intron1	-	ATT T	139 3	TTAATCACTGAGAAT GAGCTATTTGATGG	339 9	UUUAAUCACUGAGAAU GAGCUAUUUGAUGG
STMN2_ intron1	-	CTT G	139 4	TAGCATTTTTTAATCA CTGAGAATGAGCTA	340 0	UAGCAUUUUUAAUCA CUGAGAAUGAGCUA
STMN2_ intron1	-	ATT G	139 5	TAGCCTCTGTAGCAT TTTTTAATCACTGA	340 1	UAGCCUCUUGUAGCAU UUUUUAAUCACUGA
STMN2_ intron1	-	TTTC	139 6	CTGAATCTGAGTAAAT TGTAGCCTCTTGTA	340 2	CUGAAUCUGAGUAAA UGUAGCCUCUUGUA
STMN2_ intron1	-	TTT A	139 7	GAATAGAATAATTTA CTACAAATCTGTAAG	340 3	GAAUAGAAUAAUUUAC UACAAAUCUGUAAG
STMN2_ intron1	-	ATT T	139 8	ACTACAAATCTGTAA GTCACATTATTGTAA	340 4	ACUACAAAUCUGUAAG UCACAUUAAUUGUAA
STMN2_ intron1	-	TTT A	139 9	CTACAAATCTGTAAGT CACATTATTGTAAA	340 5	CUACAAAUCUGUAAGU CACAUUAAUUGUAAA
STMN2_ intron1	-	ATT A	140 0	TTGTAAAAAAAACCC ATTGTGAATTTTGAC	340 6	UUGUAAAAAAAACCA UUGUGAAUUUUGAC
STMN2_ intron1	-	CTT A	140 1	CTCACCTGGTATAAAC TAAATACATGAGAT	340 7	CUCACCUGGUAAUAAAC UAAAUACAUGAGAU
STMN2_ intron1	-	ATT G	140 2	CAGGCTCAGCTTACTC ACCTGGTATAAACT	340 8	CAGGCUCAGCUUACUC ACCUGGUAAUAAACU
STMN2_ intron1	-	TTT A	140 3	TTGCAGGCTCAGCTTA CTCACCTGGTATAA	340 9	UUGCAGGCUCAGCUUA CUCACCUGGUAAUA
STMN2_ intron1	-	GTT T	140 4	ATTGCAGGCTCAGCTT ACTCACCTGGTATA	341 0	AUUGCAGGCUCAGCUU ACUCACCUGGUAAUA
STMN2_ intron1	-	GTT A	140 5	CACTGGGACAGAGAG TGTTTATTGCAGGCT	341 1	CACUGGGACAGAGAGU GUUUAUUGCAGGCU
STMN2_ intron1	-	ATT C	140 6	TAGCTACCTGCGACGT GTTACACTGGGACA	341 2	UAGCUACCUGCGACGU GUUACACUGGGACA
STMN2_ intron1	-	TTT A	140 7	TCCTATCATTCTAGCT ACCTGCGACGTGTT	341 3	UCCUAUCAUUCUAGCU ACCUGCGACGUGUU

STMN2_ intron1	-	ATT T	140 8	ATCCTATCATTCTAGC TACCTGCGACGTGT	341 4	AUCCUAUCAUUCUAGC UACCUGCGACGUGU
STMN2_ intron1	-	ATT A	140 9	ATTTATCCTATCATTC TAGCTACCTGCGAC	341 5	AUUUAUCCUAUCAUUC UAGCUACCUGCGAC
STMN2_ intron1	-	TTT A	141 0	ACGTGCATAGACAAA CACCACAAGGTCTAT	341 6	ACGUGCAUAGACAAAC ACCACAAGGUCUAU
STMN2_ intron1	-	TTTT	141 1	AACGTGCATAGACAA ACACCACAAGGTCTA	341 7	AACGUGCAUAGACAAA CACCACAAGGUCUA
STMN2_ intron1	-	ATT T	141 2	TAACGTGCATAGACA AACACCACAAGGTCT	341 8	UAACGUGCAUAGACAA ACACCACAAGGUCU
STMN2_ intron1	-	TTTC	141 3	TCTCAGAGAATTTTAA CGTGCATAGACAAA	341 9	UCUCAGAGAAUUUUAA CGUGCAUAGACAAA
STMN2_ intron1	-	ATT T	141 4	CCTGAATCTGAGTAA ATTGTAGCCTCTTGT	342 0	CCUGAAUCUGAGUAAA UUGUAGCCUCUUGU
STMN2_ intron1	-	CTTT	141 5	CTCTCAGAGAATTTTA ACGTGCATAGACAA	342 1	CUCUCAGAGAAUUUUA ACGUGCAUAGACAA
STMN2_ intron1	-	TTTT	141 6	AAAATATACTTTCTCT CAGAGAATTTTAAC	342 2	AAAAUAUACUUCUCUC CAGAGAAUUUUAAC
STMN2_ intron1	-	ATT T	141 7	TAAAATATACTTTCTC TCAGAGAATTTTAA	342 3	UAAAAUAUACUUCUC UCAGAGAAUUUUA
STMN2_ intron1	-	ATT A	141 8	TCATTTTAAAATATAC TTTCTCTCAGAGAA	342 4	UCAUUUUAAAAUAUAC UUUCUCUCAGAGAA
STMN2_ intron1	-	CTT A	141 9	ATTATCATTTTAAAAT ATACTTTCTCTCAG	342 5	AUUAUCAUUUUAAAAU AUACUUCUCUCAG
STMN2_ intron1	-	TTT A	142 0	ATAGCACAAATGTCC AATCTTAATTATCAT	342 6	AUAGCACAAUGUCCA AUCUUAUUUAUCAU
STMN2_ intron1	-	TTTT	142 1	AATAGCACAAATGTC CAATCTTAATTATCA	342 7	AAUAGCACAAUGUCC AAUCUUAUUUAUCA
STMN2_ intron1	-	ATT T	142 2	TAATAGCACAAATGT CCAATCTTAATTATC	342 8	UAAUAGCACAAUGUC CAAUCUUAUUUAUC
STMN2_ intron1	-	GTT G	142 3	TAGATTTTAATAGCAC AAATGTCCAATCTT	342 9	UAGAUUUAAUAGCAC AAUGUCCAAUCUU
STMN2_ intron1	-	TTT G	142 4	ACTAAAGTTGTAGATT TTAATAGCACAAAT	343 0	ACUAAAGUUGUAGAUU UUAAUAGCACAAAU
STMN2_ intron1	-	TTTT	142 5	GACTAAAGTTGTAGA TTTTAATAGCACAAA	343 1	GACUAAAGUUGUAGAU UUUAAUAGCACAAA
STMN2_ intron1	-	ATT T	142 6	TGACTAAAGTTGTAG ATTTTAATAGCACAA	343 2	UGACUAAAGUUGUAGA UUUUAAUAGCACAA
STMN2_ intron1	-	ATT G	142 7	TGAATTTTGACTAAAG TTGTAGATTTTAAT	343 3	UGAAUUUUGACUAAAG UUGUAGAUUUUAAU
STMN2_ intron1	-	ATT G	142 8	TAAAAAAAACCATT GTGAATTTTGACTAA	343 4	UAAAAAAAACCAUUG UGAAUUUUGACUAA
STMN2_ intron1	-	TTT A	142 9	AAATATACTTTCTCTC AGAGAATTTTAACG	343 5	AAAUAUACUUCUCUC AGAGAAUUUUAACG

STMN2_ intron1	-	ATT G	143 0	ATAAACTACTGCCATT TCTTTTCAGTTTTAT	343 6	AUAAACUACUGCCA UCUUUCAGUUUUUAU
STMN2_ intron1	-	CTT A	143 1	TGGCACTCTGAAAGG ACATTTTCCTGAATCT	343 7	UGGCACUCUGAAAGGA CAUUUCCUGAAUCU
STMN2_ intron1	-	TTT A	143 2	TTATATGAATCAGCCT TATGGCACTCTGAA	343 8	UUUAUAUGAAUCAGCCU UAUGGCACUCUGAA
STMN2_ intron1	-	CTTT	143 3	TTTCAGCCTCCTGTGA GCAATGAGCTACCA	343 9	UUUCAGCCUCCUGUGA GCAAUGAGCUACCA
STMN2_ intron1	-	CTT C	143 4	CTCCTGCTCGGAGGCC AGCTTTTTTCAGCC	344 0	CUCCUGCUCGGAGGCC AGCUUUUUUCAGCC
STMN2_ intron1	-	TTT G	143 5	TGCTCTGAGCTTCCTC CTGCTCGGAGGCCA	344 1	UGCUCUGAGCUUCCUC CUGCUCGGAGGCCA
STMN2_ intron1	-	GTT T	143 6	GTGCTCTGAGCTTCCT CCTGCTCGGAGGCC	344 2	GUGCUCUGAGCUUCCU CCUGCUCGGAGGCC
STMN2_ intron1	-	GTT C	143 7	GCTATCAGCAGCTCCC AGTGGCCACGCCCA	344 3	GCUAUCAGCAGCUCCC AGUGGCCACGCCCA
STMN2_ intron1	-	CTT C	143 8	CCACGACCAAAAAAG AAACTGGTGTGAGCT	344 4	CCACGACCAAAAAAGA AACUGGUGUGAGCU
STMN2_ intron1	-	TTTC	143 9	TTCCCACGACCAAAA AAGAACTGGTGTGA	344 5	UUCCCACGACCAAAA AGAAACUGGUGUGA
STMN2_ intron1	-	TTTT	144 0	CTTCCCACGACCAAAA AAGAACTGGTGTG	344 6	CUUCCCACGACCAAAA AAGAAACUGGUGUG
STMN2_ intron1	-	TTTT	144 1	TCTTCCCACGACCAAA AAAGAACTGGTGT	344 7	UCUUCCCACGACCAAA AAAGAAACUGGUGU
STMN2_ intron1	-	GTT T	144 2	TTCTTCCCACGACCAA AAAAGAACTGGTG	344 8	UUCUUCCCACGACCAA AAAAGAAACUGGUG
STMN2_ intron1	-	CTT G	144 3	TGACAACAGGATAAT ATGTGTTTTTCTTCC	344 9	UGACAACAGGAUAAUA UGUGUUUUUCUCC
STMN2_ intron1	-	TTTC	144 4	ATATAAGGTCACAGA TCTTGTGACAACAGG	345 0	AUAUAAGGUCACAGAU CUUGUGACAACAGG
STMN2_ intron1	-	TTTT	144 5	CATATAAGGTCACAG ATCTTGTGACAACAG	345 1	CAUAUAAGGUCACAGA UCUUGUGACAACAG
STMN2_ intron1	-	TTTT	144 6	TCATATAAGGTCACA GATCTTGTGACAACA	345 2	UCAUAUAAGGUCACAG AUCUUGUGACAACA
STMN2_ intron1	-	TTTT	144 7	TTCATATAAGGTCACA GATCTTGTGACAAC	345 3	UUCAUAUAAGGUCACA GAUCUUGUGACAAC
STMN2_ intron1	-	ATT T	144 8	TTTCATATAAGGTCAC AGATCTTGTGACAA	345 4	UUUCAUAUAAGGUCAC AGAUCUUGUGACAA
STMN2_ intron1	-	ATT C	144 9	TAGCATTTTTTTCATAT AAGGTCACAGATCT	345 5	UAGCAUUUUUCAUAU AAGGUCACAGAUCU
STMN2_ intron1	-	TTT A	145 0	ATGAAAAAATTCTAG CATTTTTTCATATAA	345 6	AUGAAAAAAUUCUAGC AUUUUUUCAUAUA
STMN2_ intron1	-	TTTT	145 1	AATGAAAAAATTCTA GCATTTTTTCATATA	345 7	AAUGAAAAAAUUCUAG CAUUUUUCAUAUA

STMN2_ intron1	-	TTTT	145 2	TAATGAAAAAATTCT AGCATTTTTTCATAT	345 8	UAAUGAAAAAAUUCUA GCAUUUUUUCUAU
STMN2_ intron1	-	TTTT	145 3	TTAATGAAAAAATTCT AGCATTTTTTCATA	345 9	UUAUGAAAAAAUUCU AGCAUUUUUUCUA
STMN2_ intron1	-	CTTT	145 4	TTTAATGAAAAAATTC TAGCATTTTTTCAT	346 0	UUUAAUGAAAAAAUUC UAGCAUUUUUUCAU
STMN2_ intron1	-	TTTC	145 5	TTTTTTAATGAAAAAA TTCTAGCATTTTTT	346 1	UUUUUAAUGAAAAAA UUCUAGCAUUUUU
STMN2_ intron1	-	TTTT	145 6	CTTTTTTAATGAAAAA ATTCTAGCATTTTT	346 2	CUUUUUUAAUGAAAAA AUUCUAGCAUUUU
STMN2_ intron1	-	ATT T	145 7	TCTTTTTTAATGAAAA AATTCTAGCATTTT	346 3	UCUUUUUAAUGAAAA AAUUCUAGCAUUU
STMN2_ intron1	-	GTT C	145 8	AGTATTTTCTTTTTTA ATGAAAAAATTCTA	346 4	AGUAUUUUCUUUUUA AUGAAAAAUUCUA
STMN2_ intron1	-	GTT C	145 9	TGAAAACATCTGGGT CACTGGCTAGTTCAG	346 5	UGAAAACAUCUGGGUC ACUGGCUAGUUCAG
STMN2_ intron1	-	TTTT	146 0	TTCAGCCTCCTGTGAG CAATGAGCTACCAA	346 6	UUCAGCCUCCUGUGAG CAAUGAGCUACCAA
STMN2_ intron1	-	TTTT	146 1	TCAGCCTCCTGTGAGC AATGAGCTACCAAG	346 7	UCAGCCUCCUGUGAGC AAUGAGCUACCAAG
STMN2_ intron1	-	TTTT	146 2	CAGCCTCCTGTGAGCA ATGAGCTACCAAGG	346 8	CAGCCUCCUGUGAGCA AUGAGCUACCAAGG
STMN2_ intron1	-	TTTC	146 3	AGCCTCCTGTGAGCAA TGAGCTACCAAGGT	346 9	AGCCUCCUGUGAGCAA UGAGCUACCAAGGU
STMN2_ intron1	-	TTTT	146 4	ATTATATGAATCAGCC TTATGGCACTCTGA	347 0	AUUAUAUGAAUCAGCC UUAUGGCACUCUGA
STMN2_ intron1	-	ATT T	146 5	TATTATATGAATCAGC CTTATGGCACTCTG	347 1	UAUAUAUGAAUCAGC CUUAUGGCACUCUG
STMN2_ intron1	-	ATT A	146 6	TAGGGAAGAAACTA TTTTATTATATGAAT	347 2	UAGGGAAGAAAACUAU UUUAUAUAUGAAU
STMN2_ intron1	-	CTT A	146 7	AATTATAGGGAAGAA AACTATTTTATTATA	347 3	AAUAUAAGGGAAGAAA ACUAUUUUAUAUA
STMN2_ intron1	-	TTT G	146 8	ATCTTAAATTATAGGG AAGAAAACATTTTT	347 4	AUCUUAUUUAUAGGG AAGAAAACUAUUU
STMN2_ intron1	-	ATT T	146 9	GATCTTAAATTATAGG GAAGAAAACATTTT	347 5	GAUCUUAUUUAUAGG GAAGAAAACUAUUU
STMN2_ intron1	-	ATT C	147 0	ACAGAACTAAGTAAC TATTTGATCTTAAAT	347 6	ACAGAACUAAGUAACU AUUGAUCUUAUU
STMN2_ intron1	-	TTT G	147 1	ATAGCTACTGCTAGGT ATTCACAGAACTAA	347 7	AUAGCUACUGCUAGGU AUUCACAGAACUA
STMN2_ intron1	-	GTT T	147 2	GATAGCTACTGCTAG GTATTCACAGAACTA	347 8	GAUAGCUACUGCUAGG UAUUCACAGAACUA
STMN2_ intron1	-	ATT C	147 3	TGTTTGATAGCTACTG CTAGGTATTCACAG	347 9	UGUUUGAUAGCUACUG CUAGGUUAUUCACAG

STMN2_ intron1	-	TTT A	147 4	AAATTCTGTTTGATAG CTACTGCTAGGTAT	348 0	AAAUUCUGUUUGAUAG CUACUGCUAGGUAU
STMN2_ intron1	-	CTTT	147 5	AAAATTCTGTTTGATA GCTACTGCTAGGTA	348 1	AAAAUUCUGUUUGAUA GCUACUGCUAGGUA
STMN2_ intron1	-	TTT A	147 6	ACTTTAAAATTCTGTT TGATAGCTACTGCT	348 2	ACUUUAAAAUUCUGUU UGAUAGCUACUGCU
STMN2_ intron1	-	ATT A	147 7	TATGAATCAGCCTTAT GGCACTCTGAAAGG	348 3	UAUGAAUCAGCCUUAU GGCACUCUGAAAGG
STMN2_ intron1	-	ATT T	147 8	AACTTTAAAATTCTGT TTGATAGCTACTGC	348 4	AACUUUAAAAUUCUGU UUGAUAGCUACUGC
STMN2_ intron1	-	GTT A	147 9	GTTGTACAGATTTAAC TTTAAAATTCTGTT	348 5	GUUGUACAGAUUUAAC UUUAAAAUUCUGUU
STMN2_ intron1	-	ATT G	148 0	TTAGTTGTACAGATTT AACTTTAAAATTCT	348 6	UUAGUUGUACAGAUUU AACUUUAAAAUUCU
STMN2_ intron1	-	CTT C	148 1	ATTGTTAGTTGTACAG ATTTAACTTTAAAA	348 7	AUUGUUAGUUGUACAG AUUUAACUUUAAAA
STMN2_ intron1	-	ATT C	148 2	ATCCTCCACTTCATTG TTAGTTGTACAGAT	348 8	AUCCUCCACUUCAUUG UUAGUUGUACAGAU
STMN2_ intron1	-	ATT C	148 3	AATATGTATCGATTCA TCCTCCACTTCATT	348 9	AAUAUGUAUCGAUUCA UCCUCCACUUCAUU
STMN2_ intron1	-	CTT C	148 4	CATTCAATATGTATCG ATTCATCCTCCACT	349 0	CAUUCAAUAUGUAUCG AUUCAUCCUCCACU
STMN2_ intron1	-	TTT A	148 5	TCAATGACAAAGTCTT CCATTCAATATGTA	349 1	UCAUGACAAAGUCUU CCAUUCAAUAUGUA
STMN2_ intron1	-	ATT T	148 6	ATCAATGACAAAGTC TTCCATTCAATATGT	349 2	AUCAUGACAAAGUCU UCCAUUCAAUAUGU
STMN2_ intron1	-	TTTC	148 7	CTAAAGATGGCCTGA ATTTATCAATGACAA	349 3	CUAAAGAUGGCCUGAA UUUAUCA AUGACAA
STMN2_ intron1	-	TTTT	148 8	CCTAAAGATGGCCTG AATTTATCAATGACA	349 4	CCUAAAGAUGGCCUGA AUUUAUCA AUGACA
STMN2_ intron1	-	ATT T	148 9	TCCTAAAGATGGCCTG AATTTATCAATGAC	349 5	UCCUAAAGAUGGCCUG AAUUUAUCA AUGAC
STMN2_ intron1	-	ATT G	149 0	ATAAATCCGGAATTTT CCTAAAGATGGCCT	349 6	AUAAAUCCGGAUUUUU CCUAAAGAUGGCCU
STMN2_ intron1	-	GTT G	149 1	AAGTAAAAAATAATG GTGATTGATAAATCC	349 7	AAGUAAAAAAUAAUGG UGAUUGAUAAAUCC
STMN2_ intron1	-	GTT G	149 2	TACAGATTTAACTTTA AAATTCTGTTTGAT	349 8	UACAGAUUUAACUUUA AAAUUCUGUUUGAU
STMN2_ intron1	+	GTT C	149 3	CTCACCTTGGTGGAT TTAGTCTTTTGCAG	349 9	CUCACCCUUGGUGGAU UUAGUCUUUUGCAG
STMN2_ intron1	-	TTTC	149 4	AATCGATGAAGAAGT AAACAATGATTTTCT	350 0	AAUCGAUGAAGAAGUA AACAAUGAUUUUCU
STMN2_ intron1	+	GTT C	149 5	TGAAGCCTGTGCCAG GTATTATGAGAACAA	350 1	UGAAGCCUGUGCCAGG UAUUAUGAGAACAA

STMN2_ intron1	+	GTT A	149 6	CTTAGTTCTGTGAATA CCTAGCAGTAGCTA	350 2	CUUAGUUCUGUGAAUA CCUAGCAGUAGCUA
STMN2_ intron1	+	TTT A	149 7	AGATCAAATAGTTACT TAGTTCTGTGAATA	350 3	AGAUCAAAUAGUUACU UAGUUCUGUGAAUA
STMN2_ intron1	+	ATT T	149 8	AAGATCAAATAGTTA CTTAGTTCTGTGAAT	350 4	AAGAUCAAAUAGUUAC UUAGUUCUGUGAAU
STMN2_ intron1	+	CTT C	149 9	CCTATAATTTAAGATC AAATAGTTACTTAG	350 5	CCUAUAAUUUAAGAUC AAAUAGUUACUAG
STMN2_ intron1	+	TTTC	150 0	TTCCCTATAATTTAAG ATCAAATAGTTACT	350 6	UUCCCUAUAAUUUAAG AUCAAAUAGUUACU
STMN2_ intron1	+	TTTT	150 1	CTTCCCTATAATTTAA GATCAAATAGTTAC	350 7	CUUCCCUAUAAUUUAA GAUCAAUAGUUAC
STMN2_ intron1	+	GTT T	150 2	TCTTCCCTATAATTTA AGATCAAATAGTTA	350 8	UCUCCCUAUAAUUUA AGAUCAAUAGUUA
STMN2_ intron1	+	ATT C	150 3	ATATAATAAAATAGTT TTCTTCCCTATAAT	350 9	AUAUAAUAAAAUAGUU UUCUCCCUAUAAU
STMN2_ intron1	+	TTTC	150 4	AGAGTGCCATAAGGC TGATTCATATAATAA	351 0	AGAGUGCCAUAAAGGC GAUUCAUUAAUAA
STMN2_ intron1	+	CTTT	150 5	CAGAGTGCCATAAGG CTGATTCATATAATA	351 1	CAGAGUGCCAUAAAGGC UGAUUCAUAAUAA
STMN2_ intron1	+	ATT C	150 6	AGGAAATGTCCTTTCA GAGTGCCATAAGGC	351 2	AGGAAAUGUCCUUUCA GAGUGCCAUAAAGGC
STMN2_ intron1	+	TTT A	150 7	CTCAGATTCAGGAAA TGTCCTTTCAGAGTG	351 3	CUCAGAUUCAGGAAAU GUCCUUUCAGAGUG
STMN2_ intron1	+	ATT T	150 8	ACTCAGATTCAGGAA ATGTCCTTTCAGAGT	351 4	ACUCAGAUUCAGGAAA UGUCCUUUCAGAGU
STMN2_ intron1	+	ATT A	150 9	AAAAATGCTACAAGA GGCTACAATTTACTC	351 5	AAAAAUGCUACAAGAG GCUACAAUUUACUC
STMN2_ intron1	+	ATT C	151 0	TCAGTGATTAAAAAA TGCTACAAGAGGCTA	351 6	UCAGUGAUUAAAAAAU GCUACAAGAGGCUA
STMN2_ intron1	+	CTT C	151 1	CATCAAATAGCTCATT CTCAGTGATTAAAA	351 7	CAUCAAUAGCUCAUU CUCAGUGAUUAAAA
STMN2_ intron1	+	TTT G	151 2	GCACAATATGACTTCC ATCAAATAGCTCAT	351 8	GCACAAUAGACUCC AUCAAUAGCUCAU
STMN2_ intron1	+	ATT T	151 3	GGCACAATATGACTTC CATCAAATAGCTCA	351 9	GGCACAAUAGACUUC CAUCAAUAGCUCA
STMN2_ intron1	+	TTT A	151 4	ATCATTTGGCACAATA TGACTTCCATCAAA	352 0	AUCAUUUGGCACAAUA UGACUCCAUCAAA
STMN2_ intron1	+	ATT T	151 5	AATCATTTGGCACAAT ATGACTTCCATCAA	352 1	AAUCAUUUGGCACAAU AUGACUCCAUCAA
STMN2_ intron1	+	ATT A	151 6	CTAATGGATAGATGG TGGAATAAGCATTTA	352 2	CUAUUGGAUAGAUGGU GGAAUAAGCAUUUA
STMN2_ intron1	+	TTTC	151 7	AAATTACTAATGGAT AGATGGTGGAAATAAG	352 3	AAAUUACUAAUGGAUA GAUGGUGGAAUAAG

STMN2_ intron1	+	TTTT	151 8	CAAATTACTAATGGAT AGATGGTGGGAATAA	352 4	CAAAUUACUAAUGGAU AGAUGGUGGAAUAA
STMN2_ intron1	+	TTTT	151 9	TCAAATTACTAATGGA TAGATGGTGGGAATA	352 5	UCAAUUACUAAUGGA UAGAUGGUGGAAUA
STMN2_ intron1	+	ATT T	152 0	TTCAAATTACTAATGG ATAGATGGTGGGAAT	352 6	UUCAAAUUACUAAUGG AUAGAUGGUGGAAU
STMN2_ intron1	+	TTT A	152 1	TTTTTCAAATTACTAA TGGATAGATGGTGG	352 7	UUUUUCAAUUACUAA UGGAUAGAUGGUGG
STMN2_ intron1	+	TTTT	152 2	ATTTTTCAAATTACTA ATGGATAGATGGTG	352 8	AUUUUUCAAUUACUA AUGGAUAGAUGGUG
STMN2_ intron1	+	CTT A	152 3	GTTCTGTGAATACCTA GCAGTAGCTATCAA	352 9	GUUCUGUGAAUACCUA GCAGUAGCUAUCAA
STMN2_ intron1	+	TTTT	152 4	TATTTTTCAAATTACT AATGGATAGATGGT	353 0	UAUUUUCAAUUACU AAUGGAUAGAUGGU
STMN2_ intron1	+	GTT C	152 5	TGTGAATACCTAGCA GTAGCTATCAAACAG	353 1	UGUGAAUACCUAGCAG UAGCUAUCAAACAG
STMN2_ intron1	+	TTTT	152 6	AAAGTTAAATCTGTAC AACTAACAATGAAG	353 2	AAAGUAAAUCUGUAC AACUAACAAUGAAG
STMN2_ intron1	+	TTTT	152 7	GGTCGTGGGAAGAAA AACACATATTATCCT	353 3	GGUCGUGGGAAGAAAA ACACAUUUUAUCCU
STMN2_ intron1	+	TTTT	152 8	TGGTCGTGGGAAGAA AAACACATATTATCC	353 4	UGGUCGUGGGAAGAAA AACACAUUUUAUCC
STMN2_ intron1	+	TTTT	152 9	TTGGTCGTGGGAAGA AAAACACATATTATC	353 5	UUGGUCGUGGGAAGAA AAACACAUUUUAUC
STMN2_ intron1	+	CTTT	153 0	TTTGGTCGTGGGAAG AAAAACACATATTAT	353 6	UUUGGUCGUGGGAAGA AAAACACAUUUUAU
STMN2_ intron1	+	TTTC	153 1	TTTTTTGGTCGTGGGA AGAAAAACACATAT	353 7	UUUUUUGGUCGUGGGA AGAAAAACACAUAU
STMN2_ intron1	+	GTT T	153 2	CTTTTTTGGTCGTGGG AAGAAAAACACATA	353 8	CUUUUUUGGUCGUGGG AAGAAAAACACAU
STMN2_ intron1	+	ATT G	153 3	CTCACAGGAGGCTGA AAAAAGCTGGCCTCC	353 9	CUCACAGGAGGCUGAA AAAAGCUGGCCUCC
STMN2_ intron1	+	CTT G	153 4	GTAGCTCATTGCTCAC AGGAGGCTGAAAAA	354 0	GUAGCUCAUUGCUCAC AGGAGGCUGAAAAA
STMN2_ intron1	+	CTT C	153 5	AACTGAGTGTGACTG ATCACATGCTCAGGC	354 1	AACUGAGUGUGACUGA UCACAUGCUCAGGC
STMN2_ intron1	+	TTT A	153 6	CTTCAACTGAGTGTGA CTGATCACATGCTC	354 2	CUUCAACUGAGUGUGA CUGAUCACAUGCUC
STMN2_ intron1	+	TTTT	153 7	ACTTCAACTGAGTGTG ACTGATCACATGCT	354 3	ACUUCAACUGAGUGUG ACUGAUCACAUGCUC
STMN2_ intron1	+	TTTT	153 8	TACTTCAACTGAGTGT GACTGATCACATGC	354 4	UACUUCAACUGAGUGU GACUGAUCACAUGC
STMN2_ intron1	+	TTTT	153 9	TTACTTCAACTGAGTG TGACTGATCACATG	354 5	UUACUUCAACUGAGUG UGACUGAUCACAUG

STMN2_ intron1	+	ATT T	154 0	TTTACTTCAACTGAGT GTGACTGATCACAT	354 6	UUUACUUCAACUGAGU GUGACUGAUCACAU
STMN2_ intron1	+	ATT A	154 1	TTTTTTACTTCAACTG AGTGTGACTGATCA	354 7	UUUUUUACUUCAACUG AGUGUGACUGAUCA
STMN2_ intron1	+	TTT A	154 2	TCAATCACCATTATTT TTTACTTCAACTGA	354 8	UCAAUCACCAUUAUUU UUUACUUCAACUGA
STMN2_ intron1	+	ATT T	154 3	ATCAATCACCATTATT TTTTACTTCAACTG	354 9	AUCAAUCACCAUUAUU UUUUACUUCAACUG
STMN2_ intron1	+	ATT C	154 4	CGGATTTATCAATCAC CATTATTTTTTACT	355 0	CGGAUUUAUCAAUAC CAUUAUUUUUUACU
STMN2_ intron1	+	TTT A	154 5	GGAAAATTCCGGATTT ATCAATCACCATTA	355 1	GGAAAAUUCGGAUUU AUCAAUCACCAUUA
STMN2_ intron1	+	CTTT	154 6	AGGAAAATTCCGGAT TTATCAATCACCATT	355 2	AGGAAAAUUCGGAUU UAUCAAUACCAUU
STMN2_ intron1	+	ATT C	154 7	AGGCCATCTTTAGGA AAATTCGGGATTAT	355 3	AGGCCAUCUUUAGGAA AAUUCGGGAUUUAU
STMN2_ intron1	+	ATT G	154 8	ATAAATTCAGGCCATC TTTAGGAAAATTCC	355 4	AUAAAUUCAGGCCAUC UUUAGGAAAAUUC
STMN2_ intron1	+	TTT G	154 9	TCATTGATAAATTCAG GCCATCTTTAGGAA	355 5	UCAUUGAUAAAUUCAG GCCAUCUUUAGGAA
STMN2_ intron1	+	CTTT	155 0	GTCATTGATAAATTC GGCCATCTTTAGGA	355 6	GUCAUUGAUAAAUUC GGCCAUCUUUAGGA
STMN2_ intron1	+	ATT G	155 1	AATGGAAGACTTTGTC ATTGATAAATTCAG	355 7	AAUGGAAGACUUUGUC AUUGAUAAAUUCAG
STMN2_ intron1	+	GTT A	155 2	AATCTGTACAACAAAC AATGAAGTGGAGGA	355 8	AAUCUGUACAACUAAC AAUGAAGUGGAGGA
STMN2_ intron1	+	TTT A	155 3	AAGTTAAATCTGTACA ACTAACAATGAAGT	355 9	AAGUUAAAUCUGUACA ACUAACAAUGAAGU
STMN2_ intron1	+	ATT T	155 4	TAAAGTTAAATCTGTA CAACTAACAATGAA	356 0	UAAAGUUAAAUCUGUA CAACUAACAAUGAA
STMN2_ intron1	+	GTT T	155 5	TTATTTTTCAAATTAC TAATGGATAGATGG	356 1	UUUUUUUCAAUUUAC UAAUGGAUAGAUGG
STMN2_ intron1	+	TTT G	155 6	GGTTTTTATTTTTCAA ATTACTAATGGATA	356 2	GGUUUUUAUUUUUCA AUUACUAAUGGAUA
STMN2_ intron1	+	CTTT	155 7	GGGTTTTTATTTTTCA AATTACTAATGGAT	356 3	GGGUUUUAUUUUUCA AAUUACUAAUGGAU
STMN2_ intron1	+	TTTT	155 8	TTACAATAATGTGACT TACAGATTTGTAGT	356 4	UUACAAUAAUGUGACU UACAGAUUUGUAGU
STMN2_ intron1	+	TTTT	155 9	TTTACAATAATGTGAC TTACAGATTTGTAG	356 5	UUUACAAUAAUGUGAC UUACAGAUUUGUAG
STMN2_ intron1	+	TTTT	156 0	TTTTACAATAATGTGA CTTACAGATTTGTA	356 6	UUUUACAAUAAUGUGA CUUACAGAUUUGUA
STMN2_ intron1	+	TTTT	156 1	TTTTTACAATAATGTG ACTTACAGATTTGT	356 7	UUUUUACAAUAAUGUG ACUUACAGAUUUGU

STMN2_ intron1	+	GTT T	156 2	TTTTTTACAATAATGT GACTTACAGATTTG	356 8	UUUUUUACAAUAAUGU GACUUACAGAUUUG
STMN2_ intron1	+	ATT C	156 3	ACAATGGTTTTTTTTT ACAATAATGTGACT	356 9	ACAAUGGUUUUUUUUU ACAAUAAUGUGACU
STMN2_ intron1	+	TTT A	156 4	GTCAAAATTCACAAT GGTTTTTTTTTTACAA	357 0	GUCAAAAUUCACAAUG GUUUUUUUUUACAA
STMN2_ intron1	+	CTTT	156 5	AGTCAAAATTCACAA TGGTTTTTTTTTACA	357 1	AGUCAAAUUCACAAU GGUUUUUUUUUACA
STMN2_ intron1	+	ATT A	156 6	AAATCTACAACCTTAG TCAAAATTCACAAT	357 2	AAAUUCUACAACUUAG UCAAAAUUCACAAU
STMN2_ intron1	+	TTT G	156 7	TGCTATTAAAATCTAC AACTTTAGTCAAAA	357 3	UGCUAUUAAAAUCUAC AACUUUAGUCAAAA
STMN2_ intron1	+	ATT T	156 8	GTGCTATTAAAATCTA CAACTTTAGTCAAA	357 4	GUGCUAUUAAAAUCUA CAACUUUAGUCAAA
STMN2_ intron1	+	ATT G	156 9	GACATTTGTGCTATTA AAATCTACAACCTT	357 5	GACAUUUGUGCUAUUA AAAUUCUACAACUUU
STMN2_ intron1	+	ATT A	157 0	AGATTGGACATTTGTG CTATTAAAATCTAC	357 6	AGAUUGGACAUUUGUG CUAUUAAAAUCUAC
STMN2_ intron1	+	TTT A	157 1	AAATGATAATTAAGA TTGGACATTTGTGCT	357 7	AAAUUGAUAAUUAAGAU UGGACAUUUGUGCU
STMN2_ intron1	+	TTTT	157 2	AAAATGATAATTAAG ATTGGACATTTGTGC	357 8	AAAUGAUAAUUAAGA UUGGACAUUUGUGC
STMN2_ intron1	+	ATT T	157 3	TAAAATGATAATTAA GATTGGACATTTGTG	357 9	UAAAAUGAUAAUUAAG AUUGGACAUUUGUG
STMN2_ intron1	+	ATT C	157 4	TCTGAGAGAAAGTAT ATTTTAAAATGATAA	358 0	UCUGAGAGAAAGUAUA UUUUAAAAUGAUAA
STMN2_ intron1	+	GTT A	157 5	AAATTCTCTGAGAGA AAGTATATTTTAAAA	358 1	AAAUUCUCUGAGAGAA AGUAUAUUUUAAAA
STMN2_ intron1	+	TTT G	157 6	TCTATGCACGTTAAAA TTCTCTGAGAGAAA	358 2	UCUAUGCACGUUAAAA UUCUCUGAGAGAAA
STMN2_ intron1	+	GTT T	157 7	GTCTATGCACGTTAAA ATTCTCTGAGAGAA	358 3	GUCUAUGCACGUUAAA AUUCUCUGAGAGAA
STMN2_ intron1	+	CTT G	157 8	TGGTGTGTTGTCTATGC ACGTTAAAATTCTC	358 4	UGGUGUUUGUCUAUGC ACGUUAAAAUUCUC
STMN2_ intron1	+	ATT A	157 9	ATAGACCTGTGGTGT TTGTCTATGCACGT	358 5	AUAGACCUUGUGGUGU UUGUCUAUGCACGU
STMN2_ intron1	+	TTT A	158 0	TACCAGGTGAGTAAG CTGAGCCTGCAATAA	358 6	UACCAGGUGAGUAAGC UGAGCCUGCAAUA
STMN2_ intron1	+	GTT T	158 1	ATACCAGGTGAGTAA GCTGAGCCTGCAATA	358 7	AUACCAGGUGAGUAAG CUGAGCCUGCAAUA
STMN2_ intron1	+	TTT A	158 2	GTTTATACCAGGTGAG TAAGCTGAGCCTGC	358 8	GUUUUAUACCAGGUGAG UAAGCUGAGCCUGC
STMN2_ intron1	+	ATT T	158 3	AGTTTATACCAGGTGA GTAAGCTGAGCCTG	358 9	AGUUUAUACCAGGUGA GUAAGCUGAGCCUG

STMN2_ intron1	+	ATT A	158 4	ATCTCATGTATTTAGT TTATACCAGGTGAG	359 0	AUCUCAUGUAUUUAGU UUUAUACCAGGUGAG
STMN2_ intron1	+	TTTT	158 5	TACAATAATGTGACTT ACAGATTTGTAGTA	359 1	UACAAUAAUGUGACUU ACAGAUUUGUAGUA
STMN2_ intron1	+	TTTT	158 6	ACAATAATGTGACTTA CAGATTTGTAGTAA	359 2	ACAAUAAUGUGACUUA CAGAUUUGUAGUAA
STMN2_ intron1	+	TTT A	158 7	CAATAATGTGACTTAC AGATTTGTAGTAAA	359 3	CAAUAAUGUGACUUAC AGAUUUGUAGUAAA
STMN2_ intron1	+	CTT A	158 8	CAGATTTGTAGTAAAT TATTCTATTCTAAA	359 4	CAGAUUUGUAGUAAA UAUUCUAUUCUAAA
STMN2_ intron1	+	ATT A	158 9	CTTTGGGTTTTTATTTT TCAAATTACTAAT	359 5	CUUUGGGUUUUUAUUU UUCAAAUAUACUAAU
STMN2_ intron1	+	TTT A	159 0	ATTACTTTGGGTTTTT ATTTTTCAAATTAC	359 6	AUUACUUUGGGUUUUU AUUUUCAAUUUAC
STMN2_ intron1	+	TTTT	159 1	AATTACTTTGGGTTTT TATTTTTCAAATTA	359 7	AAUUACUUUGGGUUUU UAUUUUUCAAUUUA
STMN2_ intron1	+	GTT T	159 2	TAATTACTTTGGGTTT TTATTTTTCAAATT	359 8	UAAUUACUUUGGGUUU UUUUUUUCAAUUU
STMN2_ intron1	+	ATT G	159 3	AAAGCAGTTTTAATTA CTTTGGGTTTTTAT	359 9	AAAGCAGUUUUAAUUA CUUUGGGUUUUUAU
STMN2_ intron1	+	GTT G	159 4	CATTGAAAGCAGTTTT AATTACTTTGGGTT	360 0	CAUUGAAAGCAGUUUU AAUUACUUUGGGUU
STMN2_ intron1	+	TTT G	159 5	TTGCATTGAAAGCAGT TTTAATTACTTTGG	360 1	UUGCAUUGAAAGCAGU UUUAAUUACUUUGG
STMN2_ intron1	+	ATT T	159 6	GTTGCATTGAAAGCA GTTTAAATTACTTTG	360 2	GUUGCAUUGAAAGCAG UUUUAAUUACUUUG
STMN2_ intron1	+	TTT A	159 7	TTTGTTGCATTGAAAG CAGTTTAAATTACT	360 3	UUUGUUGCAUUGAAAG CAGUUUUAAUUACU
STMN2_ intron1	+	TTTT	159 8	ATTTGTTGCATTGAAA GCAGTTTAAATTAC	360 4	AUUUGUUGCAUUGAAA GCAGUUUUAAUUAC
STMN2_ intron1	+	CTTT	159 9	TATTTGTTGCATTGAA AGCAGTTTTAATTA	360 5	UAUUUGUUGCAUUGAA AGCAGUUUUAAUUA
STMN2_ intron1	+	TTT A	160 0	GCAAACTTTTATTTGT TGCATTGAAAGCAG	360 6	GCAAACUUUUUUUUUGU UGCAUUGAAAGCAG
STMN2_ intron1	+	TTTT	160 1	AGCAAACTTTTATTTG TTGCATTGAAAGCA	360 7	AGCAAACUUUUUUUUUG UUGCAUUGAAAGCA
STMN2_ intron1	+	TTT G	160 2	GTCGTGGGAAGAAAA ACACATATTATCCTG	360 8	GUCGUGGGAAGAAAAA CACAUUUUAUCCUG
STMN2_ intron1	+	TTTT	160 3	TAGCAAACTTTTATTT GTTGCATTGAAAGC	360 9	UAGCAAACUUUUUUUU GUUGCAUUGAAAGC
STMN2_ intron1	+	ATT A	160 4	ATATTTTTAGCAAAC TTTATTTGTTGCAT	361 0	AUAUUUUUAGCAAACU UUUAUUUGUUGCAU
STMN2_ intron1	+	ATT A	160 5	CCTCATTAATATTTTT AGCAAACTTTTATT	361 1	CCUCAUUAAUAUUUUU AGCAAACUUUUUAU

STMN2_ intron1	+	GTT A	160 6	CAGCTATTACCTCATT AATATTTTTAGCAA	361 2	CAGCUAUUACCUCAU AAUAUUUUUAGCAA
STMN2_ intron1	+	ATT G	160 7	TTACAGCTATTACCTC ATTAATATTTTTAG	361 3	UUACAGCUAUUACCUC AUUAAUAUUUUUAG
STMN2_ intron1	+	TTT A	160 8	TTGTTACAGCTATTAC CTCATTAATATTTT	361 4	UUGUUACAGCUAUUAC CUCAUUAUAUUUU
STMN2_ intron1	+	TTTT	160 9	ATTGTTACAGCTATTA CCTCATTAATATTT	361 5	AUUGUUACAGCUAUUA CCUCAUUAUAUUUU
STMN2_ intron1	+	TTTT	161 0	TATTGTTACAGCTATT ACCTCATTAATATT	361 6	UAUUGUUACAGCUAUU ACCUCAUUAUAUU
STMN2_ intron1	+	GTT T	161 1	TTATTGTTACAGCTAT TACCTCATTAATAT	361 7	UUAUUGUUACAGCUAU UACCUCAUUAUAU
STMN2_ intron1	+	ATT C	161 2	TAAAAGAGAAATGAG TGTTTTTATTGTTAC	361 8	UAAAAGAGAAAUGAGU GUUUUUAUUGUUAC
STMN2_ intron1	+	ATT C	161 3	TATTCTAAAAGAGAA ATGAGTGTTTTTATT	361 9	UAUUCUAAAAGAGAAA UGAGUGUUUUUAUU
STMN2_ intron1	+	ATT A	161 4	TTCTATTCTAAAAGAG AAATGAGTGTTTTT	362 0	UUCUAUUCUAAAAGAG AAAUGAGUGUUUUU
STMN2_ intron1	+	TTT G	161 5	TAGTAAATTATTCTAT TCTAAAAGAGAAAT	362 1	UAGUAAAUAUUCUAU UCUAAAAGAGAAAU
STMN2_ intron1	+	ATT T	161 6	GTAGTAAATTATTCTA TTCTAAAAGAGAAA	362 2	GUAGUAAAUAUUCUA UUCUAAAAGAGAAA
STMN2_ intron1	+	ATT T	161 7	TTAGCAAACCTTTTATT TGTTGCATTGAAAG	362 3	UUAGCAAACUUUUUAU UGUUGCAUUGAAAG
STMN2_ intron1	+	ATT A	161 8	TCCTGTTGTCACAAGA TCTGTGACCTTATA	362 4	UCCUGUUGUCACAAGA UCUGUGACCUUAUA
STMN2_ intron1	+	GTT G	161 9	TCACAAGATCTGTGAC CTTATATGAAAAAA	362 5	UCACAAGAUCUGUGAC CUUAUAUGAAAAAA
STMN2_ intron1	+	CTT A	162 0	TATGAAAAAATGCTA GAATTTTTTCATTAA	362 6	UAUGAAAAAAUGCUAG AAUUUUUUCAUUAA
STMN2_ intron1	+	TTTT	162 1	AAATCTAATCCAATGT GATTTCAATCTAGT	362 7	AAUUCUAAUCCAAUGU GAUUUCAUUCUAGU
STMN2_ intron1	+	TTTT	162 2	TAAATCTAATCCAATG TGATTTCAATCTAG	362 8	UAAAUUCUAAUCCAAUG UGAUUUCUAAUCUAG
STMN2_ intron1	+	CTTT	162 3	TTAAATCTAATCCAAT GTGATTTCAATCTA	362 9	UUAAAUCUAAUCCAAU GUGAUUUCUAAUCUA
STMN2_ intron1	+	TTT A	162 4	AAGATACCTTTTTAAA TCTAATCCAATGTG	363 0	AAGAUACCUUUUAAAA UCUAAUCCAAUGUG
STMN2_ intron1	+	ATT T	162 5	AAAGATACCTTTTTAA ATCTAATCCAATGT	363 1	AAAGAUACCUUUUAAA AUCUAAUCCAAUGU
STMN2_ intron1	+	TTTC	162 6	CATTTAAAGATACCTT TTTAAATCTAATCC	363 2	CAUUUAAAGAUACCUU UUUAAAUCUAAUCC
STMN2_ intron1	+	TTTT	162 7	CCATTTAAAGATACCT TTTTAAATCTAATC	363 3	CCAUUUAAAGAUACCU UUUUAAAUCUAAUC

STMN2_ intron1	+	CTTT	162 8	TCCATTTAAAGATACC TTTTTAAATCTAAT	363 4	UCCAUUUAAAGAUACC UUUUUAAAUCUAAU
STMN2_ intron1	+	TTTC	162 9	TTTTCCATTTAAAGAT ACCTTTTTTAAATCT	363 5	UUUUCCAUUUAAAGAU ACCUUUUUAAAUCU
STMN2_ intron1	+	CTTT	163 0	CTTTTCCATTTAAAGA TACCTTTTTTAAATC	363 6	CUUUUCCAUUUAAAGA UACCUUUUUAAAUC
STMN2_ intron1	+	CTT C	163 1	TAAGTCTGTCTTTCTT TTCCATTTAAAGAT	363 7	UAAGUCUGUCUUUCUU UCCAUUUAAAGAU
STMN2_ intron1	+	TTTC	163 2	CCATCTTCTAAGTCTG TCTTTCTTTTCCAT	363 8	CCAUCUUCUAAGUCUG UCUUUCUUUCCA
STMN2_ intron1	+	TTTT	163 3	CCCATCTTCTAAGTCT GTCTTTCTTTTCCA	363 9	CCCAUCUUCUAAGUCU GUCUUUCUUUCCA
STMN2_ intron1	+	TTTT	163 4	TCCCATCTTCTAAGTC TGTCTTTCTTTTCC	364 0	UCCCAUCUUCUAAGUC UGUCUUUCUUUCC
STMN2_ intron1	+	ATT T	163 5	TTCCCATCTTCTAAGT CTGTCTTTCTTTTC	364 1	UCCCAUCUUCUAAGU CUGUCUUUCUUUUC
STMN2_ intron1	+	GTT A	163 6	TTTTTCCCATCTTCTA AGTCTGTCTTTCTT	364 2	UUUUUCCCAUCUUCUA AGUCUGUCUUUCUU
STMN2_ intron1	+	CTT A	163 7	GCGAGTAAACAGGC AGGTATGTGATACTG	364 3	GCGAGUAAACAGGCA GGUAUGUGAUACUG
STMN2_ intron1	+	GTT C	163 8	AGAGCACATCTGAAT ATCAGAGTCTCCACC	364 4	AGAGCACAUUCUGAAUA UCAGAGUCUCCACC
STMN2_ intron1	+	ATT G	163 9	AAATGTGCCCCCTGTT CAGAGCACATCTGA	364 5	AAAUGUGCCCCCUGUU CAGAGCACAUUCUGA
STMN2_ intron1	+	CTT C	164 0	ATCGATTGAAATGTGC CCCCTGTTCCAGAGC	364 6	AUCGAUUGAAAUGUGC CCCCUGUUCAGAGC
STMN2_ intron1	+	CTT C	164 1	TTCATCGATTGAAATG TGCCCCCTGTTCCAG	364 7	UUCAUCGAUUGAAAUG UGCCCCCUGUUCAG
STMN2_ intron1	+	TTT A	164 2	CTTCTTCATCGATTGA AATGTGCCCCCTGT	364 8	CUUCUUCAUUCGAUUGA AAUGUGCCCCCUGU
STMN2_ intron1	+	GTT T	164 3	ACTTCTTCATCGATTG AAATGTGCCCCCTG	364 9	ACUUCUUCAUUCGAUUG AAAUGUGCCCCCUG
STMN2_ intron1	+	ATT G	164 4	TTTACTTCTTCATCGA TTGAAATGTGCCCC	365 0	UUUACUUCUUCAUUCGA UUGAAAUGUGCCCC
STMN2_ intron1	+	ATT A	164 5	AAGAAAATCATTGTTT ACTTCTTCATCGAT	365 1	AAGAAAUCAUUGUUU ACUUCUUCAUUCGAU
STMN2_ intron1	+	CTT A	164 6	AAAATAAAGGAATAA ATTAAAGAAAATCAT	365 2	AAAUAAGGAUAAA UUAAGAAAUAU
STMN2_ intron1	+	TTT A	164 7	ATGCTTAAAAATAAA GGAATAAATTAAAGA	365 3	AUGCUUAAAAUAAAG GAAUAAAUAAGA
STMN2_ intron1	+	TTT A	164 8	AATCTAATCCAATGTG ATTTCAATCTAGTT	365 4	AAUCUAAUCCAUUGUG AUUCAAUCUAGUU
STMN2_ intron1	+	ATT T	164 9	CAATCTAGTTTATCA GATTTCAACAATTA	365 5	CAAUCUAGUUUAUCA GAUUUCAACAAUA

STMN2_ intron1	+	TTTC	165 0	AATCTAGTTTTATCAG ATTTCAACAATTAT	365 6	AAUCUAGUUUUAUCAG AUUUCAACAAUUAU
STMN2_ intron1	+	GTT T	165 1	TATCAGATTTCAACAA TTATTGAGCATCTC	365 7	UAUCAGAUUUCAACAA UUAUUGAGCAUCUC
STMN2_ intron1	+	ATT T	165 2	TTTGATTACATTTTAT GTAATTCTAATCCA	365 8	UUUGAUUACAUUUUUAU GUAAUUCUAAUCCA
STMN2_ intron1	+	ATT A	165 3	TTTTTTGATTACATTTT ATGTAATTCTAAT	365 9	UUUUUUGAUUACAUUU UAUGUAAUUCUAAU
STMN2_ intron1	+	ATT G	165 4	ATAGAATTATTTTTTG ATTACATTTTATGT	366 0	AUAGAAUUAUUUUUUG AUUACAUUUUUAUGU
STMN2_ intron1	+	TTT A	165 5	AATATGCATTGATAG AATTATTTTTTGATT	366 1	AAUAUGCAUUGAUAGA AUUAUUUUUUGAUU
STMN2_ intron1	+	TTTT	165 6	AAATATGCATTGATA GAATTATTTTTTGAT	366 2	AAUAUGCAUUGAUAG AAUUAUUUUUUGAU
STMN2_ intron1	+	TTTT	165 7	TAAATATGCATTGATA GAATTATTTTTTGA	366 3	UAAUAUGCAUUGAUA GAAUUAUUUUUUGA
STMN2_ intron1	+	TTTT	165 8	TTAAATATGCATTGAT AGAATTATTTTTTG	366 4	UUAAUAUGCAUUGAU AGAAUUAUUUUUUG
STMN2_ intron1	+	ATT T	165 9	TTTAAATATGCATTGA TAGAATTATTTTTT	366 5	UUUAAUAUGCAUUGA UAGAAUUAUUUUUU
STMN2_ intron1	+	TTT G	166 0	GGTATCATCAAAAGT GGATTTTTTAAATAT	366 6	GGUAUCAUCAAAAGUG GAUUUUUUUAAUAU
STMN2_ intron1	+	TTTT	166 1	GGGTATCATCAAAAG TGGATTTTTTAAATA	366 7	GGGUCAUCAUCAAAAGU GGAUUUUUUUAAUA
STMN2_ intron1	+	ATT T	166 2	TGGGTATCATCAAAA GTGGATTTTTTAAAT	366 8	UGGGUACAUCAAAAG UGGAUUUUUUUAAAU
STMN2_ intron1	+	TTT A	166 3	ACGAAGTAAGAAGAA ATATATAAGTATAAA	366 9	ACGAAGUAAGAAGAAA UAUAUAAGUAUAAA
STMN2_ intron1	+	TTTT	166 4	AACGAAGTAAGAAGA AATATATAAGTATAA	367 0	AACGAAGUAAGAAGAA AUUAUAAGUAUAA
STMN2_ intron1	+	TTTT	166 5	AATGCTTAAAAATAA AGGAATAAATTAAAG	367 1	AAUGCUUAAAAAUAAA GGAAUAAAUUAAAG
STMN2_ intron1	+	ATT T	166 6	TAACGAAGTAAGAAG AAATATATAAGTATA	367 2	UAACGAAGUAAGAAGA AAUAUAUAAGUAUA
STMN2_ intron1	+	ATT A	166 7	GAAAATCGATGTTAA TTTAAACGAAGTAAG	367 3	GAAAUCGAUGUUAAU UUUAACGAAGUAAG
STMN2_ intron1	+	TTT A	166 8	TTAGAAAATCGATGTT AATTTTAAACGAAGT	367 4	UUAGAAAUCGAUGUU AAUUUUAACGAAGU
STMN2_ intron1	+	GTT T	166 9	ATTAGAAAATCGATG TTAATTTTAAACGAAG	367 5	AUUAGAAAUCGAUGU UAAUUUUAACGAAG
STMN2_ intron1	+	TTTC	167 0	TGTTTATTAGAAAATC GATGTTAATTTTAA	367 6	UGUUUAUUAGAAAUC GAUGUAAUUUUAA
STMN2_ intron1	+	TTTT	167 1	CTGTTTATTAGAAAAT CGATGTTAATTTTA	367 7	CUGUUUAUUAGAAAUC CGAUGUAAUUUUAA

STMN2_ intron1	+	GTT T	167 2	TCTGTTTATTAGAAAA TCGATGTTAATTTT	367 8	UCUGUUUUAUUAGAAAA UCGAUGUUAUUUUU
STMN2_ intron1	+	CTT G	167 3	TAGTGGTTTTCTGTTT ATTAGAAAATCGAT	367 9	UAGUGGUUUUCUGUUU AUUAGAAAAUCGAU
STMN2_ intron1	+	ATT G	167 4	AGCATCTCCTTGTAGT GGTTTTCTGTTTAT	368 0	AGCAUCUCCUUGUAGU GGUUUUCUGUUUAU
STMN2_ intron1	+	ATT A	167 5	TTGAGCATCTCCTTGT AGTGGTTTTCTGTT	368 1	UUGAGCAUCUCCUUGU AGUGGUUUUCUGUU
STMN2_ intron1	+	TTTC	167 6	AACAATTATTGAGCAT CTCCTTGTAGTGGT	368 2	AACAAUUUUUGAGCAU CUCCUUGUAGUGGU
STMN2_ intron1	+	ATT T	167 7	CAACAATTATTGAGC ATCTCCTTGTAGTGG	368 3	CAACAAUUUUUGAGCA UCUCCUUGUAGUGG
STMN2_ intron1	+	TTT A	167 8	TCAGATTCAACAATT ATTGAGCATCTCCT	368 4	UCAGAUUUCACAAUU AUUGAGCAUCUCCU
STMN2_ intron1	+	TTTT	167 9	ATCAGATTCAACAAT TATTGAGCATCTCC	368 5	AUCAGAUUUCACAAU UAUUGAGCAUCUCC
STMN2_ intron1	+	GTT A	168 0	ATTTTAACGAAGTAA GAAGAAATATATAAG	368 6	AUUUUAACGAAGUAAG AAGAAUAUAUAAG
STMN2_ intron1	+	TTT A	168 1	TCAATTAATCTCATGT ATTTAGTTTATACC	368 7	UCAAUUAAUCUCAUGU AUUUAGUUUAUACC
STMN2_ intron1	+	ATT T	168 2	TAATGCTTAAAAATA AAGGAATAAATTTAA	368 8	UAAUGCUUAAAAAUAA AGGAUAAAUUAAA
STMN2_ intron1	+	ATT T	168 3	AGCAGCCGAATATTTT AATGCTTAAAAATA	368 9	AGCAGCCGAUUUUUU AAUGCUUAAAAUA
STMN2_ intron1	+	TTT A	168 4	CCAGGAACATTCAAG TGTTTATTCAATAAG	369 0	CCAGGAACAUUCAAGU GUUUUUUCAUAAG
STMN2_ intron1	+	TTTT	168 5	ACCAGGAACATTCAA GTGTTTATTCAATAA	369 1	ACCAGGAACAUUCAAG UGUUUAUUCAAUA
STMN2_ intron1	+	CTTT	168 6	TACCAGGAACATTCA AGTGTTTATTCAATA	369 2	UACCAGGAACAUUCA GUGUUUAUUCAAUA
STMN2_ intron1	+	TTTC	168 7	TTTTACCAGGAACATT CAAGTGTTTATTCA	369 3	UUUUACCAGGAACAU CAAGUGUUUAUUC
STMN2_ intron1	+	TTTT	168 8	CTTTTACCAGGAACAT TCAAGTGTTTATTC	369 4	CUUUUACCAGGAACAU UCAAGUGUUUAUUC
STMN2_ intron1	+	CTTT	168 9	TCTTTTACCAGGAACA TTCAAGTGTTTATT	369 5	UCUUUUACCAGGAACA UUCAAGUGUUUAUU
STMN2_ intron1	+	TTT A	169 0	ATAAAATCTTTTCTTT TACCAGGAACATTC	369 6	AUAAAAUCUUUCUUU UACCAGGAACAUUC
STMN2_ intron1	+	GTT T	169 1	AATAAAATCTTTTCTT TTACCAGGAACATT	369 7	AAUAAAAUCUUUCUU UUACCAGGAACAUU
STMN2_ intron1	+	ATT A	169 2	ACTGTTTAATAAAATC TTTTCTTTTACCAG	369 8	ACUGUUUAAUAAAAUC UUUCUUUUACCAG
STMN2_ intron1	+	GTT C	169 3	CAAATATTAAGTGT AATAAAATCTTTTC	369 9	CAAAUAUUAACUGUUU AAUAAAAUCUUUC

STMN2_ intron1	+	ATT G	169 4	ATGTAAACCTAGTTCC AAATATTAACGTGT	370 0	AUGUAAACCUAGUUCC AAAUAUUAAACUGUU
STMN2_ intron1	+	GTT C	169 5	TCTAAAAAAGCAGAT GATTGATGTAAACCT	370 1	UCUAAAAAAGCAGAUG AUUGAUGUAAACCU
STMN2_ intron1	+	TTTC	169 6	ACCACACTAGAGGGC AATCATGTTCTCTAA	370 2	ACCACACUAGAGGGCA AUCAUGUUCUCUAA
STMN2_ intron1	+	TTTT	169 7	CACCACACTAGAGGG CAATCATGTTCTCTA	370 3	CACCACACUAGAGGGC AAUCAUGUUCUCUA
STMN2_ intron1	+	CTTT	169 8	TCACCACACTAGAGG GCAATCATGTTCTCT	370 4	UCACCACACUAGAGGG CAAUCAUGUUCUCU
STMN2_ intron1	+	ATT A	169 9	ACTTTTCACCACACTA GAGGGCAATCATGT	370 5	ACUUUUCACCACACUA GAGGGCAAUCAUGU
STMN2_ intron1	+	ATT G	170 0	GAAAACCTCGGTGTCT GCATTAACCTTTTCA	370 6	GAAAACCUCGGUGUCU GCAUUAACUUUUA
STMN2_ intron1	+	GTT C	170 1	TGTCCATTGGAAAACC TCGGTGTCTGCATT	370 7	UGUCCAUUGGAAAACC UCGGUGUCUGCAUU
STMN2_ intron1	+	TTTC	170 2	AGAACCTAGACTGGT TCTGTCCATTGGAAA	370 8	AGAACCUAGACUGGUU CUGUCCAUUGGAAA
STMN2_ intron1	+	TTTT	170 3	CAGAACCTAGACTGG TTCTGTCCATTGGAA	370 9	CAGAACCUAGACUGGU UCUGUCCAUUGGAA
STMN2_ intron1	+	GTT T	170 4	TCAGAACCTAGACTG GTTCTGTCCATTGGA	371 0	UCAGAACCUAGACUGG UUCUGUCCAUUGGA
STMN2_ intron1	+	ATT A	170 5	AAAAAGAAAATACTG AACTAGCCAGTGACC	371 1	AAAAAGAAAAUACUGA ACUAGCCAGUGACC
STMN2_ intron1	+	TTTC	170 6	ATTAAAAAAGAAAAT ACTGAACTAGCCAGT	371 2	AUUAAAAAAGAAAAUA CUGAACUAGCCAGU
STMN2_ intron1	+	TTTT	170 7	CATTAAAAAAGAAAA TACTGAACTAGCCAG	371 3	CAUUAAAAAAGAAAAU ACUGAACUAGCCAG
STMN2_ intron1	+	TTTT	170 8	TCATTAAAAAAGAAA ATACTGAACTAGCCA	371 4	UCAUUAAAAAAGAAAA UACUGAACUAGCCA
STMN2_ intron1	+	TTTT	170 9	TTCATTAAAAAAGAA AATACTGAACTAGCC	371 5	UUCAUUAAAAAAGAAA AUACUGAACUAGCC
STMN2_ intron1	+	ATT T	171 0	TTTCATTAAAAAAGA AAATACTGAACTAGC	371 6	UUUCAUUAAAAAAGAA AAUACUGAACUAGC
STMN2_ intron1	+	ATT C	171 1	AAGTGTTTATTCAATA AGCTGATGCCATGC	371 7	AAGUGUUUAUUCAAUA AGCUGAUGCCAUGC
STMN2_ intron1	+	GTT T	171 2	ATTCAATAAGCTGATG CCATGCTTTACCCT	371 8	AUUCAAUAAGCUGAUG CCAUGCUUUACCCU
STMN2_ intron1	+	TTT A	171 3	TTCAATAAGCTGATGC CATGCTTTACCCTA	371 9	UUCAUAAGCUGAUGC CAUGCUUUACCCUA
STMN2_ intron1	+	ATT C	171 4	AATAAGCTGATGCCA TGCTTTACCCTAGTG	372 0	AAUAAGCUGAUGCCAU GCUUUACCCUAGUG
STMN2_ intron1	+	GTT A	171 5	TTTAGCAGCCGAATAT TTAATGCTTAAAA	372 1	UUUAGCAGCCGAUAU UUUAAUGCUUAAAA

STMN2_ intron1	+	TTT G	171 6	TAGTGGATAAATAGT AGAAAAATGTCAGTA	372 2	UAGUGGAUAAAUAGUA GAAAAAUGUCAGUA
STMN2_ intron1	+	TTTT	171 7	GTAGTGGATAAATAG TAGAAAAATGTCAGT	372 3	GUAGUGGAUAAAUAGU AGAAAAAUGUCAGU
STMN2_ intron1	+	ATT T	171 8	TGTAGTGGATAAATA GTAGAAAAATGTCAG	372 4	UGUAGUGGAUAAAUAG UAGAAAAAUGUCAG
STMN2_ intron1	+	CTT C	171 9	TGAGATTTTGTAGTGG ATAAATAGTAGAAA	372 5	UGAGAUUUUGUAGUGG AUAAAUAGUAGAAA
STMN2_ intron1	+	GTT A	172 0	CTTCTGAGATTTTGTA GTGGATAAATAGTA	372 6	CUUCUGAGAUUUUGUA GUGGAUAAAUAGUA
STMN2_ intron1	+	TTT A	172 1	TGTTACTTCTGAGATT TTGTAGTGGATAAA	372 7	UGUUACUUCUGAGAUU UUGUAGUGGAUAAA
STMN2_ intron1	+	ATT T	172 2	ATGTTACTTCTGAGAT TTTGTAGTGGATAA	372 8	AUGUUACUUCUGAGAU UUUGUAGUGGAUAA
STMN2_ intron1	+	ATT A	172 3	TAATACCATTTATGTT ACTTCTGAGATTTT	372 9	UAAUACCAUUUAUGUU ACUUCUGAGAUUUU
STMN2_ intron1	+	GTT A	172 4	TTATAATACCATTTAT GTTACTTCTGAGAT	373 0	UUAUAAUACCAUUUAU GUUACUUCUGAGAU
STMN2_ intron1	+	ATT G	172 5	TTATTATAATACCATT TATGTTACTTCTGA	373 1	UUAUUAAUAAUACCAU UAUGUUACUUCUGA
STMN2_ intron1	+	ATT A	172 6	CATTGTTATTATAATA CCATTTATGTTACT	373 2	CAUUGUUUUUAUAAUA CCAUUUAUGUUACU
STMN2_ intron1	+	TTT A	172 7	TTACATTGTTATTATA ATACCATTTATGTT	373 3	UUACAUUGUUUUUAUA AUACCAUUUAUGUU
STMN2_ intron1	+	TTT A	172 8	GCAGCCGAATATTTTA ATGCTTAAAAATAA	373 4	GCAGCCGAUAUUUUUA AUGCUUAAAAAUAA
STMN2_ intron1	+	TTTT	172 9	ATTACATTGTTATTAT AATACCATTTATGT	373 5	AUUACAUGUUUAUUUA AAUACCAUUUAUGU
STMN2_ intron1	+	CTT C	173 0	TCAGTTTTATTACATT GTTATTATAATACC	373 6	UCAGUUUUUAUUACA GUUAUUUAUAAUACC
STMN2_ intron1	+	TTT A	173 1	CTTCTCAGTTTTATTA CATTGTTATTATAA	373 7	CUUCUCAGUUUUUAUA CAUUGUUUAUUUA
STMN2_ intron1	+	TTTT	173 2	ACTTCTCAGTTTTATT ACATTGTTATTATA	373 8	ACUUCUCAGUUUUUAU ACAUUGUUUAUUUA
STMN2_ intron1	+	GTT T	173 3	TACTTCTCAGTTTTAT TACATTGTTATTAT	373 9	UACUUCUCAGUUUUUA UACAUGUUUAUUUA
STMN2_ intron1	+	ATT C	173 4	CCTGATGGTTTTACTT CTCAGTTTTATTAC	374 0	CCUGAUGGUUUUACU CUCAGUUUUUAUAC
STMN2_ intron1	+	ATT A	173 5	TTCCCTGATGGTTTTA CTTCTCAGTTTTAT	374 1	UUCCUGAUGGUUUUA CUUCUCAGUUUUUA
STMN2_ intron1	+	GTT A	173 6	ATTATTCCCTGATGGT TTACTTCTCAGTT	374 2	AUUAUUCCUGAUGGU UUUACUUCUCAGUU
STMN2_ intron1	+	TTTC	173 7	AAGGAGACAGGATGA AATGAGTGGTCATAA	374 3	AAGGAGACAGGAUGAA AUGAGUGGUCAUAA

STMN2_ intron1	+	TTTT	173 8	CAAGGAGACAGGATG AAATGAGTGGTCATA	374 4	CAAGGAGACAGGAUGA AAUGAGUGGUCAUA
STMN2_ intron1	+	ATT T	173 9	TCAAGGAGACAGGAT GAAATGAGTGGTCAT	374 5	UCAAGGAGACAGGAUG AAAUGAGUGGUCAU
STMN2_ intron1	+	CTT G	174 0	TACAATTTTCAAGGAG ACAGGATGAAATGA	374 6	UACAAUUUUCAAGGAG ACAGGAUGAAAUGA
STMN2_ intron1	+	TTT A	174 1	CCCTAGTGGATGAAC AGAGCTTGTACAATT	374 7	CCCUAGUGGAUGAACA GAGCUUGUACAAUU
STMN2_ intron1	+	CTTT	174 2	ACCCTAGTGGATGAA CAGAGCTTGTACAAT	374 8	ACCCUAGUGGAUGAAC AGAGCUUGUACAAU
STMN2_ intron1	+	GTT T	174 3	TATTACATTGTTATTA TAATACCATTTATG	374 9	UAUUACAUGUUUAUUA UAAUACCAUUUAUG
STMN2_ intron1	+	TTTT	174 4	TTGATTACATTTTATG TAATTCTAATCCAG	375 0	UUGAUUACAUUUUUUG UAAUUCUAAUCCAG
STMN2_ intron1	+	GTT T	174 5	ATCAATTAATCTCATG TATTTAGTTTATAC	375 1	AUCAUUAAUCUCAUG UAUUUAGUUUAUAC
STMN2_ intron1	+	ATT T	174 6	CAGGATAAAACTGAA AGAAATGGCAGTAGT	375 2	CAGGAUAAAACUGAAA GAAAUGGCAGUAGU
STMN2_ intron1	+	GTT T	174 7	GCGGGAAAAGCTTCT AGAACCTAGACATGT	375 3	GCGGGAAAAGCUUCUA GAACCUAGACAUGU
STMN2_ intron1	+	TTT G	174 8	ATCGTTTGCGGGAAA AGCTTCTAGAACCTA	375 4	AUCGUUUGCGGGAAAA GCUUCUAGAACCUA
STMN2_ intron1	+	CTTT	174 9	GATCGTTTGCGGGAA AAGCTTCTAGAACCT	375 5	GAUCGUUUGCGGGAAA AGCUUCUAGAACCU
STMN2_ intron1	+	TTT G	175 0	AAGACCTTTGATCGTT TGCGGGAAAAGCTT	375 6	AAGACCUUGAUCGUU UGCGGGAAAAGCUU
STMN2_ intron1	+	CTTT	175 1	GAAGACCTTTGATCGT TTGCGGGAAAAGCT	375 7	GAAGACCUUGAUCGU UUGCGGGAAAAGCU
STMN2_ intron1	+	GTT C	175 2	TTTGAAGACCTTTGAT CGTTTGCGGGAAAA	375 8	UUUGAAGACCUUGAU CGUUUGCGGGAAAA
STMN2_ intron1	+	TTT A	175 3	GACATAGACACAGAT AAAGGGTTCTTTGAA	375 9	GACAUAGACACAGUA AAGGGUUCUUUGAA
STMN2_ intron1	+	GTT T	175 4	AGACATAGACACAGA TAAAGGGTTCTTTGA	376 0	AGACAUAGACACAGAU AAAGGGUUCUUUGA
STMN2_ intron1	+	ATT A	175 5	CATAGAGTGTTTAGAC ATAGACACAGATAA	376 1	CAUAGAGUGUUUAGAC AUAGACACAGAUAA
STMN2_ intron1	+	TTTC	175 6	GGAAGCAAATTACAT AGAGTGTTTAGACAT	376 2	GGAAGCAAUUACAUA GAGUGUUUAGACAU
STMN2_ intron1	+	TTTT	175 7	CGGAAGCAAATTACA TAGAGTGTTTAGACA	376 3	CGGAAGCAAUUACA AGAGUGUUUAGACA
STMN2_ intron1	+	CTTT	175 8	TCGGAAGCAAATTAC ATAGAGTGTTTAGAC	376 4	UCGGAAGCAAUUACA UAGAGUGUUUAGAC
STMN2_ intron1	+	TTTC	175 9	TTTTCGGAAGCAAATT ACATAGAGTGTTTA	376 5	UUUUCGGAAGCAAUU ACAUAGAGUGUUUA

STMN2_ intron1	+	TTTT	176 0	CTTTTCGGAAGCAAAT TACATAGAGTGTTT	376 6	CUUUUCGGAAGCAAAU UACAUAGAGUGUUU
STMN2_ intron1	+	TTTT	176 1	TCTTTTTCGGAAGCAAA TTACATAGAGTGTT	376 7	UCUUUUCGGAAGCAAA UUACAUAGAGUGUU
STMN2_ intron1	+	ATT T	176 2	TTCTTTTCGGAAGCAA ATTACATAGAGTGT	376 8	UUCUUUUCGGAAGCAA AUUACAUAGAGUGU
STMN2_ intron1	+	GTT A	176 3	ACATTTTCTTTTCGG AAGCAAATTACATA	376 9	ACAUUUUUCUUUUCGG AAGCAAAUACAU
STMN2_ intron1	+	TTT A	176 4	AGAGAGATGGGAAAA GTGGGTAAACATTTT	377 0	AGAGAGAUGGGAAAAAG UGGGUUAACAUUUU
STMN2_ intron1	+	TTTT	176 5	AAGAGAGATGGGAAA AGTGGGTAAACATTT	377 1	AAGAGAGAUGGGAAAA GUGGGUUAACAUUU
STMN2_ intron1	+	CTTT	176 6	TAAGAGAGATGGGAA AAGTGGGTAAACATT	377 2	UAAGAGAGAUGGGAAA AGUGGGUUAACAUU
STMN2_ intron1	+	GTT C	176 7	TGCTTTTAAGAGAGAT GGGAAAAGTGGGT	377 3	UGCuuuUAAGAGAGAU GGGAAAAGUGGGUU
STMN2_ intron1	+	ATT G	176 8	TTCTGCTTTTAAGAGA GATGGGAAAAGTGG	377 4	UUCUGCUUUUAAGAGA GAUGGGAAAAGUGG
STMN2_ intron1	+	CTT C	176 9	CAAGAGAGACCTGAC CACTGACCCCGCCCT	377 5	CAAGAGAGACCUGACC ACUGACCCCGCCCU
STMN2_ intron1	+	ATT C	177 0	GAAAGGGGGTTCGGGT GGGGAGCGCAGCGTG	377 6	GAAAGGGGGUCGGGUG GGGAGCGCAGCGUG
STMN2_ intron1	+	CTT C	177 1	ATTCGAAAGGGGGTC GGGTGGGGAGCGCAG	377 7	AUUCGAAAGGGGGUCG GGUGGGGAGCGCAG
STMN2_ intron1	+	TTT G	177 2	TGTGCGGACCAGCGG TCCCGGGGGGAGGCA	377 8	UGUGCGGACCAGCGGU CCCGGGGGGAGGCA
STMN2_ intron1	+	CTTT	177 3	GTGTGCGGACCAGCG GTCCCGGGGGGAGGC	377 9	GUGUGCGGACCAGCGG UCCCGGGGGGAGGC
STMN2_ intron1	+	TTT G	177 4	CGGGAAAAGCTTCTA GAACCTAGACATGTG	378 0	CGGGAAAAGCUUCUAG AACCUAGACAUGUG
STMN2_ intron1	+	TTTC	177 5	TTTGTGTGCGGACCAG CGGTCCCGGGGGGA	378 1	UUUGUGUGCGGACCAG CGGUCCCGGGGGGA
STMN2_ intron1	+	CTT C	177 6	TAGAACCTAGACATG TGTATGTATAATAAT	378 2	UAGAACCUAGACAUGU GUAUGUAUAAUAAU
STMN2_ intron1	+	GTT A	177 7	AGCCACGCGAAATTTT CGTTTTGTGGGTCA	378 3	AGCCACGCGAAAUUUC CGUUUUGUGGGUCA
STMN2_ intron1	+	CTTT	177 8	TTTTCCCCCAGCCCAA GCCCCCGCCACC	378 4	UUUUCCCCCAGCCCAA GCCCCCGCCACC
STMN2_ intron1	+	CTT C	177 9	TCGCCCACCCACGGTC CGCGGAGCTCGGGG	378 5	UCGCCCACCCACGGUCC GCGGAGCUCGGGG
STMN2_ intron1	+	ATT C	178 0	AGGGAGGGCTGTCTC TTCTCGCCCACCCAC	378 6	AGGGAGGGCUGUCUCU UCUCGCCCACCCAC
STMN2_ intron1	+	CTT C	178 1	CCAGGGATTGAGGGA GGGCTGTCTCTTCTC	378 7	CCAGGGAUUCAGGGAG GGCUGUCUCUUCUC

STMN2_ intron1	+	CTT G	178 2	ATGTGCGCAGACCCCC GGCGTGGCTCTCAG	378 8	AUGUGCGCAGACCCCC GGCGUGGCUCUCAG
STMN2_ intron1	+	TTTC	178 3	AGCCCCGCAGTCCAC AACGGCCCCGAGCACC	378 9	AGCCCCGCAGUCCACA ACGGCCCCGAGCACC
STMN2_ intron1	+	TTTT	178 4	CAGCCCCGCAGTCCAC AACGGCCCCGAGCAC	379 0	CAGCCCCGCAGUCCAC AACGGCCCCGAGCAC
STMN2_ intron1	+	TTTT	178 5	TCAGCCCCGCAGTCCA CAACGGCCCCGAGCA	379 1	UCAGCCCCGCAGUCCA CAACGGCCCCGAGCA
STMN2_ intron1	+	TTTT	178 6	TTCAGCCCCGCAGTCC ACAACGGCCCCGAGC	379 2	UUCAGCCCCGCAGUCC ACAACGGCCCCGAGC
STMN2_ intron1	+	CTTT	178 7	TTTCAGCCCCGCAGTC CACAACGGCCCCGAG	379 3	UUUCAGCCCCGCAGUC CACAACGGCCCCGAG
STMN2_ intron1	+	GTT G	178 8	AGCTGTATGCAGTCCT GGAACCTCTTTTTT	379 4	AGCUGUAUGCAGUCCU GGAACCUCUUUUUU
STMN2_ intron1	+	GTT G	178 9	CAGGATGCGGAGACA GGGAAAGCTGCCGAA	379 5	CAGGAUGCGGAGACAG GGAAAGCUGCCGAA
STMN2_ intron1	+	CTT G	179 0	GTTGCAGGATGCGGA GACAGGGAAAGCTGC	379 6	GUUGCAGGAUGCAGGAG ACAGGGAAAGCUGC
STMN2_ intron1	+	GTT C	179 1	TGGCGCTCAGTGGCCC CGGGGTGAAAAGGC	379 7	UGGCGCUCAGUGGCCC CGGGGUGAAAAGGC
STMN2_ intron1	+	CTT G	179 2	AGTGCCACGTTCTG GCGCTCAGTGGCCC	379 8	AGUGCCACGGUUCUG GCGCUCAGUGGCCC
STMN2_ intron1	+	CTT G	179 3	TGCCTTGAGTGCCAC GGTTCTGCGCTCA	379 9	UGCCUUGAGUGCCAC GGUUCUGGCGCUCA
STMN2_ intron1	+	ATT G	179 4	GTCTTGTCCTTGAGT GCCCACGGTTCTGG	380 0	GUCUUGUGCCUUGAGU GCCCACGGUUCUGG
STMN2_ intron1	+	CTT C	179 5	ATCCGCAATTGGTCTT GTGCCTTGAGTGCC	380 1	AUCCGCAAUUGGUCUU GUGCCUUGAGUGCC
STMN2_ intron1	+	ATT C	179 6	AGGGCCTTCATCCGCA ATTGGTCTTGAGTCC	380 2	AGGGCCUUCAUCCGCA AUUGGUCUUGUGCC
STMN2_ intron1	+	ATT C	179 7	TGGATTCAGGGCCTTC ATCCGCAATTGGTC	380 3	UGGAUUCAGGGCCUUC AUCCGCAAUUGGUC
STMN2_ intron1	+	TTTC	179 8	ATAAGCTCAGAGAGA CAAGACAGTGGAGAC	380 4	AUAAGCUCAGAGAGAC AAGACAGUGGAGAC
STMN2_ intron1	+	ATT T	179 9	CATAAGCTCAGAGAG ACAAGACAGTGGAGA	380 5	CAUAAGCUCAGAGAGA CAAGACAGUGGAGA
STMN2_ intron1	+	TTT G	180 0	TGGGTCAGACAGTGC CAAATATCGGCAATT	380 6	UGGGUCAGACAGUGCC AAAUUUCGGCAAU
STMN2_ intron1	+	TTTT	180 1	GTGGGTCAGACAGTG CCAAATATCGGCAAT	380 7	GUGGGUCAGACAGUGC CAAAUUCGGCAAU
STMN2_ intron1	+	GTT T	180 2	TGTGGGTCAGACAGT GCCAAATATCGGCAA	380 8	UGUGGGUCAGACAGUG CCAAUUCGGCAA
STMN2_ intron1	+	TTTC	180 3	CGTTTTGTGGGTCAGA CAGTGCCAAATATC	380 9	CGUUUUGUGGGUCAGA CAGUGCCAAUUAUC

STMN2_ intron1	+	ATT T	180 4	CCGTTTTGTGGGTCAG ACAGTGCCAAATAT	381 0	CCGUUUUGUGGGUCAG ACAGUGCCAAAUAU
STMN2_ intron1	+	CTT A	180 5	AGTTAAGCCACGCGA AATTTCCGTTTTGTG	381 1	AGUUAAGCCACGCGAA AUUUCGUUUUGUG
STMN2_ intron1	+	GTT T	180 6	CTTTGTGTGCGGACCA GCGGTCCCGGGGGG	381 2	CUUUGUGUGCGGACCA GCGGUCCCGGGGGG
STMN2_ intron1	+	CTT C	180 7	GAAGGCGCTGGGGTG GGGTTTCTTTGTGTG	381 3	GAAGGCGCUGGGGUGG GGUUUCUUUGUGUG
STMN2_ intron1	+	TTT A	180 8	GGGCAAGGGAGGGGA AGGAGAGAGGAAGTC	381 4	GGGCAAGGGAGGGGAA GGAGAGAGGAAGUC
STMN2_ intron1	+	CTT A	180 9	AGGGACATTTTGGAA AGTGCTTTATAACGA	381 5	AGGGACAUUUUGGAAA GUGCUUUAUAACGA
STMN2_ intron1	+	CTT A	181 0	AATGGGCTTAAGGGA CATTTTGGAAGTGC	381 6	AAUGGGCUUAAGGGAC AUUUUGGAAAGUGC
STMN2_ intron1	+	TTT G	181 1	CCTTAAATGGGCTTAA GGGACATTTTGGAA	381 7	CCUUAUUUGGGCUUAA GGGACAUUUUGGAA
STMN2_ intron1	+	GTT T	181 2	GCCTTAAATGGGCTTA AGGGACATTTTGGAA	381 8	GCCUUAUUUGGGCUUA AGGGACAUUUUGGA
STMN2_ intron1	+	CTT A	181 3	ACTGTTTGCCTTAAAT GGGCTTAAGGGACA	381 9	ACUGUUUGCCUUAUAAU GGGCUUAAGGGACA
STMN2_ intron1	+	ATT A	181 4	GGACTCAATCGTGAG GGGAGGAAGCTACCT	382 0	GGACUCAUUCGUGAGG GGAGGAAGCUACCU
STMN2_ intron1	+	TTT A	181 5	AAATTAGGACTCAAT CGTGAGGGGAGGAAG	382 1	AAAUUAGGACUCAUUC GUGAGGGGAGGAAG
STMN2_ intron1	+	ATT T	181 6	AAAATTAGGACTCAA TCGTGAGGGGAGGAA	382 2	AAAAUAGGACUCAAU CGUGAGGGGAGGAA
STMN2_ intron1	+	TTTC	181 7	CATATTTAAAATTAGG ACTCAATCGTGAGG	382 3	CAUAUUUAAAAUUAGG ACUCAUUCGUGAGG
STMN2_ intron1	+	GTT T	181 8	CCATATTTAAAATTAG GACTCAATCGTGAG	382 4	CCAUAUUUAAAAUUAG GACUCAUUCGUGAG
STMN2_ intron1	+	ATT C	181 9	TGTTTCCATATTTAAA ATTAGGACTCAATC	382 5	UGUUUCCAUAUUUAAA AUUAGGACUCAUUC
STMN2_ intron1	+	TTT A	182 0	TTCTGTTTCCATATTT AAAATTAGGACTCA	382 6	UUCUGUUUCCAUAUUU AAAAUUAGGACUCA
STMN2_ intron1	+	ATT T	182 1	ATTCTGTTTCCATATT TAAAATTAGGACTC	382 7	AUUCUGUUUCCAUAUU UAAAAUUAGGACUC
STMN2_ intron1	+	GTT G	182 2	CCCTCCTATGGGTAGA GAATTTATTCTGTT	382 8	CCCUCCUAUGGGUAGA GAAUUUAUUCUGUU
STMN2_ intron1	+	TTT A	182 3	AAAGGTAGAAGCGGG TAAGTTGCCCTCCTA	382 9	AAAGGUAGAAGCGGGU AAGUUGCCCUCCUA
STMN2_ intron1	+	TTTT	182 4	AAAAGGTAGAAGCGG GTAAGTTGCCCTCCT	383 0	AAAAGGUAGAAGCGGG UAAGUUGCCCUCCU
STMN2_ intron1	+	CTTT	182 5	TAAAAGGTAGAAGCG GGTAAGTTGCCCTCC	383 1	UAAAAGGUAGAAGCGG GUAAGUUGCCCUCC

STMN2_ intron1	+	TTTC	182 6	TTTTAAAAGGTAGAA GCGGGTAAGTTGCCC	383 2	UUUUAAAAGGUAGAAG CGGGUAAAGUUGCCC
STMN2_ intron1	+	ATT T	182 7	CTTTTAAAAGGTAGA AGCGGGTAAGTTGCC	383 3	CUUUUAAAAGGUAGAA GCGGGUAAAGUUGCC
STMN2_ intron1	+	GTT C	182 8	TGGGGGAGGTGGGAG GGCAGAGAAGAGGTC	383 4	UGGGGGAGGUGGGAGG GCAGAGAAGAGGUC
STMN2_ intron1	+	GTT A	182 9	ATGGTAACACAGGAC CAGGAAGGACAGGGC	383 5	AUGGUAACACAGGACC AGGAAGGACAGGGC
STMN2_ intron1	+	TTT A	183 0	TAAAGAAAAAGATGT TAATGGTAACACAGG	383 6	UAAAGAAAAAGAUGUU AAUGGUAACACAGG
STMN2_ intron1	+	TTTT	183 1	ATAAAGAAAAAGATG TTAATGGTAACACAG	383 7	AUAAAGAAAAAGAUGU UAAUGGUAACACAG
STMN2_ intron1	+	ATT T	183 2	TATAAAGAAAAAGAT GTAAATGGTAACACA	383 8	UAUAAAGAAAAAGAUG UUAUGGUAACACA
STMN2_ intron1	+	ATT C	183 3	AGAGATATTTTATAAA GAAAAAGATGTTAA	383 9	AGAGAUUUUUUAUAAA GAAAAAGAUGUAAA
STMN2_ intron1	+	CTT G	183 4	AGCTCTAGAAGCATTC AGAGATATTTTATA	384 0	AGCUCUAGAAGCAUUC AGAGAUUUUUUAUA
STMN2_ intron1	+	ATT A	183 5	TGAGAACAAAAATAA AAATGTTCTCACC	384 1	UGAGAACAAAAUAAA AAUGUCCUCACC
STMN2_ intron1	+	ATT T	183 6	TGGAAAGTGCTTTATA ACGACCTTTTTTTT	384 2	UGGAAAGUGCUUUUAU ACGACCUUUUUUUU
STMN2_ intron1	+	TTTT	183 7	GGAAAGTGCTTTATA ACGACCTTTTTTTT	384 3	GGAAAGUGCUUUUAUA CGACCUUUUUUUUU
STMN2_ intron1	+	TTT G	183 8	GAAAGTGCTTTATAAC GACCTTTTTTTTTT	384 4	GAAAGUGCUUUUAUAAC GACCUUUUUUUUUU
STMN2_ intron1	+	CTTT	183 9	ATAACGACCTTTTTTT TTTTTATTTCTTCT	384 5	AUAACGACCUUUUUUU UUUUUAUUUCUUCU
STMN2_ intron1	+	TTTT	184 0	AGGGCAAGGGAGGGG AAGGAGAGAGGAAGT	384 6	AGGGCAAGGGAGGGGA AGGAGAGAGGAAGU
STMN2_ intron1	+	GTT T	184 1	TAGGGCAAGGGAGGG GAAGGAGAGAGGAAG	384 7	UAGGGCAAGGGAGGGG AAGGAGAGAGGAAG
STMN2_ intron1	+	TTT G	184 2	TTTTAGGGCAAGGGA GGGGAAGGAGAGAGG	384 8	UUUUAGGGCAAGGGAG GGGAAGGAGAGAGG
STMN2_ intron1	+	CTTT	184 3	GTTTTAGGGCAAGGG AGGGGAAGGAGAGAG	384 9	GUUUUAGGGCAAGGGA GGGGAAGGAGAGAG
STMN2_ intron1	+	ATT G	184 4	TCTCGTCGAAGAAACC GCTAGTCCTGGGGT	385 0	UCUCGUCGAAGAAACC GCUAGUCCUGGGGU
STMN2_ intron1	+	TTT A	184 5	CGGTATTGTCTCGTCG AAGAAACCGCTAGT	385 1	CGGUUUGUCUCGUCG AAGAAACCGCUAGU
STMN2_ intron1	+	TTTT	184 6	ACGGTATTGTCTCGTC GAAGAAACCGCTAG	385 2	ACGGUAUUGUCUCGUC GAAGAAACCGCUAG
STMN2_ intron1	+	ATT T	184 7	TACGGTATTGTCTCGT CGAAGAAACCGCTA	385 3	UACGGUAUUGUCUCGU CGAAGAAACCGCUA

STMN2_ intron1	+	TTT G	184 8	AAAGATGGGTGGAGA CGGGGGGAGGGGATG	385 4	AAAGAUGGGUGGAGAC GGGGGGAGGGGAUG
STMN2_ intron1	+	GTT T	184 9	GAAAGATGGGTGGAG ACGGGGGGAGGGGAT	385 5	GAAAGAUGGGUGGAGA CGGGGGGAGGGGAU
STMN2_ intron1	+	ATT G	185 0	CAAAGTCAAAGCGGT CCCATCCCGCTGTTT	385 6	CAAAGUCAAGCGGUC CCAUCCCCGUGUUU
STMN2_ intron1	+	TTT A	185 1	AGAAGAAAATAGGAA AGGGGTAAAGGGAAG	385 7	AGAAGAAAUAAGGAAA GGGGUAAAGGGAAG
STMN2_ intron1	+	GTT T	185 2	AAGAAGAAAATAGGA AAGGGGTAAAGGGAAG	385 8	AAGAAGAAAUAAGGAA AGGGGUAAAGGGAAG
STMN2_ intron1	+	TTTT	185 3	TTTCCCCCAGCCCAAG CCCCCGCCCACCC	385 9	UUUCCCCCAGCCCAAG CCCCCGCCCACCC
STMN2_ intron1	+	CTT C	185 4	TCTAGTTTAAGAAGA AAATAGGAAAGGGGT	386 0	UCUAGUUUAAGAAGAA AAUAGGAAAGGGGU
STMN2_ intron1	+	ATT T	185 5	CTTCTCTAGTTTAAGA AGAAAATAGGAAAG	386 1	CUUCUCUAGUUUAAGA AGAAAUAAGGAAAG
STMN2_ intron1	+	TTT A	185 6	TTTCTTCTCTAGTTTA AGAAGAAAATAGGA	386 2	UUUCUUCUCUAGUUUA AGAAGAAAUAAGGA
STMN2_ intron1	+	TTTT	185 7	ATTTCTTCTCTAGTTT AAGAAGAAAATAGG	386 3	AUUUCUUCUCUAGUUU AAGAAGAAAUAAGG
STMN2_ intron1	+	TTTT	185 8	TATTTCTTCTCTAGTTT AAGAAGAAAATAG	386 4	UAUUUCUUCUCUAGUU UAAGAAGAAAUAAG
STMN2_ intron1	+	TTTT	185 9	TTATTTCTTCTCTAGTT TAAGAAGAAAATA	386 5	UUAUUUCUUCUCUAGU UUAAGAAGAAAUA
STMN2_ intron1	+	TTTT	186 0	TTTATTTCTTCTCTAGT TTAAGAAGAAAAT	386 6	UUUAUUUCUUCUCUAG UUUAAGAAGAAAUA
STMN2_ intron1	+	TTTT	186 1	TTTTATTTCTTCTCTAG TTTAAGAAGAAAA	386 7	UUUUAUUUCUUCUCUA GUUUAAGAAGAAAA
STMN2_ intron1	+	TTTT	186 2	TTTTTATTTCTTCTCTA GTTTAAGAAGAAA	386 8	UUUUUAUUUCUUCUCU AGUUUAAGAAGAAA
STMN2_ intron1	+	TTTT	186 3	TTTTTTATTTCTTCTCT AGTTTAAGAAGAA	386 9	UUUUUUAUUUCUUCUC UAGUUUAAGAAGAA
STMN2_ intron1	+	TTTT	186 4	TTTTTTTTATTTCTTCTC TAGTTTAAGAAGA	387 0	UUUUUUUAUUUCUUCU CUAGUUUAAGAAGA
STMN2_ intron1	+	TTTT	186 5	TTTTTTTTATTTCTTCTC CTAGTTTAAGAAG	387 1	UUUUUUUUAUUUCUUC UCUAGUUUAAGAAG
STMN2_ intron1	+	CTTT	186 6	TTTTTTTTATTTCTTC TCTAGTTTAAGAA	387 2	UUUUUUUUUAUUUCUU CUCUAGUUUAAGAA
STMN2_ intron1	+	TTT A	186 7	TAACGACCTTTTTTTT TTTTATTTCTTCTC	387 3	UAACGACCUUUUUUUU UUUUAUUUCUUCUC
STMN2_ intron1	+	TTTC	186 8	TTCTCTAGTTTAAGAA GAAAATAGGAAAGG	387 4	UUCUCUAGUUUAAGAA GAAAUAAGGAAAGG
STMN2_ intron1	+	TTTT	186 9	TTCCCCCAGCCCAAGC CCCCCGCCCACCCT	387 5	UUCCCCCAGCCCAAGCC CCCCGCCCACCCU

STMN2_ intron1	+	TTTT	187 0	TCCCCAGCCCAAGCC CCCCGCCACCCTC	387 6	UCCCCAGCCCAAGCCC CCCCGCCACCUC
STMN2_ intron1	+	TTTT	187 1	CCCCAGCCCAAGCCC CCCCGCCACCCTCT	387 7	CCCCAGCCCAAGCCCC CCGCCACCUCUCU
STMN2_ intron1	+	TTTC	187 2	TGGCCATAATTTAACT GCATTTGCAAATCA	387 8	UGGCCAUAAUUAACU GCAUUUGCAAUA
STMN2_ intron1	+	CTTT	187 3	CTGGCCATAATTTAAC TGCATTTGCAAATC	387 9	CUGGCCAUAAUUAAC UGCAUUUGCAAUC
STMN2_ intron1	+	CTTG	187 4	ATACAGCCTCAATCCT ACACAGATACATGG	388 0	AUACAGCCUCAAUCCU ACACAGAUACAUGG
STMN2_ intron1	+	ATTC	187 5	TTGATACAGCCTCAAT CCTACACAGATACA	388 1	UUGAUACAGCCUCAU CCUACACAGAUACA
STMN2_ intron1	+	CTTC	187 6	CAACTGCTGATTCTTG ATACAGCCTCAATC	388 2	CAACUGCUGAUUCUUG AUACAGCCUCAUC
STMN2_ intron1	+	GTTT	187 7	TTCCAAGTCTGATTC TTGATACAGCCTCA	388 3	UCCAACUGCUGAUUC UUGAUACAGCCUCA
STMN2_ intron1	+	TTTC	187 8	CCCTGAAACTGTTCTT CCAAGTCTGATTC	388 4	CCCUGAAACUGUUCU CCAACUGCUGAUUC
STMN2_ intron1	+	TTTT	187 9	CCCCTGAAACTGTTCT TCCAAGTCTGATT	388 5	CCCUGAAACUGUUCU UCCAACUGCUGAUU
STMN2_ intron1	+	TTTT	188 0	TCCCCTGAAACTGTTT TTCCAAGTCTGAT	388 6	UCCCUGAAACUGUUC UCCAACUGCUGAU
STMN2_ intron1	+	TTTT	188 1	TTCCCCTGAAACTGTT CTTCCAAGTCTGA	388 7	UCCCCUGAAACUGUU CUCCAACUGCUGA
STMN2_ intron1	+	GTTT	188 2	TTTCCCCTGAAACTGT TCTTCCAAGTCTG	388 8	UUCCCCUGAAACUGU UCUCCAACUGCUG
STMN2_ intron1	+	TTTA	188 3	AGTTTTTTCCCCTGAA ACTGTTCTTCCAAC	388 9	AGUUUUUUCCCCUGAA ACUGUUCUCCAAC
STMN2_ intron1	+	TTTT	188 4	AAGTTTTTTCCCCTGA AACTGTTCTTCCAA	389 0	AAGUUUUUUCCCCUGA AACUGUUCUCCA
STMN2_ intron1	+	ATTT	188 5	TAAGTTTTTTCCCCTG AACTGTTCTTCCA	389 1	UAAGUUUUUUCCCCUG AAACUGUUCUCCA
STMN2_ intron1	+	TTTA	188 6	TGCACAAAATTTTAAG TTTTTTCCCCTGAA	389 2	UGCACAAA AUUUUAAG UUUUUUCCCCUGAA
STMN2_ intron1	+	GTTT	188 7	ATGCACAAAATTTTAA GTTTTTTCCCCTGA	389 3	AUGCACAAA AUUUUAA GUUUUUUCCCCUGA
STMN2_ intron1	+	GTTT	188 8	TATCTATAAATATATA AATATAGTTTATGC	389 4	UAUCUAUAAAUUAUA AAUAUAGUUUAUGC
STMN2_ intron1	+	CTTT	188 9	AACATAAGGTTATATC TATAAATATATAAA	389 5	AACAUAGGUUAUAUC UAUAAAUAUAUAAA
STMN2_ intron1	+	ATTT	189 0	AGATGATCTTCAACAT AAGGTTATATCTAT	389 6	AGAUGAUCUACAACAU AAGGUUAUAUCUAU
STMN2_ intron1	+	TTTG	189 1	TGGCTGCAATGGGTG AGAATACACATATAT	389 7	UGGCTGCA AUGGGUGA GAAUACACAUUAU

STMN2_ intron1	+	GTT T	189 2	GTGGCTGCAATGGGT GAGAATACACATATA	389 8	GUGGCUGCAAUGGGUG AGAAUACACAUUA
STMN2_ intron1	+	ATT G	189 3	TTTGTGGCTGCAATGG GTGAGAATACACAT	389 9	UUUGUGGCUGCAAUGG GUGAGAAUACACAU
STMN2_ intron1	+	ATT C	189 4	TCTGCAAAGAATTGTT TGTGGCTGCAATGG	390 0	UCUGCAAAGAAUUGUU UGUGGCUGCAAUGG
STMN2_ intron1	+	ATT G	189 5	CTGGAAAATTCTCTGC AAAGAATTGTTTGT	390 1	CUGGAAAAUUCUCUGC AAAGAAUUGUUUGU
STMN2_ intron1	+	TTT G	189 6	TGTGCCAACGATTGCT GGAAAATTCTCTGC	390 2	UGUGCCAACGAUUGCU GGAAAAUUCUCUGC
STMN2_ intron1	+	GTT T	189 7	GTGTGCCAACGATTGC TGGAAAATTCTCTG	390 3	GUGUGCCAACGAUUGC UGGAAAAUUCUCUG
STMN2_ intron1	+	CTT G	189 8	CTAAGAGCAGGGTTT GTGTGCCAACGATTG	390 4	CUAAGAGCAGGGUUUG UGUGCCAACGAUUG
STMN2_ intron1	+	ATT T	189 9	AACTGCATTTGCAAT CATGAAAAAACAC	390 5	AACUGCAUUUGCAAAU CAUGAAAAAACAC
STMN2_ intron1	+	ATT T	190 0	GCAAATCATGAAAAA AACACTACTTCTGCA	390 6	GCAAUACAUGAAAAAA ACACUACUUCUGCA
STMN2_ intron1	+	TTT G	190 1	CAAATCATGAAAAA ACACTACTTCTGCAG	390 7	CAAAUCAUGAAAAAA CACUACUUCUGCAG
STMN2_ intron1	+	CTT C	190 2	TGCAGTATTAATAA ATAGATTTTGAAATT	390 8	UGCAGUAUUAUAAUAA UAGAUUUUGAAAUA
STMN2_ intron1	+	TTT G	190 3	GTCAGAATTTGAGGAT AAAACGAAAGAAA	390 9	GUCAGAAUUUCAGGAU AAAACUGAAAGAAA
STMN2_ intron1	+	ATT T	190 4	GGTCAGAATTTGAGG ATAAACTGAAAGAA	391 0	GGUCAGAAUUUCAGGA UAAAACUGAAAGAA
STMN2_ intron1	+	CTT C	190 5	TGAATGGATATATAA GTAAGTAGAAATGAA	391 1	UGAAUGGAUUAUAUAG UAACUAGAAAUAGAA
STMN2_ intron1	+	TTTC	190 6	TAATGAAGTGGGCAC CTTCTGAATGGATAT	391 2	UAAUGAAGUGGGCACC UUCUGAAUGGAUAU
STMN2_ intron1	+	TTTT	190 7	CTAATGAAGTGGGCA CCTTCTGAATGGATA	391 3	CUAAUGAAGUGGGCAC CUUCUGAAUGGAUA
STMN2_ intron1	+	CTTT	190 8	TCTAATGAAGTGGGC ACCTTCTGAATGGAT	391 4	UCUAAUGAAGUGGGCA CCUUCUGAAUGGAU
STMN2_ intron1	+	ATT A	190 9	TCTTTTCTAATGAAGT GGGCACCTTCTGAA	391 5	UCUUUUCUAAUGAAGU GGGCACCUUCUGAA
STMN2_ intron1	+	ATT C	191 0	CCCATTATCTTTTCTA ATGAAGTGGGCACC	391 6	CCCAUUAUCUUUUCUA AUGAAGUGGGCACC
STMN2_ intron1	+	ATT G	191 1	TAAGAGGTGCATATA ATATTCCCCATTATC	391 7	UAAGAGGUGCAUAUAA UAUUCUCCCAUUAUC
STMN2_ intron1	+	ATT C	191 2	AGCATGATTGTAAGA GGTGCATATAATATT	391 8	AGCAUGAUUGUAAGAG GUGCAUAUAAUAUU
STMN2_ intron1	+	ATT A	191 3	TGTATTGAGCATGATT GTAAGAGGTGCATA	391 9	UGUAUUCAGCAUGAUU GUAAGAGGUGCAUA

STMN2_ intron1	+	ATT A	191 4	AACAATTATGTATTCA GCATGATTGTAAGA	392 0	AACAAUUAUGUAUUCA GCAUGAUUGUAAGA
STMN2_ intron1	+	ATT C	191 5	ATTAAACAATTATGTA TTCAGCATGATTGT	392 1	AUUAACAUAUUAUGUA UUCAGCAUGAUUGU
STMN2_ intron1	+	GTT C	191 6	ATGTGGCTAAGATAC ATGTGCAAGTGCTTG	392 2	AUGUGGCUAAGAUACA UGUGCAAGUGCUUG
STMN2_ intron1	+	TTTC	191 7	CTGATTCATTAAACAA TTATGTATTCAGCA	392 3	CUGAUUCAUUAACAA UUAUGUAUUCAGCA
STMN2_ intron1	+	TTTT	191 8	TCCTGATTCATTAAAC AATTATGTATTCAG	392 4	UCCUGAUUCAUUAAC AAUUAUGUAUUCAG
STMN2_ intron1	+	TTTT	191 9	TTCCTGATTCATTAAA CAATTATGTATTCA	392 5	UUCUGAUUCAUUA CAAUUAUGUAUUCA
STMN2_ intron1	+	CTTT	192 0	TTTCTGATTCATTAA ACAATTATGTATTC	392 6	UUUCCUGAUUCAUUA ACAAUUAUGUAUUC
STMN2_ intron1	+	ATT A	192 1	TCAGGGCGAGTGCTTT TTTCTGATTCATT	392 7	UCAGGGCGAGUGCUUU UUUCCUGAUUCAU
STMN2_ intron1	+	ATT A	192 2	ATTATCAGGGCGAGT GCTTTTTTCCTGATT	392 8	AUUAUCAGGGCGAGUG CUUUUUUCCUGAUU
STMN2_ intron1	+	TTTC	192 3	AAAGATAATTAATTAT CAGGGCGAGTGCTT	392 9	AAAGAUAAUUAUUAU CAGGGCGAGUGCUU
STMN2_ intron1	+	ATT T	192 4	CAAAGATAATTAATT ATCAGGGCGAGTGCT	393 0	CAAAGAUAAUUAUUA UCAGGGCGAGUGCU
STMN2_ intron1	+	ATT C	192 5	CAATTTCAAAGATAAT TAATTATCAGGGCG	393 1	CAAUUCAAAGAUAAU UAAUUAUCAGGGCG
STMN2_ intron1	+	ATT A	192 6	ATTCCAATTTCAAAGA TAATTAATTATCAG	393 2	AUCCAAUUUCAAGA UAAUUAUUAUCAG
STMN2_ intron1	+	TTT G	192 7	AAATTAATTCCAATTT CAAAGATAATTAAT	393 3	AAAUAAUUCCAAUUU CAAAGAUAAUUAU
STMN2_ intron1	+	TTTT	192 8	GAAATTAATTCCAATT TCAAAGATAATTAA	393 4	GAAAUAAUUCCAAUU UCAAGAUAAUUA
STMN2_ intron1	+	ATT T	192 9	TGAAATTAATTCCAAT TTCAAAGATAATTA	393 5	UGAAAUAAUUCCAAU UUCAAAGAUAAUUA
STMN2_ intron1	+	ATT A	193 0	AAATAATAGATTTTGA AATTAATTCCAATT	393 6	AAAUAAUAGAUUUUGA AAUUAUUCCAAUU
STMN2_ intron1	+	TTTT	193 1	CCTGATTCATTAAACA ATTATGTATTCAGC	393 7	CCUGAUUCAUUAACA AUUAUGUAUUCAGC
STMN2_ intron1	+	TTTC	193 2	AGGATAAACTGAAA GAAATGGCAGTAGTT	393 8	AGGAUAAAACUGAAAG AAUUGGCAGUAGUU
STMN2_ intron1	+	ATT A	193 3	TGTATGTTTCATGTGGC TAAGATACATGTGC	393 9	UGUAUGUUC AUGUGGC UAAGAUACAUGUGC
STMN2_ intron1	+	TTT G	193 4	CTTCTGCCAGGATTA TGTATGTTTCATGTG	394 0	CUUCCUGCCAGGAUUA UGUAUGUUC AUGUG
STMN2_ intron1	+	TTT A	193 5	ATGATTCAGTAGCCTT GTTTGTTCCTCATTT	394 1	AUGAUUCAGUAGCCUU GUUUGUUCUCAUUU

STMN2_ intron1	+	ATT T	193 6	AATGATTTCAGTAGCCT TGTTTGTTCCTCATT	394 2	AAUGAUUCAGUAGCCU UGUUUGUUCUCAUU
STMN2_ intron1	+	ATT A	193 7	TTTAATGATTTCAGTAG CCTTGTTTGTTCCTC	394 3	UUUAAUGAUUCAGUAG CCUUGUUUGUUCUC
STMN2_ intron1	+	GTT A	193 8	TTATTTAATGATTTCAG TAGCCTTGTTTGT	394 4	UUAUUUAAUGAUUCAG UAGCCUUGUUUGUU
STMN2_ intron1	+	GTT G	193 9	TTATTATTTAATGATT CAGTAGCCTTGTTT	394 5	UUAUUUUUAAUGAUU CAGUAGCCUUGUUU
STMN2_ intron1	+	TTTC	194 0	AAATCGTTGTTATTAT TTAATGATTTCAGTA	394 6	AAAUCGUUGUUAUUUAU UUAAGAUUCAGUA
STMN2_ intron1	+	ATT T	194 1	CAAATCGTTGTTATTA TTTAATGATTTCAGT	394 7	CAAUCGUUGUUAUUA UUUAAUGAUUCAGU
STMN2_ intron1	+	ATT A	194 2	TCATTTCAAATCGTTG TTATTATTTAATGA	394 8	UCAUUUCAAUCGUUG UUAUUUUUAAUGA
STMN2_ intron1	+	ATT A	194 3	TTATCATTTCAAATCG TTGTTATTATTTAA	394 9	UUAUCAUUUCAAUCG UUGUUUAUUUUAA
STMN2_ intron1	+	TTTC	194 4	CGCTGCAGGCTAGTG GCTGCAAACATCATCG	395 0	CGCUGCAGGCUAGUGG CUGCAAACUCAUCG
STMN2_ intron1	+	GTT T	194 5	CCGCTGCAGGCTAGTG GCTGCAAACATCATC	395 1	CCGCUGCAGGCUAGUG GCUGCAAACUCAUC
STMN2_ intron1	+	TTTC	194 6	TGCACCCCTCAGAAA GGTTTCCGCTGCAGG	395 2	UGCACCCCUAGAAAAG GUUUCGCGUCAGG
STMN2_ intron1	+	CTTT	194 7	CTGCACCCCTCAGAAA GGTTTCCGCTGCAG	395 3	CUGCACCCCUAGAAA GGUUUCGCGUCAG
STMN2_ intron1	+	GTT C	194 8	TGAGAATGGGTGGTG GGGGCGATCTCGCCT	395 4	UGAGAAUGGGUGGUGG GGGCGAUCUCGCCU
STMN2_ intron1	+	GTT C	194 9	ACTCGCACGTCCAGA AAGGTTCTGAGAATG	395 5	ACUCGCACGUCCAGAA AGGUUCUGAGAAUG
STMN2_ intron1	+	ATT C	195 0	GCAGTTCACCTCGCACG TCCAGAAAGGTTCT	395 6	GCAGUUCACUCGCACG UCCAGAAAGGUUCU
STMN2_ intron1	+	TTTC	195 1	CACAATTCGCAGTTCA CTCGCACGTCCAGA	395 7	CACAAUUCGCAGUUCA CUCGCACGUCCAGA
STMN2_ intron1	+	CTTT	195 2	CCACAATTCGCAGTTC ACTCGCACGTCCAG	395 8	CCACAAUUCGCAGUUC ACUCGCACGUCCAG
STMN2_ intron1	+	TTTC	195 3	TGCGCAGTGTCTCTGAG CTACCCCCGCTTTC	395 9	UGCGCAGUGUCCUGAG CUACCCCCGCUUUC
STMN2_ intron1	+	GTT T	195 4	CTGCGCAGTGTCTCTGA GCTACCCCCGCTTT	396 0	CUGCGCAGUGUCCUGA GCUACCCCCGCUUU
STMN2_ intron1	+	GTT G	195 5	GGCGCTCGCCCCGCG GTGCAGCCGGGGAG	396 1	GGCGCUCGCCCCGCG GUGCAGCCGGGGAG
STMN2_ intron1	+	CTT C	195 6	TCTAAGGGAGACCCTC GCTCCTCCAGCGGG	396 2	UCUAAGGGAGACCCUC GCUCCUCCAGCGGG
STMN2_ intron1	+	TTTC	195 7	CAGAATGGAGACCCC GCGAGGGGCTTCTCT	396 3	CAGAAUGGAGACCCCG CGAGGGGCUUCUCU

STMN2_ intron1	+	TTTT	195 8	CCAGAATGGAGACCC CGCGAGGGGCTTCTC	396 4	CCAGAAUGGAGACCCC GCGAGGGGCUUCUC
STMN2_ intron1	+	ATT T	195 9	TCCAGAATGGAGACC CCGCGAGGGGCTTCT	396 5	UCCAGAAUGGAGACCC CGCGAGGGGCUUCU
STMN2_ intron1	+	GTT C	196 0	TCTATGATTTTCCAGA ATGGAGACCCCGCG	396 6	UCUAUGAUUUUCCAGA AUGGAGACCCCGCG
STMN2_ intron1	+	TTTC	196 1	CCCCAGCCCCAAGCCCC CGCCCCACCCTCTG	396 7	CCCCAGCCCCAAGCCCC CGCCCCACCUCUG
STMN2_ intron1	+	ATT C	196 2	AGTAGCCTTGTTTGT CTCATTTGTTCAAA	396 8	AGUAGCCUUGUUUGUU CUCAUUUGUUCAAA
STMN2_ intron1	+	CTT G	196 3	TTTGTTCTCATTTGTTC AAAAGGGACGTGG	396 9	UUUGUUCUCAUUUGUU CAAAAGGGACGUGG
STMN2_ intron1	+	GTT T	196 4	GTTCTCATTTGTTCAA AAGGGACGTGGATT	397 0	GUUCUCAUUUGUUCAA AAGGGACGUGGAUU
STMN2_ intron1	+	TTT G	196 5	TTCTCATTTGTTCAAA AGGGACGTGGATTG	397 1	UUCUCAUUUGUUCAAA AGGGACGUGGAUUG
STMN2_ intron1	+	TTTT	196 6	GCTTCCTGCCAGGATT ATGTATGTTTCATGT	397 2	GCUUCCUGCCAGGAUU AUGUAUGUUCAUGU
STMN2_ intron1	+	TTTT	196 7	TGCTTCCTGCCAGGAT TATGTATGTTTCATG	397 3	UGCUUCCUGCCAGGAU UAUGUAUGUUCAUG
STMN2_ intron1	+	ATT T	196 8	TTGCTTCCTGCCAGGA TTATGTATGTTTCAT	397 4	UUGCUUCCUGCCAGGA UUAUGUAUGUUCAU
STMN2_ intron1	+	GTT A	196 9	TAAAGCAAATATATTT TTGCTTCCTGCCAG	397 5	UAAAGCAAUAUAUUU UUGCUUCCUGCCAG
STMN2_ intron1	+	TTT A	197 0	AGTTATAAAGCAAAT ATATTTTGTCTCCT	397 6	AGUUAUAAAGCAAUA UAUUUUUGCUUCCU
STMN2_ intron1	+	TTTT	197 1	AAGTTATAAAGCAAA TATATTTTGTCTCC	397 7	AAGUUAUAAAGCAAUA UAUUUUUGCUUCC
STMN2_ intron1	+	ATT T	197 2	TAAGTTATAAAGCAA ATATATTTTGTCTC	397 8	UAAGUUAUAAAGCAA UAUAUUUUUGCUUC
STMN2_ intron1	+	GTT C	197 3	ATTTTAAGTTATAAAG CAAATATATTTTGTG	397 9	AUUUUAAGUUAUAAAG CAAUAUAUUUUUG
STMN2_ intron1	+	GTT G	197 4	TTCATTTTAAGTTATA AAGCAAATATATTT	398 0	UUCAUUUUAAGUUAUA AAGCAAUAUAUUU
STMN2_ intron1	+	TTT G	197 5	TCTCCAGTTGTTTCATT TTAAGTTATAAAGC	398 1	UCUCCAGUUGUUCAUU UUAAGUUAUAAAGC
STMN2_ intron1	+	ATT T	197 6	GTCTCCAGTTGTTTCAT TTTAAGTTATAAAG	398 2	GUCUCCAGUUGUUCAU UUUAAGUUAUAAAG
STMN2_ intron1	+	TTTC	197 7	CCCCACAAAAAGGTA AATTTGTCTCCAGTT	398 3	CCCCACAAAAAGGUAA AUUUGUCUCCAGUU
STMN2_ intron1	+	CTTT	197 8	CCCCACAAAAAGGT AAATTTGTCTCCAGT	398 4	CCCCACAAAAAGGUA AAUUGUCUCCAGU
STMN2_ intron1	+	CTT C	197 9	CTGCCAGGATTATGTA TGTTTCATGTGGCTA	398 5	CUGCCAGGAUUAUGUA UGUUCAUGUGGCUA

STMN2_ intron1	+	ATT G	198 0	CCCTCATCCCTTTCCC CCACAAAAAGGTAA	398 6	CCCUCAUCCCUUUCCCC CACAAAAAGGUAA
STMN2_ intron1	+	TTT G	198 1	CTTCCTCCTAATTGCC CTCATCCCTTTCCC	398 7	CUUCCUCCUAAUUGCC CUCAUCCCUUUC
STMN2_ intron1	+	CTTT	198 2	GCTTCCTCCTAATTGC CCTCATCCCTTTCC	398 8	GCUUCCUCCUAAUUGC CCUCAUCCCUUUC
STMN2_ intron1	+	GTT C	198 3	GCTTTGCTTCCTCCTA ATTGCCCTCATCCC	398 9	GCUUUGCUUCCUCCUA AUUGCCCUCAUCCC
STMN2_ intron1	+	GTT G	198 4	CGTTCGCTTTGCTTCC TCCTAATTGCCCTC	399 0	CGUUCGCUUUGCUUCC UCCUAAUUGCCCUC
STMN2_ intron1	+	CTT G	198 5	TTGCGTTCGCTTTGCT TCCTCCTAATTGCC	399 1	UUGCGUUCGCUUUGCU UCCUCCUAAUUGCC
STMN2_ intron1	+	ATT A	198 6	ACCCTTGTTGCGTTCG CTTTGCTTCCTCCT	399 2	ACCCUUGUUGCGUUCG CUUUGCUUCCUCCU
STMN2_ intron1	+	GTT A	198 7	AGGATTAACCCTTGTT GCGTTCGCTTTGCT	399 3	AGGAUUAACCCUUGUU GCGUUCGCUUUGCU
STMN2_ intron1	+	CTT G	198 8	GTTAAGGATTAACCCT TGTTGCGTTCGCTT	399 4	GUUAAGGAUUAACCCU UGUUGCGUUCGCUU
STMN2_ intron1	+	ATT G	198 9	CTCTTGTTAAGGATT AACCCTTGTTGCGT	399 5	CUCUUGGUUAAGGAUU AACCCUUGUUGCGU
STMN2_ intron1	+	GTT C	199 0	AAAAGGGACGTGGAT TGCTCTTGTTAAGG	399 6	AAAAGGGACGUGGAUU GCUCUUGGUUAAGG
STMN2_ intron1	+	TTT G	199 1	TTCAAAAGGGACGTG GATTGCTCTTGTTA	399 7	UUCAAAAGGGACGUGG AUUGCUCUUGGUUA
STMN2_ intron1	+	ATT T	199 2	GTTCAAAAGGGACGT GGATTGCTCTTGTT	399 8	GUUCAAAAGGGACGUG GAUUGCUCUUGGUU
STMN2_ intron1	+	GTT C	199 3	TCATTTGTTCAAAAGG GACGTGGATTGCTC	399 9	UCAUUUGUUCAAAAGG GACGUGGAUUGCUC
STMN2_ intron1	+	CTT C	199 4	CTCCTAATTGCCCTCA TCCCTTTCCCCCAC	400 0	CUCCUAAUUGCCCUCA UCCCUUCCCCCAC
STMN2_ intron1	+	TTTT	199 5	TGATTACATTTTATGT AATTCTAATCCAGC	400 1	UGAUUACAUUUAUGU AAUUCUAAUCCAGC
STMN2_ intron1	+	TTT A	199 6	ACTGCATTTGCAAATC ATGAAAAAAACACT	400 2	ACUGCAUUUGCAAUUC AUGAAAAAAACACU
STMN2_ intron1	+	TTT G	199 7	ATTACATTTTATGTAA TTCTAATCCAGCTA	400 3	AUUACAUUUAUGUAA UUCUAAUCCAGCUA
STMN2_ intron1	+	GTT C	199 8	GCACATTAACCATTAG TACAAGTACCCAAT	400 4	GCACAUUAACCAUAG UACAAGUACCCAAT
STMN2_ intron1	+	GTT G	199 9	GAGTTCGCACATTAAC CATTAGTACAAGTA	400 5	GAGUUCGCACAUUAAC CAUUAGUACAAGUA
STMN2_ intron1	+	TTT G	200 0	GATGTTGGAGTTCGCA CATTAAACCATTAGT	400 6	GAUGUUGGAGUUCGCA CAUUAACCAUAGU
STMN2_ intron1	+	TTTT	200 1	GGATGTTGGAGTTCGC ACATTAACCATTAG	400 7	GGAUGUUGGAGUUCGC ACAUUAACCAUAG

STMN2_ intron1	+	ATT T	200 2	TGGATGTTGGAGTTCG CACATTAACCATTA	400 8	UGGAUGUUGGAGUUCG CACAUUAACCAUUA
STMN2_ intron1	+	ATT G	200 3	TATTTTGGATGTTGGA GTTTCGCACATTAAC	400 9	UAUUUUGGAUGUUGGA GUUCGCACAUUAAC
STMN2_ intron1	+	CTT C	200 4	TGGAATAATTGTATTT TGGATGTTGGAGTT	401 0	UGGAAUAAUUGUAUUU UGGAUGUUGGAGUU
STMN2_ intron1	+	ATT C	200 5	TTCTGGAATAATTGTA TTTTGGATGTTGGA	401 1	UUCUGGAAUAAUUGUA UUUUGGAUGUUGGA
STMN2_ intron1	+	GTT A	200 6	TTCTTCTGGAATAATT GTATTTTGGATGTT	401 2	UUCUUCUGGAAUAAU GUAUUUUGGAUGUU
STMN2_ intron1	+	TTT A	200 7	GCAGTTATTCTTCTGG AATAATTGTATTTT	401 3	GCAGUUAUUCUUCUGG AAUAAUUGUAUUUU
STMN2_ intron1	+	ATT T	200 8	AGCAGTTATTCTTCTG GAATAATTGTATTT	401 4	AGCAGUUAUUCUUCUG GAAUAAUUGUAUUU
STMN2_ intron1	+	ATT G	200 9	TAAAGCAACGCCTGC AAGAGTGCCCATTTA	401 5	UAAAGCAACGCCUGCA AGAGUGCCCAUUA
STMN2_ intron1	+	TTT A	201 0	CAAAGATTGTAAAGC AACGCCTGCAAGAGT	401 6	CAAAGAUUGUAAAGCA ACGCCUGCAAGAGU
STMN2_ intron1	+	TTTT	201 1	ACAAAGATTGTAAAG CAACGCCTGCAAGAG	401 7	ACAAAGAUUGUAAAGC AACGCCUGCAAGAG
STMN2_ intron1	+	TTTT	201 2	TACAAAGATTGTAAA GCAACGCCTGCAAGA	401 8	UACAAAGAUUGUAAAG CAACGCCUGCAAGA
STMN2_ intron1	+	TTTT	201 3	TTACAAAGATTGTAA AGCAACGCCTGCAAG	401 9	UUACAAAGAUUGUAAA GCAACGCCUGCAAG
STMN2_ intron1	+	TTTT	201 4	TTTACAAAGATTGTAA AGCAACGCCTGCAA	402 0	UUUACAAAGAUUGUAA AGCAACGCCUGCAA
STMN2_ intron1	+	TTTT	201 5	TTTTACAAAGATTGTA AAGCAACGCCTGCA	402 1	UUUUACAAAGAUUGUA AAGCAACGCCUGCA
STMN2_ intron1	+	TTTT	201 6	TTTTTACAAAGATTGT AAAGCAACGCCTGC	402 2	UUUUUACAAAGAUUGU AAAGCAACGCCUGC
STMN2_ intron1	+	TTTT	201 7	TTTTTTACAAAGATTG TAAAGCAACGCCTG	402 3	UUUUUACAAAGAUUG UAAAGCAACGCCUG
STMN2_ intron1	+	TTTT	201 8	TTTTTTTACAAAGATT GTAAAGCAACGCCT	402 4	UUUUUUUACAAAGAUU GUAAAGCAACGCCU
STMN2_ intron1	+	TTTT	201 9	TTTTTTTTACAAAGAT TGTAAGCAACGCC	402 5	UUUUUUUACAAAGAU UGUAAAGCAACGCC
STMN2_ intron1	+	TTTT	202 0	TTTTTTTTTACAAAGA TTGTAAAGCAACGC	402 6	UUUUUUUUUACAAAGA UUGUAAAGCAACGC
STMN2_ intron1	+	ATT T	202 1	TTTTTTTTTTACAAAG ATTGTAAAGCAACG	402 7	UUUUUUUUUACAAAG AUUGUAAAGCAACG
STMN2_ intron1	+	ATT G	202 2	CCTAGGACTGAATGA TTTTTTTTTTTTTAC	402 8	CCUAGGACUGAAUGAU UUUUUUUUUUUAC
STMN2_ intron1	+	TTT A	202 3	TAGGGCAAAAATATT GCCTAGGACTGAATG	402 9	UAGGGCAAAAUAUUG CCUAGGACUGAAUG

STMN2_ intron1	+	TTTT	202 4	ATAGGGCAGAAAATAT TGCCTAGGACTGAAT	403 0	AUAGGGCAGAAAUAU GCCUAGGACUGAAU
STMN2_ intron1	+	ATT A	202 5	ACCATTAGTACAAGT ACCCAATATAACAAT	403 1	ACCAUAGUACAAGUA CCCAUAUAACAAU
STMN2_ intron1	+	TTTT	202 6	TATAGGGCAGAAAATA TTGCCTAGGACTGAA	403 2	UAUAGGGCAGAAAUAU UGCCUAGGACUGAA
STMN2_ intron1	+	ATT A	202 7	GTACAAGTACCCAAT ATAACAATAGATCAT	403 3	GUACAAGUACCCAUA UAACAAUAGAUCU
STMN2_ intron1	+	TTTT	202 8	AGTTGTATGTCTTTAT ATCAGGATAAAGAG	403 4	AGUUGUAUGUCUUUAU AUCAGGAUAAAGAG
STMN2_ intron1	+	TTTC	202 9	CTTATGAAATGCAGCC ATAAAGTTTAACTT	403 5	CUUAUGAAAUGCAGCC AUAAGUUUAACUU
STMN2_ intron1	+	TTTT	203 0	CCTTATGAAATGCAGC CATAAAGTTTAACT	403 6	CCUUAUGAAAUGCAGC CAUAAAGUUUAACU
STMN2_ intron1	+	TTTT	203 1	TCCTTATGAAATGCAG CCATAAAGTTTAACT	403 7	UCCUUAUGAAAUGCAG CCAUAAGUUUAAC
STMN2_ intron1	+	TTTT	203 2	TTCCTTATGAAATGCA GCCATAAAGTTTAA	403 8	UUCCUUAUGAAAUGC GCCAUAAGUUUA
STMN2_ intron1	+	TTTT	203 3	TTTCCTTATGAAATGC AGCCATAAAGTTTA	403 9	UUUCCUUAUGAAAUGC AGCCAUAAGUUUA
STMN2_ intron1	+	TTTT	203 4	TTTCCTTATGAAATG CAGCCATAAAGTTT	404 0	UUUCCUUAUGAAAUG CAGCCAUAAGUUU
STMN2_ intron1	+	GTT T	203 5	TTTTTCCTTATGAAAT GCAGCCATAAAGTT	404 1	UUUUUCCUUAUGAAU GCAGCCAUAAGUU
STMN2_ intron1	+	TTT G	203 6	GAAGTTTTTTTTTCCT ATGAAATGCAGCCA	404 2	GAAGUUUUUUUCCU AUGAAAUGCAGCCA
STMN2_ intron1	+	CTTT	203 7	GGAAGTTTTTTTTTCCT TATGAAATGCAGCC	404 3	GGAAGUUUUUUUCCU UAUGAAAUGCAGCC
STMN2_ intron1	+	ATT C	203 8	TACTCTGTCTTTGGAA GTTTTTTTTTCCTTA	404 4	UACUCUGUCUUUGGAA GUUUUUUUUCCUUA
STMN2_ intron1	+	ATT A	203 9	GCATTCTACTCTGTCT TTGGAAGTTTTTTT	404 5	GCAUUCUACUCUGUCU UUGGAAGUUUUUU
STMN2_ intron1	+	TTT A	204 0	TTAGCATTCTACTCTG TCTTTGGAAGTTTT	404 6	UUAGCAUUCUACUCUG UCUUUGGAAGUUUU
STMN2_ intron1	+	TTTT	204 1	ATTAGCATTCTACTCT GTCTTTGGAAGTTT	404 7	AUUAGCAUUCUACUCU GUCUUUGGAAGUUU
STMN2_ intron1	+	TTTT	204 2	TATTAGCATTCTACTC TGTCTTTGGAAGTT	404 8	UAUUAGCAUUCUACUC UGUCUUUGGAAGUU
STMN2_ intron1	+	ATT T	204 3	TTATTAGCATTCTACT CTGTCTTTGGAAGT	404 9	UUUUUAGCAUUCUACU CUGUCUUUGGAAGU
STMN2_ intron1	+	ATT A	204 4	AATTTTATTAGCATT CTACTCTGTCTTTG	405 0	AAUUUUUAUUAGCAUU CUACUCUGUCUUUG
STMN2_ intron1	+	GTT A	204 5	AAGTGTAATTTAAATT TTATTAGCATTCT	405 1	AAGUGUAAAUUAAAU UUUAUUAGCAUUCU

STMN2_ intron1	+	TTT A	204 6	CAAGAGAGCATGTTA AAGTGTAATTTAAAT	405 2	CAAGAGAGCAUGUUA AGUGUAAAUUAAA
STMN2_ intron1	+	TTTT	204 7	ACAAGAGAGCATGTT AAAGTGTAATTTAAA	405 3	ACAAGAGAGCAUGUUA AAGUGUAAAUUAAA
STMN2_ intron1	+	CTTT	204 8	TACAAGAGAGCATGT TAAAGTGTAATTTAA	405 4	UACAAGAGAGCAUGUU AAAGUGUAAAUUAA
STMN2_ intron1	+	TTT A	204 9	TCTAAACCTAGTCCCA CAAATACTTTTACA	405 5	UCUAAACCUAGUCCCA CAAAUACUUUUACA
STMN2_ intron1	+	ATT T	205 0	ATCTAAACCTAGTCCC ACAAATACTTTTAC	405 6	AUCUAAACCUAGUCCC ACAAAUACUUUUAC
STMN2_ intron1	+	ATT G	205 1	AGTGAAATTTATCTAA ACCTAGTCCCACAA	405 7	AGUGAAAUUUAUCUAA ACCUAGUCCCACAA
STMN2_ intron1	+	TTT A	205 2	TATCAGGATAAAGAG AATTGAGTGAAATTT	405 8	UAUCAGGAUAAAGAGA AUUGAGUGAAAUUU
STMN2_ intron1	+	CTTT	205 3	ATATCAGGATAAAGA GAATTGAGTGAAATT	405 9	AUAUCAGGAUAAAGAG AAUUGAGUGAAAUU
STMN2_ intron1	+	GTT G	205 4	TATGTCTTTATATCAG GATAAAGAGAATTG	406 0	UAUGUCUUUAUAUCAG GAUAAAGAGAAUUG
STMN2_ intron1	+	TTT A	205 5	GTTGTATGTCTTTATA TCAGGATAAAGAGA	406 1	GUUGUAUGUCUUUAUA UCAGGAUAAAGAGA
STMN2_ intron1	+	CTTT	205 6	TAGTTGTATGTCTTTA TATCAGGATAAAGA	406 2	UAGUUGUAUGUCUUUA UAUCAGGAUAAAGA
STMN2_ intron1	+	ATT T	205 7	TTATAGGGCAAAAAT ATTGCCTAGGACTGA	406 3	UUUAUAGGGCAAAAUA UUGCCUAGGACUGA
STMN2_ intron1	+	TTT A	205 8	TTTTTATAGGGCAAAA ATATTGCCTAGGAC	406 4	UUUUUAUAGGGCAAAA AUUAUUGCCUAGGAC
STMN2_ intron1	+	ATT T	205 9	ATTTTTATAGGGCAAAA AATATTGCCTAGGA	406 5	AUUUUUAUAGGGCAAAA AAUAUUGCCUAGGA
STMN2_ intron1	+	TTTC	206 0	AGCCATCATTTTGCTG GTCATGTGGAAATA	406 6	AGCCAUCAUUUUGCUG GUCAUGUGGAAAUA
STMN2_ intron1	+	ATT T	206 1	CAGCCATCATTTTGCT GGTCATGTGGAAAT	406 7	CAGCCAUCAUUUUGCU GGUCAUGUGGAAAU
STMN2_ intron1	+	ATT A	206 2	ATGCATTTCAGCCATC ATTTTGCTGGTCAT	406 8	AUGCAUUUCAGCCAUC AUUUUGCUGGUCAU
STMN2_ intron1	+	GTT A	206 3	ATTAATGCATTTTCAGC CATCATTTTGCTGG	406 9	AUUAUUGCAUUUCAGC CAUCAUUUUGCUGG
STMN2_ intron1	+	TTT A	206 4	TATGAGTGTAAGGTT AATTAATGCATTTC	407 0	UAUGAGUGUAAAGGUU AAUUAUUGCAUUUC
STMN2_ intron1	+	TTTT	206 5	ATATGAGTGTAAGG TTAATTAATGCATTT	407 1	AUAUGAGUGUAAAGGU UAAUUAAUGCAUUU
STMN2_ intron1	+	CTTT	206 6	TATATGAGTGTAAGG GTAAATTAATGCATT	407 2	UAUAUGAGUGUAAAGG UUAAUUAAUGCAUU
STMN2_ intron1	+	GTT C	206 7	TCACAAAACACTTTTA TATGAGTGTAAGG	407 3	UCACAAAACACUUUUA UAUGAGUGUAAAGG

STMN2_ intron1	+	TTT G	206 8	TTCTCACAAAACACTT TTATATGAGTGTA	407 4	UUCUCACAAAACACUU UUAUAUGAGUGUAA
STMN2_ intron1	+	ATT T	206 9	GTTCTCACAAAACACT TTATATGAGTGTA	407 5	GUUCUCACAAAACACU UUUAUAUGAGUGUA
STMN2_ intron1	+	TTT G	207 0	TGTACATTTGTTCTCA CAAAACACTTTTAT	407 6	UGUACAUUUGUUCUCA CAAAACACUUUUUAU
STMN2_ intron1	+	ATT T	207 1	GTGTACATTTGTTCTC ACAAAACACTTTTA	407 7	GUGUACAUUUGUUCUC ACAAAACACUUUUA
STMN2_ intron1	+	ATT A	207 2	AAGATAACATTTGTGT ACATTTGTTCTCAC	407 8	AAGAUAAACAUUUGUGU ACAUUUGUUCUCAC
STMN2_ intron1	+	ATT A	207 3	GTCATGATTAAAGAT AACATTTGTGTACAT	407 9	GUCAUGAUUAAAGAU ACAUUUGUGUACAU
STMN2_ intron1	+	TTT A	207 4	TTAGTCATGATTAAAG ATAACATTTGTGTA	408 0	UUAGUCAUGAUUAAAG AUAACAUUUGUGUA
STMN2_ intron1	+	TTTT	207 5	ATTAGTCATGATTAAA GATAACATTTGTGT	408 1	AUUAGUCAUGAUUAAA GAUAACAUUUGUGU
STMN2_ intron1	+	TTTT	207 6	TATTAGTCATGATTAA AGATAACATTTGTG	408 2	UAUUAGUCAUGAUUAA AGAUAAAUUUGUG
STMN2_ intron1	+	ATT T	207 7	TTATTAGTCATGATT AAGATAACATTTGT	408 3	UUUUAGUCAUGAUUA AAGAUAAAUUUGU
STMN2_ intron1	+	TTT A	207 8	TAATATCCATTTTAT TAGTCATGATTAAA	408 4	UAAUAUCCAUUUUUAU UAGUCAUGAUUAAA
STMN2_ intron1	+	GTT T	207 9	ATAATATCCATTTT TTAGTCATGATTAA	408 5	AUAAUAUCCAUUUUUA UUAGUCAUGAUUAA
STMN2_ intron1	+	CTT G	208 0	TGTTTATAATATCCAT TTTTATTAGTCATG	408 6	UGUUUAUAAUAUCCA UUUUUUUAGUCAUG
STMN2_ intron1	+	TTT G	208 1	CAGTAGTAAAGCTTGT GTTTATAATATCCA	408 7	CAGUAGUAAAGCUUGU GUUUUAUAAUAUCCA
STMN2_ intron1	+	ATT T	208 2	GCAGTAGTAAAGCTT GTGTTTATAATATCC	408 8	GCAGUAGUAAAGCUUG UGUUUAUAAUAUCC
STMN2_ intron1	+	TTT G	208 3	TCAAGGAGACATTTG CAGTAGTAAAGCTTG	408 9	UCAAGGAGACAUUUGC AGUAGUAAAGCUUG
STMN2_ intron1	+	ATT T	208 4	GTCAAGGAGACATTT GCAGTAGTAAAGCTT	409 0	GUCAAGGAGACAUUUG CAGUAGUAAAGCUU
STMN2_ intron1	+	TTT A	208 5	ATAAAGGAATCAGGC CCTGTCATTTGTCAA	409 1	AUAAAGGAAUCAGGCC CUGUCAUUUGUCA
STMN2_ intron1	+	TTTT	208 6	AATAAAGGAATCAGG CCCTGTCATTTGTCA	409 2	AAUAAAGGAAUCAGGC CCUGUCAUUUGUCA
STMN2_ intron1	+	ATT T	208 7	TGCTGGTCATGTGGAA ATATAGCTTCTTTA	409 3	UGCUGGUCAUGUGGAA AUUAAGCUUCUUUA
STMN2_ intron1	+	TTTT	208 8	GCTGGTCATGTGGAA ATATAGCTTCTTTAG	409 4	GCUGGUCAUGUGGAAA UAUAGCUUCUUUAG
STMN2_ intron1	+	TTT G	208 9	CTGGTCATGTGGAAAT ATAGCTTCTTTAGG	409 5	CUGGUCAUGUGGAAAU AUAGCUUCUUUAGG

STMN2_ intron1	+	CTT C	209 0	TTTAGGAATTGTACTT AGAGTAGGAGCCAC	409 6	UUUAGGAAUUGUACUU AGAGUAGGAGCCAC
STMN2_ intron1	+	TTT A	209 1	AAATAATTTATTTTAA TAGGGCAAAAATAT	409 7	AAAUAAUUUAUUUUUA UAGGGCAAAAUAU
STMN2_ intron1	+	ATT T	209 2	AAAATAATTTATTTTT ATAGGGCAAAAATA	409 8	AAAAUAAUUUAUUUUU AUAGGGCAAAAUA
STMN2_ intron1	+	GTT C	209 3	TCATAGAGCACATTTA AAATAATTTATTTT	409 9	UCAUAGAGCACAUUUA AAAUAAUUUAUUUU
STMN2_ intron1	+	ATT A	209 4	CAGTTCTCATAGAGCA CATTTAAAATAATT	410 0	CAGUUCUCAUAGAGCA CAUUUAAAAUAAU
STMN2_ intron1	+	TTT A	209 5	TGGCAAGAAATAGAT AATTACAGTTCTCAT	410 1	UGGCAAGAAUAGAU AUUACAGUUCUCAU
STMN2_ intron1	+	TTTT	209 6	ATGGCAAGAAATAGA TAATTACAGTTCTCA	410 2	AUGGCAAGAAUAGAU AAUACAGUUCUCA
STMN2_ intron1	+	ATT T	209 7	TATGGCAAGAAATAG ATAATTACAGTTCTC	410 3	UAUGGCAAGAAUAGA UAAUACAGUUCUC
STMN2_ intron1	+	TTT A	209 8	TTTTATGGCAAGAAAT AGATAATTACAGTT	410 4	UUUUAUGGCAAGAAU AGAUAAUACAGUU
STMN2_ intron1	+	ATT T	209 9	ATTTTATGGCAAGAA ATAGATAATTACAGT	410 5	AUUUUAUGGCAAGAAA UAGAUAAUACAGU
STMN2_ intron1	+	TTTC	210 0	AAAATTTATTTTATGG CAAGAAATAGATAA	410 6	AAAAUUUAUUUUAUGG CAAGAAUAGAUAA
STMN2_ intron1	+	GTT T	210 1	CAAAATTTATTTTATG GCAAGAAATAGATA	410 7	CAAAUUUAUUUUAUG GCAAGAAUAGAU
STMN2_ intron1	+	GTT A	210 2	TGGGTTTCAAAATTTA TTTTATGGCAAGAA	410 8	UGGGUUUCAAAAUUUA UUUUAUGGCAAGAA
STMN2_ intron1	+	TTT A	210 3	ATACTCTGAAAAGTTA TGGGTTTCAAAATT	410 9	AUACUCUGGAAAGUUA UGGGUUUCAAAAUU
STMN2_ intron1	+	CTT A	210 4	TGAAATGCAGCCATA AAGTTTAACTTCCAT	411 0	UGAAAUGCAGCCAUAA AGUUUAACUCCAU
STMN2_ intron1	+	ATT T	210 5	AATACTCTGGAAAGTT ATGGGTTTCAAAAT	411 1	AAUACUCUGGAAAGUU AUGGGUUUCAAAAU
STMN2_ intron1	+	GTT G	210 6	TTGACCTCCAGAGTAA AATATTTAATACTC	411 2	UUGACCUCCAGAGUAA AAUAUUUAUACUC
STMN2_ intron1	+	CTT G	210 7	TTGTTGACCTCCAGAG TAAAATATTTAATA	411 3	UUGUUGACCUCCAGAG UAAAAUAUUUAAUA
STMN2_ intron1	+	GTT C	210 8	TCACTTGTTGTTGACC TCCAGAGTAAAATA	411 4	UCACUUGUUGUUGACC UCCAGAGUAAAAUA
STMN2_ intron1	+	TTT G	210 9	TTCTCACTTGTTGTTG ACCTCCAGAGTAAA	411 5	UUCUCACUUGUUGUUG ACCUCCAGAGUAAA
STMN2_ intron1	+	GTT T	211 0	GTTCTCACTTGTTGTT GACCTCCAGAGTAA	411 6	GUUCUCACUUGUUGUU GACCUCCAGAGUAA
STMN2_ intron1	+	TTT A	211 1	AGTTTGTTCTCACTTG TTGTTGACCTCCAG	411 7	AGUUUGUUCUCACUUG UUGUUGACCUCCAG

STMN2_ intron1	+	TTTT	211 2	AAGTTTGTTCCTCACT GTTGTTGACCTCCA	411 8	AAGUUUGUUCUCACUU GUUGUUGACCUCCA
STMN2_ intron1	+	ATT T	211 3	TAAGTTTGTTCCTCACT TGTTGTTGACCTCC	411 9	UAAGUUUGUUCUCACU UGUUGUUGACCUCC
STMN2_ intron1	+	ATT A	211 4	TACTATAAAACCATA ACAAAAATATTTTAA	412 0	UACUAUAAAACCAUAA CAAAAAUAUUUUA
STMN2_ intron1	+	CTT A	211 5	GAGTAGGAGCCACAT ATTATACTATAAAAC	412 1	GAGUAGGAGCCACAUA UUAUACUAUAAAAC
STMN2_ intron1	+	ATT G	211 6	TACTTAGAGTAGGAG CCACATATTATACTA	412 2	UACUUAGAGUAGGAGC CACAUAUUAUACUA
STMN2_ intron1	+	TTT A	211 7	GGAATTGTACTTAGA GTAGGAGCCACATAT	412 3	GGAAUUGUACUAGAG UAGGAGCCACAUAU
STMN2_ intron1	+	CTTT	211 8	AGGAATTGTACTTAG AGTAGGAGCCACATA	412 4	AGGAAUUGUACUUAGA GUAGGAGCCACAUA
STMN2_ intron1	+	GTT G	211 9	ACCTCCAGAGTAAAA TATTTAATACTCTGG	412 5	ACCUCCAGAGUAAAAU AUUUAUACUCUGG
STMN2_ intron1	+	GTT T	212 0	AACTTCCATTAACAAA GCTGCTCACAGTAA	412 6	AACUCCAUUAACAAA GCUGCUCACAGUAA
STMN2_ intron1	+	TTT A	212 1	ACTTCCATTAACAAAG CTGCTCACAGTAAA	412 7	ACUCCAUUAACAAAG CUGCUCACAGUAAA
STMN2_ intron1	+	CTT C	212 2	CATTAACAAAGCTGCT CACAGTAAACCTAT	412 8	CAUUAACAAAGCUGCU CACAGUAAACCUAU
STMN2_ intron1	+	ATT T	212 3	AAAGATTGGTAAATTT AAGCTCAAATAATT	412 9	AAAGAUUGGUAAAUUU AAGCUCAAAUAUUU
STMN2_ intron1	+	CTT A	212 4	TTTAAAGATTGGTAAA TTTAAGCTCAAATA	413 0	UUUAAAGAUUGGUAAA UUUAAGCUCAAAUA
STMN2_ intron1	+	GTT G	212 5	TCTTATTTAAAGATTG GTAAATTTAAGCTC	413 1	UCUUAUUUAAAGAUUG GUAAAUUUAAGCUC
STMN2_ intron1	+	CTT C	212 6	ATATAATCCCTCTGAG ATGGGCATACTATA	413 2	AUAUAAUCCCUCUGAG AUGGGCAUACUAUA
STMN2_ intron1	+	TTT G	212 7	AATCTTCATATAATCC CTCTGAGATGGGCA	413 3	AAUCUUCAUUAAUCC CUCUGAGAUGGGCA
STMN2_ intron1	+	TTTT	212 8	GAATCTTCATATAATC CCTCTGAGATGGGC	413 4	GAAUCUUCAUUAAUCC CCUCUGAGAUGGGC
STMN2_ intron1	+	CTTT	212 9	TGAATCTTCATATAAT CCCTCTGAGATGGG	413 5	UGAAUCUUCAUUAAU CCCUCUGAGAUGGG
STMN2_ intron1	+	CTT C	213 0	ATCCTTTTGAATCTTC ATATAATCCCTCTG	413 6	AUCCUUUUGAAUCUUC AUAUAAUCCCUCUG
STMN2_ intron1	+	ATT C	213 1	ACCTGCTTCATCCTTT TGAATCTTCATATA	413 7	ACCUGCUUCAUCCUUU UGAAUCUUCAUUA
STMN2_ intron1	+	TTT A	213 2	GAAAACATTACCTGC TTCATCCTTTTGAA	413 8	GAAAACAUUCACCUGC UUCAUCCUUUUGAA
STMN2_ intron1	+	TTTT	213 3	AGAAAACATTACCT GCTTCATCCTTTTGA	413 9	AGAAAACAUUCACCUG CUUCAUCCUUUUGA

STMN2_ intron1	+	TTTT	213 4	TAGAAAACATTACCT GCTTCATCCTTTTG	414 0	UAGAAAACAUUCACCU GCUUCAUCCUUUUG
STMN2_ intron1	+	ATT T	213 5	TTAGAAAACATTACCC TGCTTCATCCTTTT	414 1	UUAGAAAACAUUCACC UGCUUCAUCCUUUU
STMN2_ intron1	+	CTT G	213 6	TCATTTTTAGAAAACA TTCACCTGCTTCAT	414 2	UCAUUUUUAGAAAACA UUCACCUGCUUCAU
STMN2_ intron1	+	ATT A	213 7	AATCGCATGATCTATC TATATGGGACCTTG	414 3	AAUCGCAUGAUCUAUC UAUAUGGGACCUUG
STMN2_ intron1	+	GTT C	213 8	AAAAGAAAAATTAAA TCGCATGATCTATCT	414 4	AAAAGAAAAAUAAAAU CGCAUGAUCUAUCU
STMN2_ intron1	+	TTT A	213 9	AAAGGAGCAGGCAAG CATAGAAGACTAAAA	414 5	AAAGGAGCAGGCAAGC AUAGAAGACUAAAA
STMN2_ intron1	+	TTTT	214 0	AAAAGGAGCAGGCAA GCATAGAAGACTAAA	414 6	AAAAGGAGCAGGCAAG CAUAGAAGACUAAA
STMN2_ intron1	+	TTTT	214 1	TAAAAGGAGCAGGCA AGCATAGAAGACTAA	414 7	UAAAAGGAGCAGGCAA GCAUAGAAGACUAA
STMN2_ intron1	+	TTTT	214 2	TTAAAAGGAGCAGGC AAGCATAGAAGACTA	414 8	UUAAAAGGAGCAGGCA AGCAUAGAAGACUA
STMN2_ intron1	+	GTT T	214 3	TTTAAAAGGAGCAGG CAAGCATAGAAGACT	414 9	UUUAAAAGGAGCAGGC AAGCAUAGAAGACU
STMN2_ intron1	+	CTT A	214 4	TATAGTTTTTTAAAAG GAGCAGGCAAGCAT	415 0	UAUAGUUUUUAAAAG GAGCAGGCAAGCAU
STMN2_ intron1	+	TTTC	214 5	TTATATAGTTTTTTAA AAGGAGCAGGCAAG	415 1	UUUAUAGUUUUUUA AAGGAGCAGGCAAG
STMN2_ intron1	+	TTTT	214 6	CTTATATAGTTTTTTA AAAGGAGCAGGCAA	415 2	CUUAUAGUUUUUA AAAGGAGCAGGCAA
STMN2_ intron1	+	TTTT	214 7	TCCTATATAGTTTTTT AAAAGGAGCAGGCA	415 3	UCUUAUAGUUUUUU AAAAGGAGCAGGCA
STMN2_ intron1	+	TTTT	214 8	TTCTTATATAGTTTTTT AAAAGGAGCAGGC	415 4	UUCUUAUAGUUUUU UAAAAGGAGCAGGC
STMN2_ intron1	+	TTTT	214 9	TTTCTTATATAGTTTTT TAAAAGGAGCAGG	415 5	UUUCUUAUAGUUUU UUAAAAGGAGCAGG
STMN2_ intron1	+	TTT A	215 0	AAGATTGGTAAATTTA AGCTCAAATAATTT	415 6	AAGAUUGGUAAAUUUA AGCUCAAUAUUUU
STMN2_ intron1	+	ATT G	215 1	GTAAATTTAAGCTCAA ATAATTTATTCAGT	415 7	GUAAAUUUAAGCUCAA AUAUUUAUUCAGU
STMN2_ intron1	+	ATT T	215 2	AAGCTCAAATAATTTA TTCAGTGGCAAGCC	415 8	AAGCUCAAUAUUUA UUCAGUGGCAAGCC
STMN2_ intron1	+	TTT A	215 3	AGCTCAAATAATTTAT TCAGTGGCAAGCCT	415 9	AGCUCAAUAUUUAU UCAGUGGCAAGCCU
STMN2_ intron1	+	TTT G	215 4	TTCTGAAGCCTGTGCC AGGTATTATGAGAA	416 0	UUCUGAAGCCUGUGCC AGGUUAUAUGAGAA
STMN2_ intron1	+	TTTT	215 5	GATTACATTTTATGTA ATTCTAATCCAGCT	416 1	GAUUACAUUUAUGUA AUUCUAAUCCAGCU

STMN2_ intron1	+	CTTT	215 6	GTTCTGAAGCCTGTGC CAGGTATTATGAGA	416 2	GUUCUGAAGCCUGUGC CAGGUAUUAUGAGA
STMN2_ intron1	+	ATT G	215 7	GAGCACCAACTTTGTT CTGAAGCCTGTGCC	416 3	GAGCACCAACUUUGUU CUGAAGCCUGUGCC
STMN2_ intron1	+	ATT G	215 8	ATAGTCAGTGTCACTA ACTAAAGTAAAATA	416 4	AUAGUCAGUGUCACUA ACUAAAGUAAAAUA
STMN2_ intron1	+	TTT A	215 9	AAGTCATTGATAGTCA GTGTCACCTAACTAA	416 5	AAGUCAUUGAUAGUCA GUGUCACUAACTAA
STMN2_ intron1	+	GTT T	216 0	AAAGTCATTGATAGTC AGTGTCACTAACTA	416 6	AAAGUCAUUGAUAGUC AGUGUCACUAACTA
STMN2_ intron1	+	CTT C	216 1	AGTTTAAAGTCATTGA TAGTCAGTGTCACT	416 7	AGUUUAAAGUCAUUGA UAGUCAGUGUCACU
STMN2_ intron1	+	TTT G	216 2	TCTTCAGTTTAAAGTC ATTGATAGTCAGTG	416 8	UCUUCAGUUUAAAGUC AUUGAUAGUCAGUG
STMN2_ intron1	+	ATT T	216 3	GTCTTCAGTTTAAAGT CATTGATAGTCAGT	416 9	GUCUUCAGUUUAAAGU CAUUGAUAGUCAGU
STMN2_ intron1	+	TTT A	216 4	GCACTCCCTCCACTGT CCTGTAATAAAAACA	417 0	GCACUCCCUCCACUGU CCUGUAAUAAAACA
STMN2_ intron1	+	GTT T	216 5	AGCACTCCCTCCACTG TCCTGTAATAAAAAC	417 1	AGCACUCCCUCCACUG UCCUGUAAUAAAAC
STMN2_ intron1	+	ATT C	216 6	ATGCAAAATAAGGTT TAGCACTCCCTCCAC	417 2	AUGCAAAUAAGGUUU AGCACUCCCUCCAC
STMN2_ intron1	+	ATT T	216 7	TTTTCTTATATAGTTTT TTAAAAGGAGCAG	417 3	UUUUCUUUAUAGUUU UUUAAAAGGAGCAG
STMN2_ intron1	+	TTTC	216 8	ATACATATATACACAT TCATGCAAAATAAG	417 4	AUACAUUAUACACAU UCAUGCAAAUAAG
STMN2_ intron1	+	GTT A	216 9	TATATCATGTATGTGC CTATTTTCATACATA	417 5	UAUAUCAUGUAUGUGC CUAUUUCAUACAU
STMN2_ intron1	+	TTT A	217 0	TATGTAATATATAAAT ATGTTATATATCAT	417 6	UAUGUAAUAUUAUAAU AUGUUAUUAUCAU
STMN2_ intron1	+	ATT T	217 1	ATATGTAATATATAAA TATGTTATATATCA	417 7	AUAUGUAAUAUUAUAA UAUGUUAUUAUCA
STMN2_ intron1	+	TTT A	217 2	CCTATCAAAATATTTA TATGTAATATATAA	417 8	CCUAUCAAAAUUUUA UAUGUAAUAUUAUAA
STMN2_ intron1	+	ATT T	217 3	ACCTATCAAAATATTT ATATGTAATATATA	417 9	ACCUAUCAAAUAUUU AUAUGUAAUAUUAU
STMN2_ intron1	+	ATT A	217 4	TTTACCTATCAAAATA TTTATATGTAATAT	418 0	UUUACCUAUCAAAUA UUUAUAUGUAAUUAU
STMN2_ intron1	+	GTT G	217 5	TGTATATTATTTACCT ATCAAAATATTTAT	418 1	UGUAUAUUUUUACCU AUCAAAUAUUUAU
STMN2_ intron1	+	ATT A	217 6	CATATAATAAAGTTGT GTATATTATTTACC	418 2	CAUAUAAUAAAGUUGU GUAUAUUUUUACC
STMN2_ intron1	+	ATT A	217 7	TAACATATAATATATA TATTACATATAATA	418 3	UAAUAUAUAAUUAUA UAUUACAUAUAAUA

STMN2_ intron1	+	ATT A	217 8	TATATATATTATAACA TATAATATATATAT	418 4	UAUAUAUAUAUAACA UAUAAUAUAUAUAU
STMN2_ intron1	+	ATT C	217 9	AGTGGCAAGCCTCAG AGGCAGACTCGGAAC	418 5	AGUGGCAAGCCUCAGA GGCAGACUCGGAAC
STMN2_ intron1	+	TTT A	218 0	TTCAGTGGCAAGCCTC AGAGGCAGACTCGG	418 6	UUCAGUGGCAAGCCUC AGAGGCAGACUCGG
STMN2_ intron1	+	ATT T	218 1	ATTCAGTGGCAAGCCT CAGAGGCAGACTCG	418 7	AUUCAGUGGCAAGCCU CAGAGGCAGACUCG
STMN2_ intron1	+	ATT T	218 2	CATACATATATACACA TTCATGCAAAATAA	418 8	CAUACAUUAUACACA UUCAUGCAAAAUAA
STMN2_ intron1	+	CTTT	218 3	TAATAAAGGAATCAG GCCCTGTCATTTGTC	418 9	UAAUAAAGGAUCAGG CCCUGUCAUUUGUC
STMN2_ intron1	+	TTTC	218 4	TGATGATTTTTTTCTT ATATAGTTTTTTAA	419 0	UGAUGAUUUUUUCUU AUUAAGUUUUUAA
STMN2_ intron1	+	ATT A	218 5	TATTTCTGATGATTTT TTTCTTATATAGTT	419 1	UAUUUCUGAUGAUUUU UUUCUUAUAUAGUU
STMN2_ intron1	+	CTTT	218 6	TTATTTCCAACAAAAA TATCTATTGTTATT	419 2	UUAUUUCCAACAAAAA UAUCUAUUGUUAUU
STMN2_ intron1	+	GTT A	218 7	CTTTTTATTTCCAACA AAAATATCTATTGT	419 3	CUUUUUAUUUCCAACA AAAAUAUCUAUUGU
STMN2_ intron1	+	ATT A	218 8	ATGCAGAGTTACTTTT TATTTCCAACAAAA	419 4	AUGCAGAGUUACUUUU UAUUUCCAACAAAA
STMN2_ intron1	+	TTT A	218 9	TTAATGCAGAGTTACT TTTTATTTCCAACA	419 5	UUA AUGCAGAGUUACU UUUUAUUUCCAACA
STMN2_ intron1	+	TTTT	219 0	ATTAATGCAGAGTTAC TTTTTATTTCCAAC	419 6	AUUA AUGCAGAGUUAC UUUUUAUUUCCAAC
STMN2_ intron1	+	TTTT	219 1	TATTAATGCAGAGTTA CTTTTTATTTCCAA	419 7	UAUUA AUGCAGAGUUA CUUUUUAUUUCCAA
STMN2_ intron1	+	ATT T	219 2	TTATTAATGCAGAGTT ACTTTTTATTTCCA	419 8	UUAUUA AUGCAGAGUU ACUUUUUAUUUCCA
STMN2_ intron1	+	ATT A	219 3	TTTTTATTAATGCAGA GTTACTTTTTATTT	419 9	UUUUUAUUA AUGCAGA GUUACUUUUUAUUU
STMN2_ intron1	+	CTT C	219 4	AGAACATAATTATTTT TATTAATGCAGAGT	420 0	AGAACAUAAUUAUUUU UAUUA AUGCAGAGU
STMN2_ intron1	+	ATT G	219 5	CAGCCTCCCTGGGAAC TCTGCTTCAGAACA	420 1	CAGCCUCCCUGGGAAC UCUGCUUCAGAACA
STMN2_ intron1	+	CTT A	219 6	TTGCAGCCTCCCTGGG AACTCTGCTTCAGA	420 2	UUGCAGCCUCCCUGGG AACUCUGCUUCAGA
STMN2_ intron1	+	TTT A	219 7	GGATAGACTTATTGCA GCCTCCCTGGGAAC	420 3	GGAUAGACUUAUUGCA GCCUCCCUGGGAAC
STMN2_ intron1	+	TTTT	219 8	AGGATAGACTTATTGC AGCCTCCCTGGGAA	420 4	AGGAUAGACUUAUUGC AGCCUCCCUGGGAA
STMN2_ intron1	+	CTTT	219 9	TAGGATAGACTTATTG CAGCCTCCCTGGGA	420 5	UAGGAUAGACUUAUUG CAGCCUCCCUGGGA

STMN2_ intron1	+	ATT A	220 0	ATCATCTCAGGCACTT TTAGGATAGACTTA	420 6	AUCAUCUCAGGCACUU UUAGGAUAGACUUA
STMN2_ intron1	+	ATT T	220 1	CCAGACTCTCGGGAA GAACATTAATCATCT	420 7	CCAGACUCUCGGGAAG AACAUUAAUCAUCU
STMN2_ intron1	+	GTT A	220 2	TCATTTCCAGACTCTC GGGAAGAACATTAA	420 8	UCAUUUCCAGACUCUC GGGAAGAACAUAUA
STMN2_ intron1	+	GTT A	220 3	CAAACTGAGACCAG AAAATCCCATCAAGA	420 9	CAAAACUGAGACCAGA AAAUCCCAUCAAGA
STMN2_ intron1	+	ATT G	220 4	ACTGTTACAAAACG AGACCAGAAAATCCC	421 0	ACUGUUACAAAACUGA GACCAGAAAAUCCC
STMN2_ intron1	+	CTT A	220 5	TAATATATTGACTGTT ACAAAACGAGACC	421 1	UAAUUAUUGACUGUU ACAAAACUGAGACC
STMN2_ intron1	+	CTT C	220 6	CTAGTGAGGAGCAAC CTAACTCACACGAAA	421 2	CUAGUGAGGAGCAACC UAAUCACACGAAA
STMN2_ intron1	+	TTT G	220 7	GGCTTCCTAGTGAGG AGCAACCTAACTCAC	421 3	GGCUUCCUAGUGAGGA GCAACCUAACUCAC
STMN2_ intron1	+	GTT T	220 8	GGGCTTCCTAGTGAG GAGCAACCTAACTCA	421 4	GGGCUUCCUAGUGAGG AGCAACCUAACUCA
STMN2_ intron1	+	TTTC	220 9	CCAGTTTGGGCTTCCT AGTGAGGAGCAACC	421 5	CCAGUUUGGGCUUCCU AGUGAGGAGCAACC
STMN2_ intron1	+	GTT T	221 0	CCCAGTTTGGGCTTCC TAGTGAGGAGCAAC	421 6	CCCAGUUUGGGCUUCC UAGUGAGGAGCAAC
STMN2_ intron1	+	ATT A	221 1	TAATAATAGTTTCCCA GTTTGGGCTTCCTA	421 7	UAAUAAUAGUUUCCCA GUUUGGGCUUCCUA
STMN2_ intron1	+	ATT A	221 2	ACAAAGCTGCTCACA GTAAACCTATTATAA	421 8	ACAAAGCUGCUCACAG UAAACCUAUUAUA
STMN2_ intron1	+	TTTT	221 3	TATTTCCAACAAAAT ATCTATTGTTATTA	421 9	UAUUUCCAACAAAAAU AUCUAUUGUUAUUA
STMN2_ intron1	+	TTTT	221 4	ATTTCCAACAAAAT ATCTATTGTTATTAT	422 0	AUUUCCAACAAAAUA UCUAUUGUUAUUAU
STMN2_ intron1	+	TTT A	221 5	TTTCCAACAAAATAT CTATTGTTATTATT	422 1	UUUCCAACAAAAUAU CUAUUGUUAUUAU
STMN2_ intron1	+	ATT T	221 6	CCAACAAAATATCT ATTGTTATTATTAA	422 2	CCAACAAAUAUCUA UUGUUAUUAUUA
STMN2_ intron1	+	TTT A	221 7	TTATATTTCTGATGAT TTTTTTCTTATATA	422 3	UUAUAUUUCUGAUGAU UUUUUUCUUAUAUA
STMN2_ intron1	+	TTTT	221 8	ATTATATTTCTGATGA TTTTTTCTTATAT	422 4	AUUAUAUUUCUGAUGA UUUUUUUCUUAUAU
STMN2_ intron1	+	TTTT	221 9	TATTATATTTCTGATG ATTTTTTCTTATA	422 5	UAUUAUAUUUCUGAUG AUUUUUUCUUAUA
STMN2_ intron1	+	CTTT	222 0	TTATTATATTTCTGAT GATTTTTTCTTAT	422 6	UUAUUAUAUUUCUGAU GAUUUUUUUCUUAU
STMN2_ intron1	+	ATT A	222 1	TCTTTTTATTATATTC TGATGATTTTTTT	422 7	UCUUUUUAUUAUUAU CUGAUGAUUUUUU

STMN2_ intron1	+	TTT A	222 2	AAAATTATCTTTTAT TATATTTCTGATGA	422 8	AAAAUUAUCUUUUUAU UAUAUUUCUGAUGA
STMN2_ intron1	+	CTTT	222 3	AAAAATTATCTTTTAA TTATATTTCTGATG	422 9	AAAAUUAUCUUUUUA UUUAUUUCUGAUG
STMN2_ intron1	+	CTT G	222 4	TCACCTTAAAAATTAT CTTTTATTATATT	423 0	UCACUUUAAAAAUUAU CUUUUUAUUAUAU
STMN2_ intron1	+	ATT A	222 5	CATGATCCTGCACTCT TGTCACCTTAAAAA	423 1	CAUGAUCCUGCACUCU UGUCACUUUAAAAA
STMN2_ intron1	+	TTT A	222 6	ATGACATATTACATGA TCCTGCACTCTTGT	423 2	AUGACAUAUUACAUGA UCCUGCACUCUUGU
STMN2_ intron1	+	TTTT	222 7	AATGACATATTACATG ATCCTGCACTCTTG	423 3	AAUGACAUAUUACAUG AUCCUGCACUCUUG
STMN2_ intron1	+	CTTT	222 8	TAATGACATATTACAT GATCCTGCACTCTT	423 4	UAAUGACAUAUUACAU GAUCCUGCACUCUU
STMN2_ intron1	+	GTT C	222 9	TAGTCTTTTAATGACA TATTACATGATCCT	423 5	UAGUCUUUAAUGACA UAUUACAUGAUCCU
STMN2_ intron1	+	ATT T	223 0	CTGATGATTTTTTCT TATATAGTTTTTAA	423 6	CUGAUGAUUUUUUCU UAUAUAGUUUUUA
STMN2_ intron1	+	GTT G	223 1	TTCTAGTCTTTTAATG ACATATTACATGAT	423 7	UUCUAGUCUUUAAUG ACAUAUUACAUGAU
STMN2_ intron1	+	ATT C	223 2	AAACACATGAAAAAT TACCAAAGTTGTTCT	423 8	AAACACAUGAAAAAUU ACCAAAGUUGUUCU
STMN2_ intron1	+	CTT C	223 3	TCATAATAAATATTCA AACACATGAAAAAT	423 9	UCAUAAUAAAUAUUCA AACACAUGAAAAAU
STMN2_ intron1	+	ATT A	223 4	GCACCCTTCTCATAAT AAATATTCAAACAC	424 0	GCACCCUUCUCAUAAU AAAUAUUCAACAC
STMN2_ intron1	+	ATT C	223 5	CAATTAGCACCCCTTCT CATAATAAATATTC	424 1	CAAUUAGCACCCUUCU CAUAAUAAAUUUC
STMN2_ intron1	+	TTT A	223 6	TCTGAGAAATTCCAAT TAGCACCCCTTCTCA	424 2	UCUGAGAAAUUCCAAU UAGCACCCUUCUCA
STMN2_ intron1	+	CTTT	223 7	ATCTGAGAAATTCCA ATTAGCACCCCTTCTC	424 3	AUCUGAGAAAUUCCAA UUAGCACCCUUCUC
STMN2_ intron1	+	CTT A	223 8	CAGCTTTATCTGAGAA ATTCCAATTAGCAC	424 4	CAGCUUUAUCUGAGAA AUUCCAAUAGCAC
STMN2_ intron1	+	TTT A	223 9	AGTCTTACAGCTTTAT CTGAGAAATTCCAA	424 5	AGUCUUACAGCUUUAU CUGAGAAAUUCCAA
STMN2_ intron1	+	ATT T	224 0	AAGTCTTACAGCTTTA TCTGAGAAATTCCA	424 6	AAGUCUUACAGCUUUA UCUGAGAAAUUCCA
STMN2_ intron1	+	ATT A	224 1	TTTAAGTCTTACAGCT TTATCTGAGAAATT	424 7	UUUAAGUCUUACAGCU UUAUCUGAGAAAUU
STMN2_ intron1	+	GTT A	224 2	TTATTTAAGTCTTACA GCTTTATCTGAGAA	424 8	UUAUUUAAGUCUUACA GCUUUAUCUGAGAA
STMN2_ intron1	+	ATT G	224 3	TTATTATTTAAGTCTT ACAGCTTTATCTGA	424 9	UUAUUUAUUAAGUCUU ACAGCUUUAUCUGA

STMN2_ intron1	+	TTTC	224 4	CAACAAAAATATCTA TTGTTATTATTTAAG	425 0	CAACAAAAAUUUCUAU UGUUAUUUAUUUAAG
STMN2_ intron1	+	ATT A	224 5	CCAAAGTTGTTCTAGT CTTTTAATGACATA	425 1	CCAAAGUUGUUCUAGU CUUUUAAUGACAUA
STMN2_ intron1	+	ATT A	224 6	TCTTTTAATAAAGGAA TCAGGCCCTGTCAT	425 2	UCUUUUAUAAAAGGAA UCAGGCCCUUGUCAU
STMN2_ intron1	+	TTTC	224 7	CAGACTCTCGGGAAG AACATTAATCATCTC	425 3	CAGACUCUCGGGAAGA ACAUUAAUCAUCUC
STMN2_ intron1	+	TTTT	224 8	AATTATCTTTTAATAA AGGAATCAGGCCCT	425 4	AAUUAUCUUUUAUAA AGGAAUCAGGCCCU
STMN2_ intron1	+	CTT C	224 9	ATTATTCAATTCTAAC TTTCTAAGGAAGTC	425 5	AUUAUUCAAUUCUAAC UUUCUAAGGAAGUC
STMN2_ intron1	+	CTT A	225 0	TCTAAGCCAATAAAG GATCTTCATTATTCA	425 6	UCUAAGCCAAUAAAGG AUCUUCAUUAUUCA
STMN2_ intron1	+	CTT C	225 1	TGCTTATCTAAGCCAA TAAAGGATCTTCAT	425 7	UGC UUAUCUAAGCCAA UAAAGGAUCUUCAU
STMN2_ intron1	+	TTTC	225 2	TTCTGCTTATCTAAGC CAATAAAGGATCTT	425 8	UUCUGCUUAUCUAAGC CAAUAAAGGAUCUU
STMN2_ intron1	+	TTTT	225 3	CTTCTGCTTATCTAAG CCAATAAAGGATCT	425 9	CUUCUGCUUAUCUAAG CCAAUAAAGGAUCU
STMN2_ intron1	+	GTT T	225 4	TCTTCTGCTTATCTAA GCCAATAAAGGATC	426 0	UCUUCUGCUUAUCUAA GCCAAUAAAGGAUC
STMN2_ intron1	+	TTT G	225 5	AAAAGAGTGTTTTCTT CTGCTTATCTAAGC	426 1	AAAAGAGUGUUUUCU CUGCUUAUCUAAGC
STMN2_ intron1	+	ATT T	225 6	GAAAAGAGTGTTTTCT TCTGCTTATCTAAG	426 2	GAAAAGAGUGUUUUCU UCUGCUUAUCUAAG
STMN2_ intron1	+	ATT G	225 7	AGTATGACTGTATATT TGAAAAGAGTGTTT	426 3	AGUAUGACUGUAUAUU UGAAAAGAGUGUUU
STMN2_ intron1	+	TTT A	225 8	TTGAGTATGACTGTAT ATTTGAAAAGAGTG	426 4	UUGAGUAUGACUGUAU AUUUGAAAAGAGUG
STMN2_ intron1	+	ATT T	225 9	ATTGAGTATGACTGTA TATTTGAAAAGAGT	426 5	AUUGAGUAUGACUGUA UAUUUGAAAAGAGU
STMN2_ intron1	+	CTT A	226 0	AGAATTTATTGAGTAT GACTGTATATTTGA	426 6	AGAAUUUAUUGAGUAU GACUGUAUAUUUGA
STMN2_ intron1	+	ATT C	226 1	TTAAGAATTTATTGAG TATGACTGTATATT	426 7	UUAAGAAUUUAUUGAG UAUGACUGUAUAUU
STMN2_ intron1	+	CTT C	226 2	CTGAATACCATGTGA GAAAATTCTTAAGAA	426 8	CUGAAUACCAUGUGAG AAA AUUCUUAAGAA
STMN2_ intron1	+	TTTC	226 3	TTCCTGAATACCATGT GAGAAAATTCTTAA	426 9	UUCCUGAAUACCAUGU GAGAAA AUUCUUA
STMN2_ intron1	+	ATT T	226 4	CTTCTGAATACCATG TGAGAAAATTCTTA	427 0	CUUCCUGAAUACCAUG UGAGAAA AUUCUUA
STMN2_ intron1	+	ATT C	226 5	TAAGAGTATTTCTTCC TGAATACCATGTGA	427 1	UAAGAGUAUUUCUCC UGAAUACCAUGUGA

STMN2_ intron1	+	ATT A	226 6	TTCTAAGAGTATTTCT TCCTGAATACCATG	427 2	UUCUAAGAGUAUUUCU UCCUGAAUACCAUG
STMN2_ intron1	+	TTT A	226 7	CCAAATTATTCTAAGA GTATTTCTTCCTGA	427 3	CCAAAUUAUUCUAAGA GUAUUUCUCCUGA
STMN2_ intron1	+	ATT T	226 8	ACCAAATTATTCTAAG AGTATTTCTTCCTG	427 4	ACCAAUUAUUCUAAG AGUAUUUCUCCUG
STMN2_ intron1	+	ATT A	226 9	TTTACCAAATTATTCT AAGAGTATTTCTTC	427 5	UUUACCAAUUAUUCU AAGAGUAUUUCUUC
STMN2_ intron1	+	TTT A	227 0	TTATTTACCAAATTAT TCTAAGAGTATTC	427 6	UUAUUUACCAAUUAU UCUAAGAGUAUUUC
STMN2_ intron1	+	ATT T	227 1	ATTATTTACCAAATTA TTCTAAGAGTATTT	427 7	AUUAUUUACCAAUUA UUCUAAGAGUAUUU
STMN2_ intron1	+	CTT A	227 2	TATTTATTATTTACCA AATTATTCTAAGAG	427 8	UAUUUAUUAUUUACCA AAUUAUUCUAAGAG
STMN2_ intron1	+	ATT G	227 3	CTGTCTCAATATATCT TATATTTATTATTT	427 9	CUGUCUCAUAUAUCU UAUAUUUAUUAUUU
STMN2_ intron1	+	ATT A	227 4	AAACAAAAGATTGCT GTCTCAATATATCTT	428 0	AAACAAAAGAUUGCUG UCUCAUAUAUCUU
STMN2_ intron1	+	TTT A	227 5	TGAATAGCAATACTG AAGAAATTAACAA	428 1	UGAAUAGCAAUACUGA AGAAAUUAAAACAA
STMN2_ intron1	+	ATT A	227 6	TTCAATTCTAACTTTC TAAGGAAGTCAACC	428 2	UUCAAUUCUAAACUUUC UAAGGAAGUCAACC
STMN2_ intron1	+	ATT C	227 7	AATTCTAACTTTCTAA GGAAGTCAACCTAC	428 3	AAUUCUAAACUUUCUAA GGAAGUCAACCUAC
STMN2_ intron1	+	ATT C	227 8	TAACCTTCTAAGGAAG TCAACCTACAGATC	428 4	UAACUUUCUAAAGGAAG UCAACCUACAGAUC
STMN2_ intron1	+	CTTT	227 9	CTAAGGAAGTCAACC TACAGATCAGAAAGA	428 5	CUAAGGAAGUCAACCU ACAGAUCAGAAAGA
STMN2_ intron1	+	TTT G	228 0	CAATTTCTTGACATT GAAGGAAAGGAAGA	428 6	CAAUUUCUUGUACAUI GAAGGAAAGGAAGA
STMN2_ intron1	+	TTTT	228 1	GCAATTTCTTGACAT TGAAGGAAAGGAAG	428 7	GCAAUUUCUUGUACAUI UGAAGGAAAGGAAG
STMN2_ intron1	+	TTTT	228 2	TGCAATTTCTTGACAT TTGAAGGAAAGGAA	428 8	UGCAAUUUCUUGUACA UUGAAGGAAAGGAA
STMN2_ intron1	+	ATT T	228 3	TTGCAATTTCTTGAC ATTGAAGGAAAGGA	428 9	UUGCAAUUUCUUGUAC AUUGAAGGAAAGGA
STMN2_ intron1	+	TTTC	228 4	CATTTTTCGCAATTTCT TGTACATTGAAGGA	429 0	CAUUUUUGCAAUUUCU UGUACAUIUGAAGGA
STMN2_ intron1	+	CTTT	228 5	CCATTTTTCGCAATTC TTGTACATTGAAGG	429 1	CCAUUUUUGCAAUUUC UUGUACAUIUGAAGG
STMN2_ intron1	+	TTTC	228 6	AGGGTCTCTCAGAAG CTGGGAAACTTTCCA	429 2	AGGGUCUCUCAGAAGC UGGGAAACUUUCCA
STMN2_ intron1	+	ATT T	228 7	CAGGGTCTCTCAGAA GCTGGGAAACTTTCC	429 3	CAGGGUCUCUCAGAAG CUGGGAAACUUUCC

STMN2_ intron1	+	GTT C	228 8	ATTTTCAGGGTCTCTCA GAAGCTGGGAAACT	429 4	AUUUCAGGGUCUCUCA GAAGCUGGGAAACU
STMN2_ intron1	+	GTT A	228 9	ACAGTTCATTTTCAGGG TCTCTCAGAAGCTG	429 5	ACAGUUCAUUUCAGGG UCUCUCAGAAGCUG
STMN2_ intron1	+	GTT G	229 0	TTAACAGTTCATTTCA GGGTCTCTCAGAAG	429 6	UUAACAGUUCAUUUCA GGGUCUCUCAGAAG
STMN2_ intron1	+	GTT G	229 1	TTGTTAACAGTTCATT TCAGGGTCTCTCAG	429 7	UUGUUAACAGUUCAU UCAGGGUCUCUCAG
STMN2_ intron1	+	ATT C	229 2	AGTTGTTGTTAACAGT TCATTTTCAGGGTCT	429 8	AGUUGUUGUUAACAGU UCAUUUCAGGGUCU
STMN2_ intron1	+	ATT T	229 3	ATGAATAGCAATACT GAAGAAATTAACAACA	429 9	AUGAAUAGCAAUACUG AAGAAAUAACAACA
STMN2_ intron1	+	GTT A	229 4	GCCATTCAGTTGTTGT TAACAGTTCATTTTC	430 0	GCCAUUCAGUUGUUGU UAAACAGUUCAUUUC
STMN2_ intron1	+	GTT A	229 5	CTCAACACAAAAGTTG GACTAAGTCTCAAAG	430 1	CUCAACACAAAAGUUG ACUAAGUCUCAAAAG
STMN2_ intron1	+	TTT G	229 6	CAGAATATACTGTTAC TCAACACAAAAGTTG	430 2	CAGAAUAUACUGUUA UCAACACAAAAGUUG
STMN2_ intron1	+	GTT T	229 7	GCAGAATATACTGTTA CTCAACACAAAAGTT	430 3	GCAGAAUAUACUGUUA CUCAACACAAAAGUU
STMN2_ intron1	+	CTT C	229 8	AGGGTTTGCAGAATA TACTGTTACTCAACA	430 4	AGGGUUUGCAGAAUAU ACUGUUACUCAACA
STMN2_ intron1	+	TTTC	229 9	CCAAATAGGGCACTA AAAACATGATCCCAA	430 5	CCAAAUAGGGCACUAA AAACAUGAUCCCAA
STMN2_ intron1	+	ATT T	230 0	CCCAAATAGGGCACT AAAAACATGATCCCA	430 6	CCCAAUAGGGCACUA AAAACAUGAUCCCA
STMN2_ intron1	+	ATT A	230 1	AAAAATATAACATTTTC CCAAATAGGGCACT	430 7	AAAAAUUAACAUAUUC CCAAAUAGGGCACU
STMN2_ intron1	+	ATT A	230 2	TGCTGCAAAAATGAT ACAATACACGAAATA	430 8	UGCUGCAAAAUGAUA CAAUACACGAAUA
STMN2_ intron1	+	TTTC	230 3	TGGAAATATTATGCTG CAAAAATGATACAA	430 9	UGGAAAUUAUUGCUG CAAAAUGAUACAA
STMN2_ intron1	+	CTTT	230 4	CTGGAAATATTATGCT GCAAAAATGATACA	431 0	CUGGAAAUUAUUGCU GCAAAAUGAUACA
STMN2_ intron1	+	ATT A	230 5	CCACCTTTCTGGAAAT ATTATGCTGCAAAA	431 1	CCACCUUUCUGGAAAU AUUAUGCUGCAAAA
STMN2_ intron1	+	CTT C	230 6	AAGGAATAGCATCAA AGACATAGTCAGGTC	431 2	AAGGAAUAGCAUCAAA GACAUAGUCAGGUC
STMN2_ intron1	+	TTTC	230 7	TAAGGAAGTCAACCT ACAGATCAGAAAGAG	431 3	UAAGGAAGUCAACCUA CAGAUAGAAAGAG
STMN2_ intron1	+	GTT G	230 8	GACTAAGTCTCAAAG TTAGCCATTTCAGTTG	431 4	GACUAAGUCUCAAGU UAGCCAUUCAGUUG
STMN2_ intron1	+	ATT T	230 9	CTTGTACATTGAAGGA AAGGAAGACACACT	431 5	CUUGUACAUUGAAGGA AAGGAAGACACACU

STMN2_ intron1	+	CTT A	231 0	CTATCATTTATGAATA GCAATACTGAAGAA	431 6	CUAUCAUUUAUGAAUA GCAAUACUGAAGAA
STMN2_ intron1	+	CTT G	231 1	TGGCACAGTTGACAA GGATGATAAATCAAT	431 7	UGGCACAGUUGACAAG GAUGAUAAAUCAAU
STMN2_ intron1	+	TTTT	231 2	AGGGATATTAACCTGT AATATACAGGTATC	431 8	AGGGAUAUUAACUUGU AAUAUACAGGUAUC
STMN2_ intron1	+	GTT T	231 3	TAGGGATATTAACCTG TAATATACAGGTAT	431 9	UAGGGAUAUUAACUUG UAAUAUACAGGUAU
STMN2_ intron1	+	ATT C	231 4	TGACCACTAAACACAT CAGTTTTAGGGATA	432 0	UGACCACUAAACACAU CAGUUUUAGGGUAU
STMN2_ intron1	+	CTT C	231 5	CGAACAAGCTCCCAG ATGATGCTGATTCTG	432 1	CGAACAAGCUCCCAGA UGAUGCUGAUUCUG
STMN2_ intron1	+	ATT C	231 6	TGTCTTCCGAACAAGC TCCCAGATGATGCT	432 2	UGUCUUCCGAACAAGC UCCCAGAUGAUGCU
STMN2_ intron1	+	CTT G	231 7	AGGCAGACATTCTGTC TTCCGAACAAGCTC	432 3	AGGCAGACAUUCUGUC UUCCGAACAAGCUC
STMN2_ intron1	+	ATT C	231 8	AATACATCTGGCTTGA GGCAGACATTCTGT	432 4	AAUACAUCUGGCUUGA GGCAGACAUUCUGU
STMN2_ intron1	+	ATT C	231 9	TGATTCAATACATCTG GCTTGAGGCAGACA	432 5	UGAUUCAAUACAUCUG GCUUGAGGCAGACA
STMN2_ intron1	+	ATT A	232 0	AAATGCAAATTCTGAT TCAATACATCTGGC	432 6	AAUUGCAAUUCUGAU UCAAUACAUCUGGC
STMN2_ intron1	+	TTTC	232 1	ATTAATAATGCAAATTC TGATTCAATACATC	432 7	AUUAAAAUGCAAUUC UGAUUCAAUACAUC
STMN2_ intron1	+	TTTT	232 2	CATTAAAATGCAAATT CTGATTCAATACAT	432 8	CAUUAAAAUGCAAUUC CUGAUUCAAUACAUC
STMN2_ intron1	+	ATT T	232 3	TCATTAAAATGCAAAT TCTGATTCAATACA	432 9	UCAUUAAAAUGCAAUUC UCUGAUUCAAUACA
STMN2_ intron1	+	TTT G	232 4	ATTTTCATTAAAATGC AAATTCTGATTCAA	433 0	AUUUUCAUUAAAAUGC AAAUUCUGAUUCAA
STMN2_ intron1	+	CTTT	232 5	GATTTTCATTAAAATG CAAATTCTGATTCA	433 1	GAUUUUCAUUAAAAUG CAAAUUCUGAUUCA
STMN2_ intron1	+	ATT A	232 6	CCTTTGATTTTCATTA AAATGCAAATTCTG	433 2	CCUUUGAUUUUCAUUA AAUUGCAAUUCUG
STMN2_ intron1	+	TTT G	232 7	ATGTGCATATGAATTA CCTTTGATTTTCAT	433 3	AUGUGCAUAUGAAUUA CCUUUGAUUUUCAU
STMN2_ intron1	+	CTTT	232 8	GATGTGCATATGAATT ACCTTTGATTTTCA	433 4	GAUGUGCAUAUGAAUUC ACCUUGAUUUUCA
STMN2_ intron1	+	GTT C	232 9	CTCAAACCTTGATGTG CATATGAATTACCT	433 5	CUCAAACUUGAUGUG CAUAUGAAUUAACCU
STMN2_ intron1	+	ATT A	233 0	CTGTGTTCTCCTCAAAC TTGATGTGCATATG	433 6	CUGUGUCCUCAAAACU UUGAUGUGCAUAUG
STMN2_ intron1	+	TTT A	233 1	ATAGTGTGCATATTACT GTGTTCTCCTCAAAC	433 7	AUAGUGUCAUAUUAACU GUGUCCUCAAAACU

STMN2_ intron1	+	ATT T	233 2	AATAGTGTCAATTAC TGTGTTCTCAAAC	433 8	AAUAGUGUCAUAUUAC UGUGUUCCUCAAAAC
STMN2_ intron1	+	ATT C	233 3	TAATCCAGCTATAAA ATATTTAATAGTGTC	433 9	UAAUCCAGCUAUAAAA UAUUUAAUAGUGUC
STMN2_ intron1	+	TTT A	233 4	TGTAATTCTAATCCAG CTATAAAATATTTA	434 0	UGUAAUUCUAAUCCAG CUAUAAAAUAUUUA
STMN2_ intron1	+	TTTT	233 5	ATGTAATTCTAATCCA GCTATAAAATATTT	434 1	AUGUAAUUCUAAUCCA GCUAUAAAAUAUUU
STMN2_ intron1	+	TTT A	233 6	ATTATCTTTTAATAAA GGAATCAGGCCCTG	434 2	AUUAUCUUUUAAUAAA GGAAUCAGGCCCCUG
STMN2_ intron1	+	ATT T	233 7	TATGTAATTCTAATCC AGCTATAAAATATT	434 3	UAUGUAAUUCUAAUCC AGCUAUAAAAUAUU
STMN2_ intron1	+	ATT A	233 8	CATTTTATGTAATTCT AATCCAGCTATAAA	434 4	CAUUUUAUGUAAUUCU AAUCCAGCUAUAAA
STMN2_ intron1	+	TTT A	233 9	GGGATATTAACCTGTA ATATACAGGTATCC	434 5	GGGAUUAUAACUUGUA AUUAUACAGGUAUCC
STMN2_ intron1	+	ATT A	234 0	ACTTGTAATATACAGG TATCCCTCCTGGTA	434 6	ACUUGUAAUUAUACAGG UAUCCCUCCUGGUA
STMN2_ intron1	+	CTT G	234 1	TAATATACAGGTATCC CTCCTGGTAAGCTC	434 7	UAAUAUACAGGUAUCC CUCCUGGUAAGCUC
STMN2_ intron1	+	ATT A	234 2	TGTCTTAACATTTTTA AATCTATGGTAATC	434 8	UGUCUUAACAUUUUUA AAUCUAUGGUAUUC
STMN2_ intron1	+	TTT G	234 3	GCTCTCTGTGTGAGCA TGTGTGCGTGTGTG	434 9	GCUCUCUGUGUGAGCA UGUGUGCGUGUGUG
STMN2_ intron1	+	ATT T	234 4	GGCTCTCTGTGTGAGC ATGTGTGCGTGTGT	435 0	GGCUCUCUGUGUGAGC AUGUGUGCGUGUGU
STMN2_ intron1	+	ATT G	234 5	CAGGACTCGGCAGAA GACCTTCGAGAGAAA	435 1	CAGGACUCGGCAGAAG ACCUUCGAGAGAAA
STMN2_ intron1	+	ATT C	234 6	ATATTGCAGGACTCG GCAGAAGACCTTCGA	435 2	AUAUUGCAGGACUCGG CAGAAGACCUUCGA
STMN2_ intron1	+	ATT A	234 7	TATTCATATTGCAGGA CTCGGCAGAAGACC	435 3	UAUUCAUUUGCAGGA CUCGGCAGAAGACC
STMN2_ intron1	+	TTT A	234 8	AAATTATATTCATATT GCAGGACTCGGCAG	435 4	AAAUUAUAUUCAUUU GCAGGACUCGGCAG
STMN2_ intron1	+	TTTT	234 9	AAAATTATATTCATAT TGCAGGACTCGGCA	435 5	AAAAUUAUAUUCAUU UGCAGGACUCGGCA
STMN2_ intron1	+	TTTT	235 0	TAAAATTATATTCATA TTGCAGGACTCGGC	435 6	UAAAAUUAUAUUCAU UUGCAGGACUCGGC
STMN2_ intron1	+	ATT T	235 1	TTAAAATTATATTCAT ATTGCAGGACTCGG	435 7	UUAAAAUUAUAUUCAU AUUGCAGGACUCGG
STMN2_ intron1	+	ATT G	235 2	GATTTTAAATTTATA TTCATATTGCAGGA	435 8	GAUUUUUAAAAUUUA UUCAUAUUGCAGGA
STMN2_ intron1	+	CTT A	235 3	ATTGGATTTTAAAT TATATTCATATTGC	435 9	AUUGGAUUUUAAAAU UAUAUUCAUUUGC

STMN2_ intron1	+	GTT C	235 4	TGCCCCATCACTCTCT CTTAATTGGATTTT	436 0	UGCCCCAUCACUCUCU CUUAAUUGGAUUUU
STMN2_ intron1	+	ATT A	235 5	TGTGTTCTGCCCCATC ACTCTCTCTTAATT	436 1	UGUGUUCUGCCCCAUC ACUCUCUCUUAAUU
STMN2_ intron1	+	GTT G	235 6	ACAAGGATGATAAAT CAATAATGCAAGCTT	436 2	ACAAGGAUGAUAAAUC AAUAAUGCAAGCUU
STMN2_ intron1	+	ATT A	235 7	CTCTGGGAATTATGTG TTCTGCCCCATCAC	436 3	CUCUGGGAAUUAUGUG UUCUGCCCCAUCAC
STMN2_ intron1	+	TTTT	235 8	ATTACTCTGGGAATTA TGTGTTCTGCCCCA	436 4	AUUACUCUGGGAAUUA UGUGUUCUGCCCCA
STMN2_ intron1	+	ATT T	235 9	TATTACTCTGGGAATT ATGTGTTCTGCCCC	436 5	UAUUACUCUGGGAAUU AUGUGUUCUGCCCC
STMN2_ intron1	+	CTT C	236 0	CGAACTCATATACCTG GGGATTTTATTACT	436 6	CGAACUCAUAUACCUG GGGAUUUUAUUACU
STMN2_ intron1	+	TTT A	236 1	CTTCCGAACATCATATA CCTGGGGATTTTAT	436 7	CUUCCGAACUCAUAUA CCUGGGGAUUUUUAU
STMN2_ intron1	+	TTTT	236 2	ACTTCCGAACATCATAT ACCTGGGGATTTTA	436 8	ACUCCGAACUCAUAU ACCUGGGGAUUUUA
STMN2_ intron1	+	ATT T	236 3	TACTTCCGAACATCATA TACCTGGGGATTTT	436 9	UACUCCGAACUCAUA UACCUGGGGAUUUU
STMN2_ intron1	+	TTT A	236 4	CAAAATATTTTACTTC CGAACTCATATACC	437 0	CAAAAUUUUUACUUC CGAACUCAUAUACC
STMN2_ intron1	+	CTTT	236 5	ACAAAATATTTTACTT CCGAACATCATATAC	437 1	ACAAAUAUUUUACUU CCGAACUCAUAUAC
STMN2_ intron1	+	TTT A	236 6	AATCTATGGTAATCTT TACAAAATATTTTA	437 2	AAUCUAUGGUAUUCUU UACAAAUAUUUUA
STMN2_ intron1	+	TTTT	236 7	AAATCTATGGTAATCT TTACAAAATATTTT	437 3	AAUCUAUGGUAUUCUU UUACAAAUAUUUU
STMN2_ intron1	+	TTTT	236 8	TAAATCTATGGTAATC TTACAAAATATTTT	437 4	UAAAUUCUAUGGUAUUC UUUACAAAUAUUUU
STMN2_ intron1	+	ATT T	236 9	TTAAATCTATGGTAAT CTTTACAAAATATT	437 5	UUAAAUUCUAUGGUAU CUUUACAAAUAUU
STMN2_ intron1	+	CTT A	237 0	ACATTTTAAATCTAT GGTAATCTTTACAA	437 6	ACAUUUUUAAAUCUAU GGUAUUCUUUACAA
STMN2_ intron1	+	TTT A	237 1	TTACTCTGGGAATTAT GTGTTCTGCCCCAT	437 7	UUACUCUGGGAAUUUAU GUGUUCUGCCCCAU
STMN2_ intron1	+	TTTC	237 2	TTGTACATTGAAGGA AAGGAAGACACACTT	437 8	UUGUACAUUGAAGGAA AGGAAGACACACUU
STMN2_ intron1	+	CTT C	237 3	GAGAGAAAGGTAGAA AATAAGAATTTGGCT	437 9	GAGAGAAAGGUAGAAA AUAAGAAUUUGGCU
STMN2_ intron1	+	ATT G	237 4	AAGGAAAGGAAGACA CACTTAAGACAGCAT	438 0	AAGGAAAGGAAGACAC ACUUAAGACAGCAU
STMN2_ intron1	+	CTT A	237 5	ATCTCCTCAGTCCCAT CATGGTTAGCACAT	438 1	AUCUCCUCAGUCCCAU CAUGGUUAGCACAU

STMN2_ intron1	+	ATT G	237 6	ACTTAATCTCCTCAGT CCCATCATGGTTAG	438 2	ACUUAUAUCUCCUCAGU CCCAUCAUGGUUAG
STMN2_ intron1	+	GTT C	237 7	CAGAAATAACATTGA CTTAATCTCCTCAGT	438 3	CAGAAUAACAUIUGAC UUAUAUCUCCUCAGU
STMN2_ intron1	+	TTTC	237 8	TGGTGGGAACACACT CTGATGACCAGTTCC	438 4	UGGUGGGAACACACUC UGAUGACCAGUUC
STMN2_ intron1	+	ATT T	237 9	CTGGTGGGAACACAC TCTGATGACCAGTTC	438 5	CUGGUGGGAACACACU CUGAUGACCAGUUC
STMN2_ intron1	+	GTT C	238 0	TGCAGGCTCAGCACA GCATCGATTTCTGGT	438 6	UGCAGGCUCAGCACAG CAUCGAUUUCUGGU
STMN2_ intron1	+	GTT G	238 1	TAACGTATGAGACAC ATGGCGTTCTGCAGG	438 7	UAACGUAUGAGACACA UGGCGUUCUGCAGG
STMN2_ intron1	+	TTT G	238 2	GGAGAAAGAGAGCTA TGAGGCCGTGTGGGT	438 8	GGAGAAAGAGAGCUAU GAGGCCGUGUGGGU
STMN2_ intron1	+	CTTT	238 3	GGGAGAAAGAGAGCT ATGAGGCCGTGTGGG	438 9	GGGAGAAAGAGAGCUA UGAGGCCGUGUGGG
STMN2_ intron1	+	TTT A	238 4	GGCTTTGGGAGAAAG AGAGCTATGAGGCCG	439 0	GGCUUUGGGAGAAAGA GAGCUAUGAGGCCG
STMN2_ intron1	+	ATT T	238 5	AGGCTTTGGGAGAAA GAGAGCTATGAGGCC	439 1	AGGCUUUGGGAGAAAG AGAGCUAUGAGGCC
STMN2_ intron1	+	ATT G	238 6	CCATGATTTAGGCTTT GGGAGAAAGAGAGC	439 2	CCAUGAUUUAGGCUUU GGGAGAAAGAGAGC
STMN2_ intron1	+	ATT C	238 7	AAATAATTGCCATGAT TTAGGCTTTGGGAG	439 3	AAAUAAUUGCCAUGAU UUAGGCUUUGGGAG
STMN2_ intron1	+	CTT A	238 8	TTCAAATAATTGCCAT GATTTAGGCTTTGG	439 4	UUCAAAUAUUGCCAU GAUUUAGGCUUUGG
STMN2_ intron1	+	CTT A	238 9	CCTGGGGCTTATTCAA ATAATTGCCATGAT	439 5	CCUGGGGCUUAUUCAA AUAAUUGCCAUGAU
STMN2_ intron1	+	TTT A	239 0	ATAGCTTACCTGGGGC TTATTCAAATAATT	439 6	AUAGCUUACCUGGGGC UUAUUCAAAUAUU
STMN2_ intron1	+	TTTT	239 1	AATAGCTTACCTGGG GCTTATTCAAATAAT	439 7	AAUAGCUUACCUGGGG CUUAUUCAAAUAUU
STMN2_ intron1	+	GTT T	239 2	TAATAGCTTACCTGGG GCTTATTCAAATAA	439 8	UAAUAGCUUACCUGGG GCUUAUUCAAAUA
STMN2_ intron1	+	ATT G	239 3	ATGCCTAGTTTAAATA GCTTACCTGGGGCT	439 9	AUGCCUAGUUUAAUA GCUUACCUGGGGCU
STMN2_ intron1	+	CTT C	239 4	CAAATTGATGCCTAGT TTTAATAGCTTACC	440 0	CAAAUUGAUGCCUAGU UUUAAUAGCUUACC
STMN2_ intron1	+	CTT G	239 5	AAGAGAAAATACTTC CAAATTGATGCCTAG	440 1	AAGAGAAAUAUACUCC AAAUUGAUGCCUAG
STMN2_ intron1	+	TTTC	239 6	TGATCACAGACTCACC TTGAAGAGAAAATA	440 2	UGAUCACAGACUCACC UUGAAGAGAAAUA
STMN2_ intron1	+	CTTT	239 7	CTGATCACAGACTCAC CTTGAAGAGAAAAT	440 3	CUGAUCACAGACUCAC CUUGAAGAGAAAUA

STMN2_ intron1	+	CTT C	239 8	TCCTTTCTGATCACAG ACTCACCTTGAAGA	440 4	UCCUUUCUGAUCACAG ACUCACCUUGAAGA
STMN2_ intron1	+	TTT A	239 9	AACAGACCAGAGATG GTCTTCTCCTTTCTG	440 5	AACAGACCAGAGAUGG UCUUCUCCUUUCUG
STMN2_ intron1	+	ATT T	240 0	AAACAGACCAGAGAT GGTCTTCTCCTTTCT	440 6	AAACAGACCAGAGAUG GUCUUCUCCUUUCU
STMN2_ intron1	+	TTT A	240 1	TTTAAACAGACCAGA GATGGTCTTCTCCTT	440 7	UUUAAACAGACCAGAG AUGGUCUUCUCCUU
STMN2_ intron1	+	GTT A	240 2	GCACATTTCAAAATGC CTCCTTAACACTT	440 8	GCACAUUUCAAAAUGC CUCCUUAACUACUU
STMN2_ intron1	+	TTTT	240 3	TAATTATCTTTTAATA AAGGAATCAGGCC	440 9	UAAUUAUCUUUAAUA AAGGAAUCAGGCC
STMN2_ intron1	+	TTTC	240 4	AAAATGCCTCCTTAAC TACTTCCATAGGCC	441 0	AAAUGCCUCCUUAAC UACUUCCAUAGGCC
STMN2_ intron1	+	CTT A	240 5	ACTACTTCCATAGGCC AGAGATATTTAGTT	441 1	ACUACUCCAUAGGCC AGAGAUUUUAGUU
STMN2_ intron1	+	ATT T	240 6	TTAATTATCTTTAAT AAAGGAATCAGGCC	441 2	UUAAUUAUCUUUAAU AAAGGAAUCAGGCC
STMN2_ intron1	+	CTT G	240 7	TGAAACATTTTAATT ATCTTTTAATAAAG	441 3	UGAAACAUUUUAAUU AUCUUUUAUAAAG
STMN2_ intron1	+	CTT G	240 8	TACATTGAAGGAAAG GAAGACACACTTAAG	441 4	UACAUUGAAGGAAAGG AAGACACACUUAAG
STMN2_ intron1	+	TTT G	240 9	AATCCCTTGTGAAACA TTTTTAATTATCTT	441 5	AAUCCCUUGUGAAACA UUUUUAAUUAUCUU
STMN2_ intron1	+	TTTT	241 0	GAATCCCTTGTGAAAC ATTTTAAATTATCT	441 6	GAAUCCCUUGUGAAAC AUUUUAAUUAUCU
STMN2_ intron1	+	GTT T	241 1	TGAATCCCTTGTGAAA CATTTTAAATTATC	441 7	UGAAUCCCUUGUGAAA CAUUUUUAAUUAUC
STMN2_ intron1	+	ATT A	241 2	CCATCAAAGCAGGCA GGCAGGCAGGAGAGA	441 8	CCAUCAAAGCAGGCAG GCAGGCAGGAGAGA
STMN2_ intron1	+	CTT C	241 3	ATATTACCATCAAAGC AGGCAGGCAGGCAG	441 9	AUAUUACCAUCAAGC AGGCAGGCAGGCAG
STMN2_ intron1	+	ATT C	241 4	TCTTCATATTACCATC AAAGCAGGCAGGCA	442 0	UCUUCAUAUUACCAUC AAAGCAGGCAGGCA
STMN2_ intron1	+	TTTC	241 5	AAGATTCTCTTCATAT TACCATCAAAGCAG	442 1	AAGAUUCUCUUCAUAU UACCAUCAAGCAG
STMN2_ intron1	+	ATT T	241 6	CAAGATTCTCTTCATA TTACCATCAAAGCA	442 2	CAAGAUUCUCUUCAU UUACCAUCAAGCA
STMN2_ intron1	+	GTT A	241 7	TTCAAGATTCTCTTC ATATTACCATCAAA	442 3	UUUCAAGAUUCUCUUC AUAUUACCAUCAA
STMN2_ intron1	+	ATT A	241 8	GATGTTATTTCAAGAT TCTCTTCATATTAC	442 4	GAUGUUUUUCAAGAU UCUCUUCAUUUAC
STMN2_ intron1	+	TTTT	241 9	ATTTAAACAGACCAG AGATGGTCTTCTCCT	442 5	AUUUAAACAGACCAGA GAUGGUCUUCUCCU

STMN2_ intron1	+	TTT A	242 0	ATATAACTATTAGATG TTATTTCAAGATTC	442 6	AUAUAACUAUUAGAUG UUUUUUAAGAUUC
STMN2_ intron1	+	ATT C	242 1	ACATTTAATATAACTA TTAGATGTTATTTTC	442 7	ACAUUUAAUAUAACUA UUAGAUGUUUUUC
STMN2_ intron1	+	TTT A	242 2	CACATTCACATTTAAT ATAACTATTAGATG	442 8	CACAUUCACAUUUAU AUAACUAUUAGAUG
STMN2_ intron1	+	ATT T	242 3	ACACATTCACATTTAA TATAACTATTAGAT	442 9	ACACAUUCACAUUUA UAUAACUAUUAGAU
STMN2_ intron1	+	GTT G	242 4	AATAAAATAAATTTA CACATTCACATTTAA	443 0	AAUAAAAUAAUUUAC ACAUUCACAUUUA
STMN2_ intron1	+	TTT G	242 5	TTGAATAAAATAAATT TACACATTCACATT	443 1	UUGAAUAAAAUAAU UACACAUUCACAU
STMN2_ intron1	+	TTTT	242 6	GTTGAATAAAATAAA TTTACACATTCACAT	443 2	GUUGAAUAAAAUAAU UUACACAUUCACAU
STMN2_ intron1	+	ATT T	242 7	TGTTGAATAAAATAA ATTTACACATTCACA	443 3	UGUUGAAUAAAAUAA UUUACACAUUCACA
STMN2_ intron1	+	TTT A	242 8	ACATTTTGTGTAATAA AATAAATTTACACA	443 4	ACAUUUUGUUGAAUA AAUAAAUUUACACA
STMN2_ intron1	+	TTTT	242 9	AACATTTTGTGTAATA AAATAAATTTACAC	443 5	AACAUUUUGUUGAAU AAUAAAUUUACAC
STMN2_ intron1	+	GTT T	243 0	TAACATTTTGTGTAAT AAAATAAATTTACA	443 6	UAACAUUUUGUUGAAU AAAUAUAAUUUACA
STMN2_ intron1	+	TTT A	243 1	GTTTTAACATTTTGT GAATAAAATAAATT	443 7	GUUUUAACAUUUUGU GAUAAAAUAAAU
STMN2_ intron1	+	ATT T	243 2	AGTTTTAACATTTGT TGAATAAAATAAAT	443 8	AGUUUUAACAUUUUGU UGAAUAAAAUAAU
STMN2_ intron1	+	CTT C	243 3	CATAGGCCAGAGATA TTTAGTTTAAACATT	443 9	CAUAGGCCAGAGAUU UUAGUUUUAACAUU
STMN2_ intron1	+	ATT T	243 4	AATATACTATTAGAT GTTATTTCAAGATT	444 0	AAUAUAACUAUUAGAU GUUAUUUCAAGAUU
STMN2_ intron1	+	ATT T	243 5	TATTTAAACAGACCA GAGATGGTCTTCTCC	444 1	UAUUAAAACAGACCAG AGAUGGUCUUCUCC
STMN2_ intron1	+	ATT T	243 6	CAAAATGCCTCCTTAA CTACTTCCATAGGC	444 2	CAAAAUGCCUCCUUA CUACUCCAUAGGC
STMN2_ intron1	+	GTT A	243 7	GAGGTGAGCTCCCATT GCAGAGGTCACACC	444 3	GAGGUGAGCUCCAU GCAGAGGUCACACC
STMN2_ intron1	+	TTTC	243 8	TGGTGATTTCATAAAT TCCAGATTCTCTAT	444 4	UGGUGUAUUCAUAAU UCCAGAUUCUCUAU
STMN2_ intron1	+	TTTT	243 9	CTGGTGATTTCATAAA TTCCAGATTCTCTA	444 5	CUGGUGUAUUCAUAAA UCCAGAUUCUCUA
STMN2_ intron1	+	TTTT	244 0	TCTGGTGATTTCATAA ATTCCAGATTCTCT	444 6	UCUGGUGUAUUCAUAA AUCCAGAUUCUCU
STMN2_ intron1	+	GTT T	244 1	TTCTGGTGATTTCATA AATTCCAGATTCTC	444 7	UUCUGGUGUAUUCAU AAUCCAGAUUCUC

STMN2_ intron1	+	TTTC	244 2	AACTGTTTTTCTGGTG TATTCATAAATTCC	444 8	AACUGUUUUUCUGGUG UAUUCAUAAAUUCC
STMN2_ intron1	+	CTTT	244 3	CAACTGTTTTTCTGGT GTATTCATAAATTCC	444 9	CAACUGUUUUUCUGGU GUAUUCAUAAAUUC
STMN2_ intron1	+	TTTC	244 4	TTTCAACTGTTTTTCT GGTGTATTCATAAA	445 0	UUUCAACUGUUUUUCU GGUGUAUUCAUAAA
STMN2_ intron1	+	CTTT	244 5	CTTCAACTGTTTTTC TGGTGTATTCATAA	445 1	CUUUCAACUGUUUUUC UGGUGUAUUCAUAA
STMN2_ intron1	+	TTTC	244 6	CCGCAATGGTGCTTTC TTTCAACTGTTTTT	445 2	CCGCAAUGGUGCUUUC UUUCAACUGUUUUU
STMN2_ intron1	+	TTTT	244 7	CCC GCAATGGTGCTTT CTTCAACTGTTTTT	445 3	CCC GCAAUGGUGCUUU CUUUCAACUGUUUU
STMN2_ intron1	+	ATT T	244 8	TCCCGCAATGGTGCTT TCTTTCAACTGTTT	445 4	UCCCGCAAUGGUGCUU UCUUUCAACUGUUU
STMN2_ intron1	+	TTT A	244 9	CTCAAACATTTTCCCG CAATGGTGCTTTCT	445 5	CUCAAACAUUUUCCCG CAAUGGUGCUUUCU
STMN2_ intron1	+	TTTC	245 0	TTTACTCAAACATTTT CCCGCAATGGTGCT	445 6	UUUACUCAAAACAUUU CCCGCAAUGGUGCU
STMN2_ intron1	+	ATT C	245 1	ATAAATTCCAGATTCT CTATGGGAAGTAAC	445 7	AUAAAUCCAGAUUCU CUAUGGGAAGUAAC
STMN2_ intron1	+	ATT T	245 2	CTTACTCAAACATTT TCCCGCAATGGTGCT	445 8	CUUUACUCAAAACAUU UCCCGCAAUGGUGC
STMN2_ intron1	+	CTT G	245 3	AGGGCCTCGAGCCAA TAAGTCTTCTATTT	445 9	AGGGCCUCGAGCCAAU AAGUCUCCUAUUU
STMN2_ intron1	+	TTT G	245 4	GAGATGACAAAAATC TAAACTTGAGGGCCT	446 0	GAGAUGACAAAAAUCU AAACUUGAGGGCCU
STMN2_ intron1	+	ATT T	245 5	GGAGATGACAAAAAT CTAAACTTGAGGGCC	446 1	GGAGAUGACAAAAAUC UAAACUUGAGGGCC
STMN2_ intron1	+	ATT C	245 6	TGGCAGTCGGGCAGG GCTCTCTGTATAACC	446 2	UGGCAGUCGGGCAGGG CUCUCUGUAUAACC
STMN2_ intron1	+	TTT A	245 7	ATTCTGGCAGTCGGGC AGGGCTCTCTGTAT	446 3	AUUCUGGCAGUCGGGC AGGGCUCUCUGUAU
STMN2_ intron1	+	GTT T	245 8	AATTCTGGCAGTCGG GCAGGGCTCTCTGTA	446 4	AAUUCUGGCAGUCGGG CAGGGCUCUCUGUA
STMN2_ intron1	+	TTT A	245 9	AATGTTTAATTCTGGC AGTCGGGCAGGGCT	446 5	AAUGUUUAAUUCUGGC AGUCGGGCAGGGCU
STMN2_ intron1	+	TTTT	246 0	AAATGTTTAATTCTGG CAGTCGGGCAGGGC	446 6	AAAUGUUUAAUUCUGG CAGUCGGGCAGGGC
STMN2_ intron1	+	GTT T	246 1	TAAATGTTTAATTCTG GCAGTCGGGCAGGG	446 7	UAAAUGUUUAAUUCUG GCAGUCGGGCAGGG
STMN2_ intron1	+	ATT G	246 2	CAGAGGTCACACCTGT GATATCACCATTTT	446 8	CAGAGGUCACACCUGU GAUAUCACCAUUUU
STMN2_ intron1	+	ATT C	246 3	ATGTTTTAAATGTTTA ATTCTGGCAGTCGG	446 9	AUGUUUUAAAUGUUUA AUUCUGGCAGUCGG

STMN2_ intron1	+	ATT A	246 4	CAAAAGTAATTCATGT TTTAAATGTTTAAT	447 0	CAAAAGUAAUUCAUGU UUUAAAUGUUUAAU
STMN2_ intron1	+	CTT A	246 5	AGACAGCATTACAAA AGTAATTCATGTTTT	447 1	AGACAGCAUUACAAAA GUAAUUCAUGUUUU
STMN2_ intron1	+	CTT C	246 6	CTATTTCTTTACTCAA ACATTTTCCCGCAA	447 2	CUAUUUUCUUUACUCAA ACAUUUUCCCGCAA
STMN2_ intron1	+	ATT C	246 7	CAGATTCTCTATGGGA AGTAACTTTTATTG	447 3	CAGAUUCUCUAUGGGA AGUAACUUUUAUUG
STMN2_ intron1	+	CTTT	246 8	ACTCAAACATTTTCCC GCAATGGTGCTTTC	447 4	ACUCAAACAUUUCCCC GCAAUGGUGCUUUC
STMN2_ intron1	+	CTT A	246 9	CTCAAGGTCACACAGT TAGTCAGATCCAGA	447 5	CUCAAGGUCACACAGU UAGUCAGAUCCAGA
STMN2_ intron1	+	ATT C	247 0	TCTATGGGAAGTAACT TTTATTGATTGATT	447 6	UCUAUGGGAAGUAAACU UUUAUUGAUUGAUU
STMN2_ intron1	+	TTTC	247 1	ACCGATTGCTGCTAGT CTCATATCTGTTCC	447 7	ACCGAUUGCUGCUAGU CUCAUAUCUGUCC
STMN2_ intron1	+	CTTT	247 2	CACCGATTGCTGCTAG TCTCATATCTGTTC	447 8	CACCGAUUGCUGCUAG UCUCAUAUCUGUUC
STMN2_ intron1	+	CTT C	247 3	GGAATCCATCTTTCAC CGATTGCTGCTAGT	447 9	GGAAUCCAUCUUUCAC CGAUUGCUGCUAGU
STMN2_ intron1	+	TTT G	247 4	GGCCCAGGCCATCTG GCTTCGGAATCCATC	448 0	GGCCCAGGCCAUCUGG CUUCGGAAUCCAUC
STMN2_ intron1	+	ATT T	247 5	GGGCCCAGGCCATCT GGCTTCGGAATCCAT	448 1	GGGCCCAGGCCAUCUG GCUUCGGAAUCCAUC
STMN2_ intron1	+	GTT A	247 6	GTCAGATCCAGAATTT GGGCCCAGGCCATC	448 2	GUCAGAUCCAGAAUUU GGGCCCAGGCCAUC
STMN2_ intron1	+	GTT G	247 7	AAGTATCTTACTCAAG GTCACACAGTTAGT	448 3	AAGUAUCUUACUCAAG GUCACACAGUUAGU
STMN2_ intron1	+	ATT A	247 8	CAGATATGGAACTG AGGCACAGAAAGTTG	448 4	CAGAU AUGGAAACUGA GGCACAGAAAGUUG
STMN2_ intron1	+	GTT C	247 9	TATTACAGATATGGA AACTGAGGCACAGAA	448 5	UAUUACAGAU AUGGAA ACUGAGGCACAGAA
STMN2_ intron1	+	ATT G	248 0	CTGCTAGTCTCATATC TGTTCCATGTTAGA	448 6	CUGCUAGUCUCAUAUC UGUCCAUGUUAGA
STMN2_ intron1	+	GTT A	248 1	ATCACTTAATAATCCT AAGTAGGTTCTATT	448 7	AUCACUUAAUAAUCCU AAGUAGGUUCUAUU
STMN2_ intron1	+	GTT C	248 2	CATGTTAGAGGTGAG CTCCATTGCAGAGG	448 8	CAUGUUAGAGGUGAGC UCCCAUUGCAGAGG
STMN2_ intron1	+	CTT A	248 3	ATAATCCTAAGTAGGT TCTATTACAGATAT	448 9	AUAAUCCUAAGUAGGU UCUAUUACAGAUAU
STMN2_ intron1	+	TTTC	248 4	CACATATTAAGTGTGT TAATCACTTAATAA	449 0	CACAU AUUAACUGUGU UAAUCACUAAUAA
STMN2_ intron1	+	CTTT	248 5	TATTGATTGATTTAAC CCTTGTATAGCACA	449 1	UAUUGAUUGAUUUAAC CCUUGUAUAGCACA

STMN2_ intron1	+	TTTT	248 6	ATTGATTGATTTAACC CTTGTATAGCACAT	449 2	AUUGAUUGAUUUAACC CUUGUAUAGCACAU
STMN2_ intron1	+	TTT A	248 7	TTGATTGATTTAACCC TTGTATAGCACATA	449 3	UUGAUUGAUUUAACCC UUGUAUAGCACAU
STMN2_ intron1	+	ATT G	248 8	ATTGATTTAACCCTTG TATAGCACATATAA	449 4	AUUGAUUUAACCCUUG UAUAGCACAUUAA
STMN2_ intron1	+	ATT G	248 9	ATTTAACCCCTTGATA GCACATATAACATG	449 5	AUUUAACCCUUGUAUA GCACAUUAACAUG
STMN2_ intron1	+	ATT A	249 0	ACTGTGTAAATCACTT AATAATCCTAAGTA	449 6	ACUGUGUUAUACACUU AAUAAUCCUAAGUA
STMN2_ intron1	+	ATT T	249 1	AACCCCTGTATAGCAC ATATAACATGCAAG	449 7	AACCCUUGUAUAGCAC AUUAACAUGCAAG
STMN2_ intron1	+	CTT G	249 2	TATAGCACATATAAC ATGCAAGGCATTGTT	449 8	UAUAGCACAUUAACA UGCAAGGCAUUGUU
STMN2_ intron1	+	ATT G	249 3	TTCTAAGAACTTTCCA CATATTAAGTGTGT	449 9	UUCUAAGAACUUUCCA CAUAUUAACUGUGU
STMN2_ intron1	+	GTT C	249 4	TAAGAAGTTTCCACAT ATTAAGTGTGTAA	450 0	UAAGAACUUUCCACAU AUUAACUGUGUAA
STMN2_ intron1	+	CTTT	249 5	CCACATATTAAGTGTG TTAATCACTTAATA	450 1	CCACAUUAUUAACUGUG UUAUACACUUAUA
STMN2_ intron1	+	TTT A	249 6	ACCCTTGTATAGCACA TATAACATGCAAGG	450 2	ACCCUUGUAUAGCACA UAUAACAUGCAAGG

* The three 3' nucleotides represent the 5'-TTN-3' motif.

The present disclosure includes all combinations of the direct repeat sequences and
5 spacer sequences listed above, consistent with the present disclosure herein.

In some embodiments, a spacer sequence described herein comprises a uracil (U). In some
embodiments, a spacer sequence described herein comprises a thymine (T). In some embodiments,
a spacer sequence according to Table 5A or 5B comprises a sequence comprising a thymine in one
or more (*e.g.*, all) places indicated as uracil in Table 5A or 5B.

10 The present disclosure includes RNA guides that comprise any and all combinations of
the direct repeats and spacers described herein (*e.g.*, as set forth in Table 5A or 5B, above).

In some embodiments, the RNA guide has at least 90% identity (*e.g.*, at least 90%, 91%,
92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to any one of SEQ ID NOs: 4505-4562.
In some embodiments, the RNA guide has at least 95% identity (*e.g.*, at least 95%, 96%, 97%,
15 98% or 99% identity to any one of SEQ ID NOs: 4505-4562. In some embodiments, the RNA
guide has a sequence set forth in any one of SEQ ID NOs: 4505-4562.

In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID
NOs: 4508, 4512, 4559, and 4561, or the second nucleic acid encodes an RNA guide comprising
any one of SEQ ID NOs: 4508, 4512, 4559, and 4561.

In some embodiments, the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 5 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.

B. Nucleic Acid Modifications

The RNA guide may include one or more covalent modifications with respect to a reference sequence, in particular the parent polyribonucleotide, which are included within the 10 scope of this disclosure.

Exemplary modifications can include any modification to the sugar, the nucleobase, the internucleoside linkage (e.g., to a linking phosphate/to a phosphodiester linkage/to the phosphodiester backbone), and any combination thereof. Some of the exemplary modifications provided herein are described in detail below.

15 The RNA guide may include any useful modification, such as to the sugar, the nucleobase, or the internucleoside linkage (e.g., to a linking phosphate/to a phosphodiester linkage/to the phosphodiester backbone). One or more atoms of a pyrimidine nucleobase may be replaced or substituted with optionally substituted amino, optionally substituted thiol, optionally substituted alkyl (e.g., methyl or ethyl), or halo (e.g., chloro or fluoro). In certain embodiments, 20 modifications (e.g., one or more modifications) are present in each of the sugar and the internucleoside linkage. Modifications may be modifications of ribonucleic acids (RNAs) to deoxyribonucleic acids (DNAs), threose nucleic acids (TNAs), glycol nucleic acids (GNAs), peptide nucleic acids (PNAs), locked nucleic acids (LNAs) or hybrids thereof. Additional modifications are described herein.

25 In some embodiments, the modification may include a chemical or cellular induced modification. For example, some nonlimiting examples of intracellular RNA modifications are described by Lewis and Pan in “RNA modifications and structures cooperate to guide RNA-protein interactions” from Nat Reviews Mol Cell Biol, 2017, 18:202-210.

Different sugar modifications, nucleotide modifications, and/or internucleoside linkages 30 (e.g., backbone structures) may exist at various positions in the sequence. One of ordinary skill in the art will appreciate that the nucleotide analogs or other modification(s) may be located at any position(s) of the sequence, such that the function of the sequence is not substantially decreased. The sequence may include from about 1% to about 100% modified nucleotides (either in relation to overall nucleotide content, or in relation to one or more types of nucleotide, i.e. any 35 one or more of A, G, U or C) or any intervening percentage (e.g., from 1% to 20%>, from 1% to

25%, from 1% to 50%, from 1% to 60%, from 1% to 70%, from 1% to 80%, from 1% to 90%, from 1% to 95%, from 10% to 20%, from 10% to 25%, from 10% to 50%, from 10% to 60%, from 10% to 70%, from 10% to 80%, from 10% to 90%, from 10% to 95%, from 10% to 100%, from 20% to 25%, from 20% to 50%, from 20% to 60%, from 20% to 70%, from 20% to 80%,
5 from 20% to 90%, from 20% to 95%, from 20% to 100%, from 50% to 60%, from 50% to 70%, from 50% to 80%, from 50% to 90%, from 50% to 95%, from 50% to 100%, from 70% to 80%, from 70% to 90%, from 70% to 95%, from 70% to 100%, from 80% to 90%, from 80% to 95%, from 80% to 100%, from 90% to 95%, from 90% to 100%, and from 95% to 100%).

In some embodiments, sugar modifications (e.g., at the 2' position or 4' position) or
10 replacement of the sugar at one or more ribonucleotides of the sequence may, as well as backbone modifications, include modification or replacement of the phosphodiester linkages. Specific examples of a sequence include, but are not limited to, sequences including modified backbones or no natural internucleoside linkages such as internucleoside modifications, including modification or replacement of the phosphodiester linkages. Sequences having
15 modified backbones include, among others, those that do not have a phosphorus atom in the backbone. For the purposes of this application, and as sometimes referenced in the art, modified RNAs that do not have a phosphorus atom in their internucleoside backbone can also be considered to be oligonucleosides. In particular embodiments, a sequence will include ribonucleotides with a phosphorus atom in its internucleoside backbone.

20 Modified sequence backbones may include, for example, phosphorothioates, chiral phosphorothioates, phosphorodithioates, phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates such as 3'-alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates such as 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates,
25 thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'. Various salts, mixed salts and free acid forms are also included. In some embodiments, the sequence may be negatively or positively charged.

The modified nucleotides, which may be incorporated into the sequence, can be modified
30 on the internucleoside linkage (e.g., phosphate backbone). Herein, in the context of the polynucleotide backbone, the phrases "phosphate" and "phosphodiester" are used interchangeably. Backbone phosphate groups can be modified by replacing one or more of the oxygen atoms with a different substituent. Further, the modified nucleosides and nucleotides can include the wholesale replacement of an unmodified phosphate moiety with another
35 internucleoside linkage as described herein. Examples of modified phosphate groups include, but

are not limited to, phosphorothioate, phosphoroselenates, boranophosphates, boranophosphate esters, hydrogen phosphonates, phosphoramidates, phosphorodiamidates, alkyl or aryl phosphonates, and phosphotriesters. Phosphorodithioates have both non-linking oxygens replaced by sulfur. The phosphate linker can also be modified by the replacement of a linking
5 oxygen with nitrogen (bridged phosphoramidates), sulfur (bridged phosphorothioates), and carbon (bridged methylene-phosphonates).

The α -thio substituted phosphate moiety is provided to confer stability to RNA and DNA polymers through the unnatural phosphorothioate backbone linkages. Phosphorothioate DNA and RNA have increased nuclease resistance and subsequently a longer half-life in a cellular
10 environment.

In specific embodiments, a modified nucleoside includes an alpha-thio-nucleoside (e.g., 5'-O-(1-thiophosphate)-adenosine, 5'-O-(1-thiophosphate)-cytidine (a-thio-cytidine), 5'-O-(1-thiophosphate)-guanosine, 5'-O-(1-thiophosphate)-uridine, or 5'-O-(1-thiophosphate)-pseudouridine).

Other internucleoside linkages that may be employed according to the present disclosure, including internucleoside linkages which do not contain a phosphorous atom, are described herein.

In some embodiments, the sequence may include one or more cytotoxic nucleosides. For example, cytotoxic nucleosides may be incorporated into sequence, such as bifunctional
20 modification. Cytotoxic nucleoside may include, but are not limited to, adenosine arabinoside, 5-azacytidine, 4'-thio-aracytidine, cyclopentenylcytosine, cladribine, clofarabine, cytarabine, cytosine arabinoside, 1-(2-C-cyano-2-deoxy-beta-D-arabino-pentofuranosyl)-cytosine, decitabine, 5-fluorouracil, fludarabine, floxuridine, gemcitabine, a combination of tegafur and uracil, tegafur ((RS)-5-fluoro-1-(tetrahydrofuran-2-yl)pyrimidine-2,4(1H,3H)-dione),
25 troxacitabine, tezacitabine, 2'-deoxy-2'-methylidenecytidine (DMDC), and 6-mercaptopurine. Additional examples include fludarabine phosphate, N4-behenoyl-1-beta-D-arabinofuranosylcytosine, N4-octadecyl-1-beta-D-arabinofuranosylcytosine, N4-palmitoyl-1-(2-C-cyano-2-deoxy-beta-D-arabino-pentofuranosyl) cytosine, and P-4055 (cytarabine 5'-elaidic acid ester).

In some embodiments, the sequence includes one or more post-transcriptional modifications (e.g., capping, cleavage, polyadenylation, splicing, poly-A sequence, methylation, acylation, phosphorylation, methylation of lysine and arginine residues, acetylation, and nitrosylation of thiol groups and tyrosine residues, etc.). The one or more post-transcriptional modifications can be any post-transcriptional modification, such as any of the more than one
35 hundred different nucleoside modifications that have been identified in RNA (Rozenski, J, Crain,

P, and McCloskey, J. (1999). The RNA Modification Database: 1999 update. Nucl Acids Res 27: 196-197) In some embodiments, the first isolated nucleic acid comprises messenger RNA (mRNA). In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of pyridin-4-one ribonucleoside, 5-aza-uridine, 2-thio-5-aza-uridine, 2-thiouridine, 4-thio-pseudouridine, 2-thio-pseudouridine, 5-hydroxyuridine, 3-methyluridine, 5-carboxymethyl-uridine, 1-carboxymethyl-pseudouridine, 5-propynyl-uridine, 1-propynyl-pseudouridine, 5-taurinomethyluridine, 1-taurinomethyl-pseudouridine, 5-taurinomethyl-2-thio-uridine, 1-taurinomethyl-4-thio-uridine, 5-methyl-uridine, 1-methyl-pseudouridine, 4-thio-1-methyl-pseudouridine, 2-thio-1-methyl-pseudouridine, 1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-1-deaza-pseudouridine, dihydrouridine, dihydropseudouridine, 2-thio-dihydrouridine, 2-thio-dihydropseudouridine, 2-methoxyuridine, 2-methoxy-4-thio-uridine, 4-methoxy-pseudouridine, and 4-methoxy-2-thio-pseudouridine. In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of 5-aza-cytidine, pseudoisocytidine, 3-methyl-cytidine, N4-acetylcytidine, 5-formylcytidine, N4-methylcytidine, 5-hydroxymethylcytidine, 1-methyl-pseudoisocytidine, pyrrolo-cytidine, pyrrolo-pseudoisocytidine, 2-thio-cytidine, 2-thio-5-methyl-cytidine, 4-thio-pseudoisocytidine, 4-thio-1-methyl-pseudoisocytidine, 4-thio-1-methyl-1-deaza-pseudoisocytidine, 1-methyl-1-deaza-pseudoisocytidine, zebularine, 5-aza-zebularine, 5-methyl-zebularine, 5-aza-2-thio-zebularine, 2-thio-zebularine, 2-methoxy-cytidine, 2-methoxy-5-methyl-cytidine, 4-methoxy-pseudoisocytidine, and 4-methoxy-1-methyl-pseudoisocytidine. In some embodiments, the mRNA comprises at least one nucleoside selected from the group consisting of 2-aminopurine, 2,6-diaminopurine, 7-deaza-adenine, 7-deaza-8-aza-adenine, 7-deaza-2-aminopurine, 7-deaza-8-aza-2-aminopurine, 7-deaza-2,6-diaminopurine, 7-deaza-8-aza-2,6-diaminopurine, 1-methyladenosine, N6-methyladenosine, N6-isopentenyladenosine, N6-(cis-hydroxyisopentenyl)adenosine, 2-methylthio-N6-(cis-hydroxyisopentenyl) adenosine, N6-glycinylicarbamoyladenosine, N6-threonylicarbamoyladenosine, 2-methylthio-N6-threonyl carbamoyladenosine, N6,N6-dimethyladenosine, 7-methyladenine, 2-methylthio-adenine, and 2-methoxy-adenine. In some embodiments, mRNA comprises at least one nucleoside selected from the group consisting of inosine, 1-methyl-inosine, wyosine, wybutosine, 7-deaza-guanosine, 7-deaza-8-aza-guanosine, 6-thio-guanosine, 6-thio-7-deaza-guanosine, 6-thio-7-deaza-8-aza-guanosine, 7-methyl-guanosine, 6-thio-7-methyl-guanosine, 7-methylinosine, 6-methoxy-guanosine, 1-methylguanosine, N2-methylguanosine, N2,N2-dimethylguanosine, 8-oxo-guanosine, 7-methyl-8-oxo-guanosine, 1-methyl-6-thio-guanosine, N2-methyl-6-thio-guanosine, and N2,N2-dimethyl-6-thio-guanosine.

The sequence may or may not be uniformly modified along the entire length of the molecule. For example, one or more or all types of nucleotides (e.g., naturally-occurring nucleotides, purine or pyrimidine, or any one or more or all of A, G, U, C, I, pU) may or may not be uniformly modified in the sequence, or in a given predetermined sequence region thereof. In
5 some embodiments, the sequence includes a pseudouridine. In some embodiments, the sequence includes an inosine, which may aid in the immune system characterizing the sequence as endogenous versus viral RNAs. The incorporation of inosine may also mediate improved RNA stability/reduced degradation. See for example, Yu, Z. et al. (2015) RNA editing by ADAR1 marks dsRNA as “self”. Cell Res. 25, 1283-1284, which is incorporated by reference in its
10 entirety.

In some embodiments, one or more of the nucleotides of an RNA guide comprises a 2'-*O*-methyl phosphorothioate modification. In some embodiments, each of the first three nucleotides of the RNA guide comprises a 2'-*O*-methyl phosphorothioate modification. In some
15 embodiments, each of the last four nucleotides of the RNA guide comprises a 2'-*O*-methyl phosphorothioate modification. In some embodiments, each of the first to last, second to last, and third to last nucleotides of the RNA guide comprises a 2'-*O*-methyl phosphorothioate modification, and wherein the last nucleotide of the RNA guide is unmodified. In some
20 embodiments, each of the first three nucleotides of the RNA guide comprises a 2'-*O*-methyl phosphorothioate modification, and each of the first to last, second to last, and third to last nucleotides of the RNA guide comprises a 2'-*O*-methyl phosphorothioate modification.

When a gene editing system disclosed herein comprises nucleic acids encoding the Cas12i polypeptide disclosed herein, e.g., mRNA molecules, such nucleic acid molecules may contain any of the modifications disclosed herein, where applicable.

25 ***C. Cas12i Polypeptide***

In some embodiments, the composition or system of the present disclosure includes a Cas12i polypeptide as described in WO/2019/178427, the relevant disclosures of which are incorporated by reference for the subject matter and purpose referenced herein.

In some embodiments, the genetic editing system of the present disclosure comprises a
30 Cas12i2 polypeptide described herein (e.g., a polypeptide comprising SEQ ID NO: 448 and/or encoded by SEQ ID NO: 447 (or a version thereof in which T's are replaced with U's)). In some embodiments, the Cas12i2 polypeptide comprises at least one RuvC domain. In some
35 embodiments, the genetic editing system of the present disclosure comprises a nucleic acid molecule (e.g., a DNA molecule or a polyribonucleotide molecule) encoding a Cas12i polypeptide.

A nucleic acid sequence encoding the Cas12i2 polypeptide described herein may be substantially identical to a reference nucleic acid sequence, *e.g.*, SEQ ID NO: 447 (or a version thereof in which T's are replaced with U's). In some embodiments, the Cas12i2 polypeptide is encoded by a nucleic acid comprising a sequence having least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the reference nucleic acid sequence, *e.g.*, SEQ ID NO: 447 (or a version thereof in which T's are replaced with U's). The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (*e.g.*, BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two nucleic acid sequences are substantially identical is that the nucleic acid molecules hybridize to the complementary sequence of the other under stringent conditions of temperature and ionic strength (*e.g.*, within a range of medium to high stringency). *See, e.g.*, Tijssen, "Hybridization with Nucleic Acid Probes. Part I. Theory and Nucleic Acid Preparation" (Laboratory Techniques in Biochemistry and Molecular Biology, Vol 24).

In some embodiments, the Cas12i2 polypeptide is encoded by a nucleic acid sequence having at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity, but not 100% sequence identity, to a reference nucleic acid sequence, *e.g.*, SEQ ID NO: 447 (or a version thereof in which T's are replaced with U's).

In some embodiments, the Cas12i2 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 448.

In some embodiments, the present disclosure describes a Cas12i2 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 448. Homology or identity can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i2 polypeptide of the present disclosure having enzymatic activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 448 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using
5 any of the previously described alignment methods.

In some embodiments, the Cas12i2 polypeptide may contain one or more mutations relative to SEQ ID NO: 448, for example, at position D581, G624, F626, P868, I926, V1030, E1035, S1046, or any combination thereof. In some instances, the one or more mutations are amino acid substitutions, for example, D581R, G624R, F626R, P868T, I926R, V1030G,
10 E1035R, S1046G, or a combination thereof.

In some embodiments, the Cas12i2 polypeptide comprises a polypeptide having a sequence of SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453. In some examples, the Cas12i2 polypeptide contains mutations at positions D581, D911, I926, and V1030. Such a Cas12i2 polypeptide may contain amino acid substitutions of
15 D581R, D911R, I926R, and V1030G (*e.g.*, SEQ ID NO: 449). In some examples, the Cas12i2 polypeptide contains mutations at positions D581, I926, and V1030. Such a Cas12i2 polypeptide may contain amino acid substitutions of D581R, I926R, and V1030G (*e.g.*, SEQ ID NO: 450). In some examples, the Cas12i2 polypeptide may contain mutations at positions D581, I926, V1030, and S1046. Such a Cas12i2 polypeptide may contain amino acid substitutions of D581R,
20 I926R, V1030G, and S1046G (*e.g.*, SEQ ID NO: 451). In some examples, the Cas12i2 polypeptide may contain mutations at positions D581, G624, F626, I926, V1030, E1035, and S1046. Such a Cas12i2 polypeptide may contain amino acid substitutions of D581R, G624R, F626R, I926R, V1030G, E1035R, and S1046G (*e.g.*, SEQ ID NO: 452). In some examples, the Cas12i2 polypeptide may contain mutations at positions D581, G624, F626, P868, I926, V1030,
25 E1035, and S1046. Such a Cas12i2 polypeptide may contain amino acid substitutions of D581R, G624R, F626R, P868T, I926R, V1030G, E1035R, and S1046G (*e.g.*, SEQ ID NO: 453).

In some embodiments, the Cas12i2 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453. In some embodiments, a Cas12i2
30 polypeptide having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453 maintains the amino acid changes (or at least 1, 2, 3 etc. of these changes) that differentiate the polypeptide from its respective parent/reference
35 sequence.

In some embodiments, the present disclosure describes a Cas12i2 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453. Homology or identity can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i2 polypeptide of the present disclosure having enzymatic activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using any of the previously described alignment methods.

In some embodiments, the composition of the present disclosure includes a Cas12i4 polypeptide described herein (*e.g.*, a polypeptide comprising SEQ ID NO: 482 and/or encoded by SEQ ID NO: 481 (or a version thereof in which T's are replaced with U's)). In some embodiments, the Cas12i4 polypeptide comprises at least one RuvC domain.

A nucleic acid sequence encoding the Cas12i4 polypeptide described herein may be substantially identical to a reference nucleic acid sequence, *e.g.*, SEQ ID NO: 481 (or a version thereof in which T's are replaced with U's). In some embodiments, the Cas12i4 polypeptide is encoded by a nucleic acid comprising a sequence having least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the reference nucleic acid sequence, *e.g.*, SEQ ID NO: 481 (or a version thereof in which T's are replaced with U's). The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (*e.g.*, BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two nucleic acid sequences are substantially identical is that the nucleic acid molecules hybridize to the complementary sequence of the other under stringent conditions of temperature and ionic strength (*e.g.*, within a range of medium to high stringency).

In some embodiments, the Cas12i4 polypeptide is encoded by a nucleic acid sequence having at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least

about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or more sequence identity, but not 100% sequence identity, to a reference nucleic acid sequence, *e.g.*, SEQ ID NO: 481 (or a version thereof in which T's are replaced with U's).

In some embodiments, the Cas12i4 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 482.

In some embodiments, the present disclosure describes a Cas12i4 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 482. Homology or identity can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i4 polypeptide of the present disclosure having enzymatic activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 482 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using any of the previously described alignment methods.

In some embodiments, the Cas12i4 polypeptide comprises a polypeptide having a sequence of SEQ ID NO: 483 or SEQ ID NO: 484.

In some embodiments, the Cas12i4 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 483 or SEQ ID NO: 484. In some embodiments, a Cas12i4 polypeptide having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 483 or SEQ ID NO: 484 maintains the amino acid changes (or at least 1, 2, 3 etc. of these changes) that differentiate it from its respective parent/reference sequence.

In some embodiments, the present disclosure describes a Cas12i4 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 483 or SEQ ID NO: 484. Homology or identity can be determined by amino acid

sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i4 polypeptide of the present disclosure having enzymatic activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 483 or SEQ ID NO: 484 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using any of the previously described alignment methods.

In some embodiments, the composition of the present disclosure includes a Cas12i1 polypeptide described herein (*e.g.*, a polypeptide comprising SEQ ID NO: 4503). In some embodiments, the Cas12i1 polypeptide comprises at least one RuvC domain.

In some embodiments, the Cas12i1 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4503.

In some embodiments, the present disclosure describes a Cas12i1 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 4503. Homology or identity can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i1 polypeptide of the present disclosure having enzymatic activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 4503 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using any of the previously described alignment methods.

In some embodiments, the composition of the present disclosure includes a Cas12i3 polypeptide described herein (*e.g.*, a polypeptide comprising SEQ ID NO: 4504). In some embodiments, the Cas12i3 polypeptide comprises at least one RuvC domain.

In some embodiments, the Cas12i3 polypeptide of the present disclosure comprises a polypeptide sequence having at least 50%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to SEQ ID NO: 4504.

In some embodiments, the present disclosure describes a Cas12i3 polypeptide having a specified degree of amino acid sequence identity to one or more reference polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at

least 98%, or even at least 99%, but not 100%, sequence identity to the amino acid sequence of SEQ ID NO: 4504. Homology or identity can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a Cas12i3 polypeptide of the present disclosure having enzymatic
5 activity, *e.g.*, nuclease or endonuclease activity, and comprising an amino acid sequence which differs from the amino acid sequences of SEQ ID NO: 4504 by 50, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, 1, or 0 amino acid residue(s), when aligned using any of the previously described alignment methods.

Although the changes described herein may be one or more amino acid changes, changes
10 to the Cas12i polypeptide may also be of a substantive nature, such as fusion of polypeptides as amino- and/or carboxyl-terminal extensions. For example, the Cas12i polypeptide may contain additional peptides, *e.g.*, one or more peptides. Examples of additional peptides may include epitope peptides for labelling, such as a polyhistidine tag (His-tag), Myc, and FLAG. In some embodiments, the Cas12i polypeptide described herein can be fused to a detectable moiety such
15 as a fluorescent protein (*e.g.*, green fluorescent protein (GFP) or yellow fluorescent protein (YFP)).

In some embodiments, the Cas12i polypeptide comprises at least one (*e.g.*, two, three, four, five, six, or more) nuclear localization signal (NLS). In some embodiments, the Cas12i polypeptide comprises at least one (*e.g.*, two, three, four, five, six, or more) nuclear export signal
20 (NES). In some embodiments, the Cas12i polypeptide comprises at least one (*e.g.*, two, three, four, five, six, or more) NLS and at least one (*e.g.*, two, three, four, five, six, or more) NES.

In some embodiments, the Cas12i polypeptide described herein can be self-inactivating. See, Epstein et al., "Engineering a Self-Inactivating CRISPR System for AAV Vectors," *Mol. Ther.*, 24 (2016): S50, which is incorporated by reference in its entirety.

25 In some embodiments, the nucleotide sequence encoding the Cas12i polypeptide described herein can be codon-optimized for use in a particular host cell or organism. For example, the nucleic acid can be codon-optimized for any non-human eukaryote including mice, rats, rabbits, dogs, livestock, or non-human primates. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at the world wide web site of
30 kazusa.or.jp/codon/ and these tables can be adapted in a number of ways. See Nakamura *et al. Nucl. Acids Res.* 28:292 (2000), which is incorporated herein by reference in its entirety. Computer algorithms for codon optimizing a particular sequence for expression in a particular host cell are also available, such as Gene Forge (Aptagen; Jacobus, PA). In some examples, the nucleic acid encoding the Cas12i polypeptides such as Cas12i2 polypeptides as disclosed herein
35 can be an mRNA molecule, which can be codon optimized.

Exemplary Cas12i polypeptide sequences and corresponding nucleotide sequences are listed in **Table 7**.

Table 7. Cas12i and STMN2 Sequences

SEQ ID NO:	Sequence	Description
447	ATGAGCAGCGCGATCAAAAGCTACAAGAGCGTTCTGCGTCCGAAC GAGCGTAAGAACCAACTGCTGAAAAGCACCATTTCAGTGCCCTGGAA GACGGTAGCGCGTTCTTTTTCAAGATGCTGCAAGGCCTGTTTGGT GGCATCACCCCGGAGATTGTTTCGTTTCAGCACCGAACAGGAGAAA CAGCAACAGGATATCGCGCTGTGGTGCGCGGTTAACTGGTTCGGT CCGGTGAGCCAAGACAGCCTGACCCACACCATTGCGAGCGATAAC CTGGTGAGAGAAGTTTGAGGAATACTATGGTGGCACCGCGAGCGAC GCGATCAAACAGTACTTCAGCGCGAGCATTGGCGAAAAGCTACTAT TGGAACGACTGCCGTCAACAGTACTATGATCTGTGCCGTGAGCTG GGTGTTGAGGTGAGCGACCTGACCCATGATCTGGAGATCCTGTGC CGTGAAAAGTGCCTGGCGGTTGCGACCGAGAGCAACCAGAACAAC AGCATCATTAGCGTTCTGTTTGGCACCGGCGAAAAAGAGGACCGT AGCGTGAAACTGCGTATCACCAAGAAAATTCTGGAGGCGATCAGC AACCTGAAAGAAATCCCGAAGAACGTTGCGCCGATTCAAGAGATC ATTCTGAACGTGGCGAAAGCGACCAAGGAAACCTTCCGTCAGGTG TATGCGGGTAACCTGGGTGCGCCGAGCACCTGGAGAAAATTTATC GCGAAGGACGGCCAAAAGAGTTTCGATCTGAAGAACTGCAGACC GACCTGAAGAAAGTTATTCGTGGTAAAAGCAAGGAGCGTGATTGG TGCTGCCAGGAAGAGCTGCGTAGCTACGTGGAGCAAAAACCCATC CAGTATGACCTGTGGGCGTGGGGCGAAATGTTCAACAAAAGCGCAC ACCGCGCTGAAAATCAAGAGCACCCGTAACCTACAACCTTTGCGAAG CAACGTCTGGAACAGTTCAAAGAGATTTCAGAGCCTGAACAACCTG CTGGTTGTGAAGAAGCTGAACGACTTTTTTCGATAGCGAATTTTTTC AGCGGCGAGGAAACCTACACCATCTGCGTTCACCATCTGGGTGGC AAGGACCTGAGCAAACCTGTATAAGGCGTGGGAGGATGATCCGGCG GACCCGGAACGCGATTGTGGTTCTGTGCGACGATCTGAAAAAC AACTTTAAGAAAGAGCCGATCCGTAACATTCTGCGTTACATCTTC ACCATTCTCAAGAATGCAGCGCGCAGGACATCCTGGCGGGCGGCG AAGTACAACCAACAGCTGGATCGTTATAAAAGCCAAAAGGCGAAC CCGAGCGTTCTGGGTAACCAGGGCTTTACCTGGACCAACGCGGTG ATCCTGCCGGAGAAGGCGCAGCGTAACGACCGTCCGAACAGCCTG GATCTGCGTATTTGGCTGTACCTGAACTGCGTCACCCGGACGGT CGTTGGAAGAAACACCATATCCCGTTCTACGATACCCGTTTCTTC CAAGAAATTTATGCGGCGGGCAACAGCCCGTTGACACCTGCCAG TTTTCGTACCCCGCGTTTTCGGTTATCACCTGCCGAAACTGACCGAT CAGACCGCGATCCGTGTTAACAAGAAACATGTGAAAGCGGCGAAG ACCGAGGCGCGTATTCGTCTGGCGATCCAACAGGGCACCTGCCG GTGAGCAACCTGAAGATCACCGAAATTAGCGCGACCATCAACAGC AAAGGTCAAGTGCGTATTCCGGTTAAGTTTGACGTGGGTGCTCAA AAAGGCACCTGCAGATCGGTGACCGTTTCTGCGGCTACGATCAA AACCAGACCGCGAGCCACGCGTATAGCCTGTGGGAAGTGGTTAAA GAGGGTCAATACCATAAAGAGCTGGGCTGCTTTGTTCGTTTCATC AGCAGCGGTGACATCGTGAGCATTACCGAGAACCGTGGCAACCAA TTTGATCAGCTGAGCTATGAAGGTCTGGCGTACCCGCAATATGCG GACTGGCGTAAGAAAGCGAGCAAGTTTCGTGAGCCTGTGGCAGATC	Nucl eotide sequence encoding Cas12i2

SEQ ID NO:	Sequence	Description
	ACCAAGAAAAACAAGAAAAAGGAAATCGTGACCGTTGAAGCGAAA GAGAAGTTTGACGCGATCTGCAAGTACCAGCCGCGTCTGTATAAA TTCAACAAGGAGTACGCGTATCTGCTGCGTGATATTGTTTCGTGGC AAAAGCCTGGTGGAACTGCAACAGATTTCGTCAAGAGATCTTTCGT TTCATTGAACAGGACTGCGGTGTTACCCGTCTGGGCAGCCTGAGC CTGAGCACCCCTGGAAACCGTGAAAGCGGTTAAGGGTATCATTAC AGCTATTTTAGCACCGCGCTGAACGCGAGCAAGAACAACCCGATC AGCGACGAACAGCGTAAAGAGTTTGATCCGGAACGTTCGCGCTG CTGGAAAAGCTGGAGCTGATTTCGTACCCGTAAAAAGAAACAAAA GTGGAACGTATCGCGAACAGCCTGATTTCAGACCTGCCTGGAGAAC AACATCAAGTTCATTTCGTGGTGAAGGCGACCTGAGCACCAAC AACGCGACCAAGAAAAAGGCGAACAGCCGTAGCATGGATTGGTTG GCGCGTGGTGTGTTTTAACAAAAATCCGTCAACTGGCGCCGATGCAC AACATTACCCGTGTTTCGGTTGCGGCAGCCTGTACACCAGCCACCAG GACCCGCTGGTGCATCGTAACCCGGATAAAGCGATGAAGTGCCGT TGGGCGGCGATCCCGGTTAAGGACATTGGCGATTGGGTGCTGCGT AAGCTGAGCCAAAACCTGCGTGCGAAAAACATCGGCACCGGCGAG TACTATACCAAGGTGTTAAAGAGTTCCTGAGCCATTATGAACTG CAGGACCTGGAGGAAGAGCTGCTGAAGTGGCGTAGCGATCGTAAA AGCAACATTCCGTGCTGGGTGCTGCAGAACCGTCTGGCGGAGAAG CTGGGCAACAAAGAAGCGGTGGTTTACATCCCGGTTTCGTGGTGGC CGTATTTATTTTTCGACCCACAAGGTGGCGACCGGTGCGGTGAGC ATCGTTTTTCGACCAAAAACAAGTGTGGGTTTGCAACGCGGATCAT GTTGCGGCGGCGAACATCGCGCTGACCGTGAAGGGTATTGGCGAA CAAAGCAGCGACGAAGAGAACCCGGATGGTAGCCGTATCAAACGTG CAGCTGACCAGC	
448	MSSAIKSYKSVLRPNERNKQLLKSTIQCLEDGSAFFFKMLQGLFG GITPEIVRFSTEQEKQQQDIALWCAVNWFRPVSQDSLTHTIASDN LVEKFEEYYGGTASDAIKQYFSASIGESYYWNCRQQYYDLCREL GVEVSDLTHDLEILCREKCLAVATESNQNNIIISVLFGTGEKEDR SVKLRIITKKILEAISNLKEIPKNVAPIQEIILNVAKATKETFRQV YAGNLGAPSTLEKFIKDGQKEFDLKKLQTDLKKVIRGKSKERDW CCQEELRSYVEQNTIQYDLWAWGEMFNKAHTALKIKSTRNYNFAK QRLEQFKEIQSLNNLLVVKKLNDFFDSEFFSGEETYITCVHHLGG KDLSKLYKAWEDDPADPENAIIVVLCDDLKNNFKKEPIRNILRYIF TIRQECQAQDILAAAKYNQQLDRYKSQKANPSVLGNQGF TWNAV ILPEKAQRNDRPNSLDLRIWLYLKL RHPDGRWKKHHIPFYDTRFF QEIIYAAGNSPVDTCQFRTPRFGYHLPKLTDTAIRVNNKKHVKA TEARIRLAIQQGTLPVSNLKITEISATINSKGQVRIPVKFDVGRQ KGTQLQIGDRFCGYDQNTASHAYSLWEVVKEGQYHKELGCFVRFI SSGDIVSITENRGNQFDQLSYEGLAYPQYADWRKKASKFVSLWQI TKKNKKKEIVTVEAKEKFDAICKYQPRLYKFNKEYAYLLRDIVRG KSLVELQQIRQEIFRFIEQDCGVTRLGSLSLSTLETVKAVKGIIY SYFSTALNASKNNPISDEQRKEFDPELFALLEKLELIRTRKKKQK VERIANSLIQTCLENNIKFIRGEGLSTTNNATKKKANSRSMDWL ARGVFNKIRQLAPMHNITLFGCGSLYTSHQDPLVHRNPDKAMKCR WAAIPVKDIGDWVLRKLSQNLRAKNIGTGEYYHQGVKEFLSHYEL QDLEELLLKWRSDRKSNI PCWVLQNLRAEKLGNKEAVVYIPVRGG RIYFATHKVATGAVSIVFDQKQVWVCNADHVAAANIALTVKGIGE QSSDEENPDGSRIKLQLTS	Cas1 2i2 amino acid sequence

SEQ ID NO:	Sequence				Description
449	MSSAIKSYKS	VLRPNERKNQ	LLKSTIQCLE	DGSAFFFFKML	Varia nt Cas12i2 of SEQ ID NO: 3 of PCT/US2021 /025257
	QGLFGGITPE	IVRFSTEQEK	QQQDIALWCA	VNWFRPVSQD	
	SLTHTIASDN	LVEKFEEYYG	GTASDAIKQY	FSASIGESYY	
	WNDCRQQYYD	LCRELGVEVS	DLTHDLEILC	REKCLAVATE	
	SNQNNSIISV	LFGTGEKEDR	SVKLRTTKKI	LEAISNLKEI	
	PKNVAPIQEI	ILNVAKATKE	TFRQVYAGNL	GAPSTLEKFI	
	AKDGQKEFDL	KKLQTDLKKV	IRGKSKERDW	CCQEELRSYV	
	EQNTIQYDLW	AWGEMFNKAH	TALKIKSTRN	YNFAKQRLEQ	
	FKEIQSLNNL	LVVKKLNDFF	DSEFFSGEET	YTICVHHLGG	
	KDLSKLYKAW	EDDPADPENA	IVVLCDDLKN	NFKKEPIRNI	
	LRYIFTIRQE	CSAQDILAAA	KYNQQLDTRYK	SQKANPSVLG	
	NQGFTWTNAV	ILPEKAQRND	RPNSLDLRIW	LYLKLRLHPDG	
	RWKKHHIPFY	DTRFFQEIYA	AGNSPVDTCQ	FRTPRFGYHL	
	PKLTDQTAIR	VNKKHVKAAC	TEARIRLAIQ	QGTLPVSNLK	
	ITEISATINS	KGQVRIPVKF	RVGRQKGTLO	IGDRFCGYDQ	
	NQTASHAYSL	WEVVKEGQYH	KELGCFVRFI	SSGDIVSITE	
	NRGNQFDQLS	YEGLAYPQYA	DWRKKASKFV	SLWQITKKNK	
	KKEIVTVEAK	EKFDAICKYQ	PRLYKFNKEY	AYLLRDIVRG	
	KSLVELQQIR	QEIFRFIEQD	CGVTRLGSL	LSTLETVKAV	
	KGIIYSYFST	ALNASKNNPI	SDEQRKEFDP	ELFALLEKLE	
	LIRTRKKKQK	VERIANSLIQ	TCLENNIKFI	RGEGLSTTN	
	NATKKKANSR	SMDWLARGVF	NKIRQLAPMH	NITLFGCGSL	
	YTSHQDPLVH	RNPDKAMKCR	WAAIPVKDIG	RWVLRKLSQN	
	LRAKNRGTGE	YYHQGVKEFL	SHYELQDLEE	ELLKWRSDRK	
	SNIPCWVLQN	RLAEKLGKNE	AVVYIPVRGG	RIYFATHKVA	
	TGAVSIVFDQ	KQVWVCNADH	VAAANIALTG	KGIGEQQSSDE	
	ENPDGSRIKL	QLTS			
450	MSSAIKSYKS	VLRPNERKNQ	LLKSTIQCLE	DGSAFFFFKML	Varia nt Cas12i2 of SEQ ID NO: 4 of PCT/US2021 /025257
	QGLFGGITPE	IVRFSTEQEK	QQQDIALWCA	VNWFRPVSQD	
	SLTHTIASDN	LVEKFEEYYG	GTASDAIKQY	FSASIGESYY	
	WNDCRQQYYD	LCRELGVEVS	DLTHDLEILC	REKCLAVATE	
	SNQNNSIISV	LFGTGEKEDR	SVKLRTTKKI	LEAISNLKEI	
	PKNVAPIQEI	ILNVAKATKE	TFRQVYAGNL	GAPSTLEKFI	
	AKDGQKEFDL	KKLQTDLKKV	IRGKSKERDW	CCQEELRSYV	
	EQNTIQYDLW	AWGEMFNKAH	TALKIKSTRN	YNFAKQRLEQ	
	FKEIQSLNNL	LVVKKLNDFF	DSEFFSGEET	YTICVHHLGG	
	KDLSKLYKAW	EDDPADPENA	IVVLCDDLKN	NFKKEPIRNI	
	LRYIFTIRQE	CSAQDILAAA	KYNQQLDTRYK	SQKANPSVLG	
	NQGFTWTNAV	ILPEKAQRND	RPNSLDLRIW	LYLKLRLHPDG	
	RWKKHHIPFY	DTRFFQEIYA	AGNSPVDTCQ	FRTPRFGYHL	
	PKLTDQTAIR	VNKKHVKAAC	TEARIRLAIQ	QGTLPVSNLK	
	ITEISATINS	KGQVRIPVKF	RVGRQKGTLO	IGDRFCGYDQ	
	NQTASHAYSL	WEVVKEGQYH	KELGCFVRFI	SSGDIVSITE	
	NRGNQFDQLS	YEGLAYPQYA	DWRKKASKFV	SLWQITKKNK	
	KKEIVTVEAK	EKFDAICKYQ	PRLYKFNKEY	AYLLRDIVRG	
	KSLVELQQIR	QEIFRFIEQD	CGVTRLGSL	LSTLETVKAV	
	KGIIYSYFST	ALNASKNNPI	SDEQRKEFDP	ELFALLEKLE	
	LIRTRKKKQK	VERIANSLIQ	TCLENNIKFI	RGEGLSTTN	
	NATKKKANSR	SMDWLARGVF	NKIRQLAPMH	NITLFGCGSL	
	YTSHQDPLVH	RNPDKAMKCR	WAAIPVKDIG	DWVLRKLSQN	
	LRAKNRGTGE	YYHQGVKEFL	SHYELQDLEE	ELLKWRSDRK	

SEQ ID NO:	Sequence				Description
	SNIPCWVLQN	RLAEKLGKNE	AVVYIPVRGG	RIYFATHKVA	
	TGAVSIVFDQ	KQVWVCNADH	VAAANIALTG	KGIGEQQSSDE	
	ENPDGSRIGL	QLTS			
451	MSSAIKSYKS	VLRPNERKNQ	LLKSTIQCLE	DGSAFFFFKML	Varia nt Cas12i2 of SEQ ID NO: 5 of PCT/US2021 /025257
	QGLFGGITPE	IVRFSTEQEK	QQQDIALWCA	VNWFRPVSQD	
	SLTHTIASDN	LVEKFEEYYG	GTASDAIKQY	FSASIGESYY	
	WNDCRQQYYD	LCRELGVEVS	DLTHDLEILC	REKCLAVATE	
	SNQNNSIISV	LFGTGEKEDR	SVKLRTTKKI	LEAISNLKEI	
	PKNVAPIQEI	ILNVAKATKE	TFRQVYAGNL	GAPSTLEKFI	
	AKDGQKEFDL	KKLQTDLKKV	IRGKSKERDW	CCQEELRSYV	
	EQNTIQYDLW	AWGEMFNKAH	TALKIKSTRN	YNFAKQRLEQ	
	FKEIQSLNNL	LVVKKLNDFF	DSEFFSGEET	YTICVHHLGG	
	KDLSKLYKAW	EDDPADPENA	IVVLCDDLKN	NFKKEPIRNI	
	LRYIFTIRQE	CSAQDILAAA	KYNQQLDTRYK	SQKANPSVLG	
	NQGFTWTNAV	ILPEKAQRND	RPNSLDLRIW	LYLKLRLHPDG	
	RWKKHHIPFY	DTRFFQEIYA	AGNSPVDTCQ	FRTPRFGYHL	
	PKLTDQTAIR	VNKKHVKAAC	TEARIRLAIQ	QGTLPVSNLK	
	ITEISATINS	KGQVRIPVKF	RVGRQKGTLO	IGDRFCGYDQ	
	NQTASHAYSL	WEVVKEGQYH	KELGCFVRFI	SSGDIVSITE	
	NRGNQFDQLS	YEGLAYPQYA	DWRKKASKFV	SLWQITKKNK	
	KKEIVTVEAK	EKFDAICKYQ	PRLYKFNKEY	AYLLRDIVRG	
	KSLVELQQIR	QEIFRFIEQD	CGVTRLGSL	LSTLETVKAV	
	KGIIYSYFST	ALNASKNNPI	SDEQRKEFDP	ELFALLEKLE	
	LIRTRKKKQK	VERIANSLIQ	TCLENNIFKI	RGEGLSTTN	
	NATKKKANSR	SMDWLARGVF	NKIRQLAPMH	NITLFGCGSL	
	YTSHQDPLVH	RNPDKAMKCR	WAAIPVKDIG	DWVLRKLSQN	
	LRAKNRGTGE	YYHQGVKEFL	SHYELQDLEE	ELLKWRSDRK	
	SNIPCWVLQN	RLAEKLGKNE	AVVYIPVRGG	RIYFATHKVA	
	TGAVSIVFDQ	KQVWVCNADH	VAAANIALTG	KGIGEQQSSDE	
	ENPDGGRIKL	QLTS			
452	MSSAIKSYKS	VLRPNERKNQ	LLKSTIQCLE	DGSAFFFFKML	Varia nt Cas12i2 of SEQ ID NO: 495 of PCT/US2021 /025257
	QGLFGGITPE	IVRFSTEQEK	QQQDIALWCA	VNWFRPVSQD	
	SLTHTIASDN	LVEKFEEYYG	GTASDAIKQY	FSASIGESYY	
	WNDCRQQYYD	LCRELGVEVS	DLTHDLEILC	REKCLAVATE	
	SNQNNSIISV	LFGTGEKEDR	SVKLRTTKKI	LEAISNLKEI	
	PKNVAPIQEI	ILNVAKATKE	TFRQVYAGNL	GAPSTLEKFI	
	AKDGQKEFDL	KKLQTDLKKV	IRGKSKERDW	CCQEELRSYV	
	EQNTIQYDLW	AWGEMFNKAH	TALKIKSTRN	YNFAKQRLEQ	
	FKEIQSLNNL	LVVKKLNDFF	DSEFFSGEET	YTICVHHLGG	
	KDLSKLYKAW	EDDPADPENA	IVVLCDDLKN	NFKKEPIRNI	
	LRYIFTIRQE	CSAQDILAAA	KYNQQLDTRYK	SQKANPSVLG	
	NQGFTWTNAV	ILPEKAQRND	RPNSLDLRIW	LYLKLRLHPDG	
	RWKKHHIPFY	DTRFFQEIYA	AGNSPVDTCQ	FRTPRFGYHL	
	PKLTDQTAIR	VNKKHVKAAC	TEARIRLAIQ	QGTLPVSNLK	
	ITEISATINS	KGQVRIPVKF	RVGRQKGTLO	IGDRFCGYDQ	
	NQTASHAYSL	WEVVKEGQYH	KELRCRVRFI	SSGDIVSITE	
	NRGNQFDQLS	YEGLAYPQYA	DWRKKASKFV	SLWQITKKNK	
	KKEIVTVEAK	EKFDAICKYQ	PRLYKFNKEY	AYLLRDIVRG	
	KSLVELQQIR	QEIFRFIEQD	CGVTRLGSL	LSTLETVKAV	
	KGIIYSYFST	ALNASKNNPI	SDEQRKEFDP	ELFALLEKLE	

SEQ ID NO:	Sequence	Description
	LIRTRKKKQK VERIANSLIQ TCLENNIKFI RGEGLSTTN NATKKKANSR SMDWLARGVF NKIRQLAPMH NITLFGCGSL YTSHQDPLVH RNPDKAMKCR WAAIPVKDIG DWVLRKLSQN LRAKNRGTGE YYHQGVKEFL SHYELQDLEE ELLKWRSDRK SNIPCWVLQN RLAEKLGNKE AVVYIPVRGG RIYFATHKVA TGAVSIVFDQ KQVWVCNADH VAAANIALTG KGIGRQSSDE ENPDGGRIKL QLTS	
453	MSSAIKSYKS VLRPNERKNQ LLKSTIQCLE DGSAFFFKML QGLFGGITPE IVRFSTEQEK QQQDIALWCA VNWFRPVSQD SLTHTIASDN LVEKFEEYYG GTASDAIKQY FSASIGESYY WNDCRQQYYD LCRELGVEVS DLTHDLEILC REKCLAVATE SNQNNSSIISV LFGTGEKEDR SVKLRTKKI LEAISNLKEI PKNVAPIQEI ILNVAKATKE TFRQVYAGNL GAPSTLEKFI AKDGQKEFDL KKLQTDLKKV IRGKSKERDW CCQEELRSYV EQNTIQYDLW AWGEMFNKAH TALKIKSTRN YNFAKQRLEQ FKEIQSLNNL LVVKKLNDFF DSEFFSGEET YTICVHHLGG KDLSKLYKAW EDDPADPENA IVVLCDDLKN NFKKEPIRNI LRYIFTIRQE CSAQDILAAA KYNQQLDRYK SQKANPSVLG NQGFTWTNAV ILPEKAQRND RPNSLDLRIW LYLKLRHPDG RWKKHHIPFY DTRFFQEIYA AGNSPVDTCQ FRTPRFGYHL PKLTDQTAIR VNKKHVKAAC TEARIRLAIQ QGTLPVSNLK ITEISATINS KGQVRIPVKF RVGRQKGTLO IGDRFCGYDQ NQTASHAYSL WEVVKEGQYH KELRCRVRFI SSGDIVSITE NRGNQFDQLS YEGLAYPQYA DWRKKASKFV SLWQITKKNK KKEIVTVEAK EKFDAICKYQ PRLYKFNKEY AYLLRDIVRG KSLVELQQIR QEIFRFIEQD CGVTRLGSL S LSTLETVKAV KGIIYSYFST ALNASKNNPI SDEQRKEFDP ELFALLEKLE LIRTRKKKQK VERIANSLIQ TCLENNIKFI RGEGLSTTN NATKKKANSR SMDWLARGVF NKIRQLATMH NITLFGCGSL YTSHQDPLVH RNPDKAMKCR WAAIPVKDIG DWVLRKLSQN LRAKNRGTGE YYHQGVKEFL SHYELQDLEE ELLKWRSDRK SNIPCWVLQN RLAEKLGNKE AVVYIPVRGG RIYFATHKVA TGAVSIVFDQ KQVWVCNADH VAAANIALTG KGIGRQSSDE ENPDGGRIKL QLTS	Variant Cas12i2 of SEQ ID NO: 496 of PCT/US2021 /025257
481	ATGGCTTCCATCTCTAGGCCATACGGCACCAAGCTGCGACCGGAC GCACGGAAGAAGGAGATGCTCGATAAGTTCTTTAATACTACTGACT AAGGGTCAGCGCGTGTTCGACAGACCTGGCCCTGTGCATCTATGGC TCCCTGACCCCTGGAGATGGCCAAGTCTCTGGAGCCAGAAAGTGAT TCAGAACTGGTGTGCGCTATTGGGTGGTTTTCGGCTGGTGGACAAG ACCATCTGGTCCAAGGATGGCATCAAGCAGGAGAATCTGGTGAAA CAGTACGAAGCCTATTCCGGAAGGAGGCTTCTGAAGTGGTCAAA ACATACCTGAACAGCCCCAGCTCCGACAAGTACGTGTGGATCGAT TGCAGGCAGAAATTCCTGAGGTTTCAGCGCGAGCTCGGCACTCGC AACCTGTCCGAGGACTTCGAATGTATGCTCTTTGAACAGTACATT AGACTGACCAAGGGCGAGATCGAAGGGTATGCCGCTATTTCAAAT ATGTTTCGGAACGGCGAGAAGGAAGACCGGAGCAAGAAAAGAATG TACGCTACACGGATGAAAGATTGGCTGGAGGCAAACGAAAATATC ACTTGGGAGCAGTATAGAGAGGCCCTGAAGAACCAGCTGAATGCT AAAAACCTGGAGCAGGTTGTGGCCAATTACAAGGGGAACGCTGGC GGGGCAGACCCCTTCTTTAAGTATAGCTTCTCAAAGAGGGAATG GTGAGCAAGAAAGAACATGCACAGCAGCTCGACAAGTTCAAAACC	Nucleotide sequence encoding Cas12i4

SEQ ID NO:	Sequence	Description
	GTCCTGAAGAACAAGCCCGGGACCTGAATTTTCCAAACAAGGAG AAGCTGAAGCAGTACCTGGAGGCCGAAATCGGCATTCCGGTCGAC GCTAACGTGTACTCCCAGATGTTCTCTAACGGGGTGAGTGAGGTC CAGCCTAAGACCACACGGAATATGTCTTTTAGTAACGAGAACTG GATCTGCTCACTGAACTGAAGGACCTGAACAAGGGCGATGGGTTT GAGTACGCCAGAGAAGTGCTGAACGGGGTTCTTTGACTCCGAGCTC CACACTACCGAGGATAAGTTTAATATCACCTCTAGGTACCTGGGA GGCGACAAATCAAACCGCCTGAGCAAACCTCTATAAGATCTGGAAG AAAGAGGGTGTGGACTGCGAGGAAGGCATTTCAGCAGTTCTGTGAA GCCGTCAAAGATAAGATGGGCCAGATCCCCATTGCAAATGTGCTG AAGTACCTGTGGCAGTTCCGGGAGACAGTCAGTGCCGAGGATTTT GAAGCAGCCGCTAAGGCTAACCATCTGGAGGAAAAGATCAGCCGG GTGAAAGCCCACCCAATCGTGATTAGCAATAGGTACTGGGCTTTT GGGACTTCCGCACTGGTGGGAAACATTATGCCCCGAGACAAGAGG CATCAGGGAGAGTATGCCGGTCAGAATTTCAAATGTGGCTGGAG GCTGAACTGCACTACGATGGCAAGAAAGCAAAGCACCATCTGCCT TTTTATAACGCCCGCTTCTTTGAGGAAGTGTACTGCTATCACCCC TCTGTGCGCGAGATCACTCCTTTCAAACCAAGCAGTTTGGCTGT GAAATCGGGAAGGACATTCCAGATTACGTGAGCGTCGCTCTGAAG GACAATCCGTATAAGAAAGCAACCAAACGAATCCTGCGTGCAATC TACAATCCCGTCGCCAACACAACCTGGCGTTGATAAGACCACAAAC TGCAGCTTCATGATCAAACGCGAGAATGACGAATATAAGCTGGTC ATCAACCGAAAAATTTCCGTGGATCGGCCTAAGAGAATCGAAGTG GGCAGGACAATTATGGGGTACGACCGCAATCAGACAGCTAGCGAT ACTTATTGGATTGGCCGGCTGGTGCCACCTGGAACCCGGGGCGCA TACCGCATCGGAGAGTGGAGCGTCCAGTATATTAAGTCCGGGCCT GTCCTGTCTAGTACTCAGGGAGTTAACAATTCCACTACCGACCAG CTGGTGTACAACGGCATGCCATCAAGCTCCGAGCGGTTCAAGGCC TGGAAGAAAGCCAGAATGGCTTTTATCCGAAAACCTCATTTCGTCAG CTGAATGACGAGGGACTGGAATCTAAGGGTCAGGATTATATCCCC GAGAACCCTTCTAGTTTTCGATGTGCGGGGCGAAACCCTGTACGTC TTTAACAGTAATTATCTGAAGGCCCTGGTGAGCAAACACAGAAAG GCCAAGAAACCTGTTGAGGGGATCCTGGACGAGATTGAAGCCTGG ACATCTAAAGACAAGGATTCATGCAGCCTGATGCGGCTGAGCAGC CTGAGCGATGCTTCCATGCAGGGAATCGCCAGCCTGAAGAGTCTG ATTAACAGCTACTTCAACAAGAATGGCTGTAAAACCATCGAGGAC AAAGAAAAGTTTAATCCCGTGCTGTATGCCAAGCTGGTTGAGGTG GAACAGCGGAGAACAAACAAGCGGTCTGAGAAAGTGGGAAGAATC GCAGGTAGTCTGGAGCAGCTGGCCCTGCTGAACGGGGTTGAGGTG GTCATCGGCGAAGCTGACCTGGGGGAGGTGAAAAAGGAAAGAGT AAGAAACAGAATTCACGGAACATGGATTGGTGCGCAAAGCAGGTG GCACAGCGGCTGGAGTACAAACTGGCCTTCCATGGAATCGGTTAC TTTGGAGTGAACCCCATGTATACCAGCCACCAGGACCCTTTTCGAA CATAGGCGCGTGGCTGATCACATCGTCATGCGAGCACGTTTTGAG GAAGTCAACGTGGAGAACATTGCCGAATGGCACGTGCGAAATTTT TCAAACCTACCTGCGTGCAGACAGCGGCACTGGGCTGTACTATAAG CAGGCCACCATGGACTTCTGAAACATTACGGTCTGGAGGAACAC GCTGAGGGCCTGGAAAATAAGAAAATCAAGTTCTATGACTTTAGA AAGATCCTGGAGGATAAAAACCTGACAAGCGTGATCATTCCAAAG AGGGGCGGGCGCATCTACATGGCCACCAACCCAGTGACATCCGAC TCTACCCCGATTACATACGCCGCAAGACTTATAATAGGTGTAAC	

SEQ ID NO:	Sequence	Description
	GCTGATGAGGTGGCAGCCGCTAATATCGTTATTTCTGTGCTGGCT CCCCGCAGTAAGAAAAACGAGGAACAGGACGATATCCCTCTGATT ACCAAGAAAAGCCGAGAGTAAGTCACCACCGAAAGACCGGAAGAGA TCAAAAACAAGCCAGCTGCCTCAGAAA	
482	MASISRPYGTKLRPDARKKEMLDKFFNTLTGKQRVFADLALCIYGS SLTLEMAKSLEPESDSELVCAIGWFRFRLVDKTIWSKDGKIQENLVK QYEAYSGKEASEVVKTYLNSPSSDKYVWIDCRQKFLRFQRELGTR NLSEDFECMLFEQYIRLTKEIEGYAAISNMFNGEKEKEDRSKKRM YATRMKDWLEANENITWEQYREALKNQLNAKNLEQVVANYKGNAG GADPFFKYFSKEGMVSKKEHAQQLDKFKTVLKNKARDLNFPNKE KLKQYLEAEIGIPVDANVYSQMF SNGVSEVQPKTTRNMSFSNEKL DLLTELKDLNKGDFEYAREVLNGFFDSELHTTEDKFNITSRYLG GDKSNRLSKLYKIWKKEGVDCEEIGQQFCEAVKDKMGQIPIRNVL KYLWQFRETVSAEDFEAAAKANHLEEKISRVKAHP IVISNRYWAF GTSALVGNIMPADKRHQGEYAGQNFKMWLEAELHYDGKKAKHHLF FYNARFFEEVYCYHPSVAEITPFTKQFGCEIGKDIPDYVSVALK DNPYKKATKRILRAIYNPVANTTGVDKTTNCSFMIKRENDEYKLV INRKISVDRPKRIEIVGRTIMGYDRNQTASDTYWIGRLVPPGTRGA YRIGESVQYIKSGPVLSSSTQGVNNSTTDQLVYNGMPSSSERFKA WKKARMAFIRKLIRQLNDEGLESKGQDYIPENPSSFDVRGETLYV FNSNYLKALVSKHRKAKKPVEGILDEIEAWTSKDKDSCSLMRLSS LSDASMQGIASLKSILNSYFNKNGCKTIEDKEKFNPLYAKLVEV EQRRTNKRSEKVGRIAGSLEQLALLNGVEVVIGEADLGEVEKGKS KKQNSRNMDWCAKQVAQRLEYKLAFFHGIGYFGVNPMTSHQDPFE HRRVADHIVMRARFEEVNVENIAEWHVRNFSNYLRADSGTGLYYK QATMDFLKHYLEEHAEGLENKKIKFYDFRKILEDKNLTSV IIPK RGGRIYMATNPVTSSTPITYAGKTYNRCNADEVAAANIVISVLA PRSKKNEEQDDIPLITKKAESKSPKDRKRSKTSQLPQK	Cas1 2i4 amino acid sequence
483	MASISRPYGT KLRPDARKKE MLDKFFNTLT KGQRVFADLA LCIYGS LTLE MAK SLEPESD SELVCAIGWF RLVDKTIWSK DGKIQENLVK QYEAYSGKEA SEVVKTYLNS PSSDKYVWID CRQKFLRFQR ELGTRNLSED FECMLFEQYI RLTKGEIEGY AAISNMFNG EKEKEDRSKKRM YATRMKDWLE ANENITWEQY REALKNQLNA KNLEQVVANY KGNAGGADPF FKYSFSKEGM VSKKEHAQQ LDKFKTVLKNK ARDLNFPNKE KLKQYLEAEI GIPVDANVYS QMF SNGVSEV QPKTTRNMSF SNEKLDLLTE LKDLNKGDF EYAREVLNGF FDSSELHTTED KFNITSRYLG GDKSNRLSKL YKIWKKEGVD CEEIGQQFCE AVKDKMGQIP IRNVLKYLWQ FRETVSAEDF EAAAKANHLE EKISRVKAHP IVISNRYWAF GTSALVGNIM PADKRHQGEY AGQNFKMWLE AELHYDGKKA KHHLFPYNAR FFEVYCYHP SVAEITPFTK KQFGCEIGKD IPDYVSVALK DNPYKKATKR ILRAIYNPVA NTTGVDKTTN CSFMIKREND EYKLVINRKI SRDRPKRIEV GRTIMGYDRN QTASDTYWIG RLVPPGTRGA YRIGESVQY IKSGPVLSS STQGVNNSTTDQ LVYNGMPSSS ERFKAWKKAR MAFIRKLIRQ LNDEGLESKG QDYIPENPSS FDVRGETLYV FNSNYLKALV SKHRKAKKPV EGILDEIEAW TSKDKDSCSL MRLSSLSDAS MQGIASLKS LINSYFNKNGC KTIEDKEKFN PLYAKLVEV EQRRTNKRSE KVGRIAGSLE QLALLNGVEV VIGEADLGEV EKGSKKQNS RNMDWCAKQV AQRLEYKLAF HGIGYFGVNP MYTSHQDPFE HRRVADHIVM RARFEEVNVE	Varia nt Cas12i4 A

SEQ ID NO:	Sequence	Description
	NIAEWHVRNF SNYLRADSGT GLYYKQATMD FLKHYGLEEH AEGLENKKIK FYDFRKILED KNLTSVIIPK RGGRIYMATN PVTSDSTPIT YAGKTYNRCN ADEVAAANIV ISVLAPRSKK NREQDDIPLI TKKAESKSP KDRKRSKTSQ LPQK	
484	MASISRPYGT KLRPDARKKE MLDKFFNTLT KGQRVFADLA LCIYGSLTLE MAKSLEPESD SELVCAIGWF RLVDKTIWSK DGIKQENLVK QYEAYSGKEA SEVVKTYLNS PSSDKYVWID CRQKFLRFQR ELGTRNLSED FECMLFEQYI RLTKGEIEGY AAISNMFGNG EKEDRSKKRM YATRMKDWLE ANENITWEQY REALKNQLNA KNLEQVVANY KGNAGGADPF FKYSFSKEGM VSKKEHAQQL DKFKTVLKNK ARDLNFPNKE KLKQYLEAEI GIPVDANVYS QMFSGNVSEV QPKTTRNMSF SNEKLDLLTE LKDLNKGDF EYAREVLNGF FDSELHTTED KFNITSRYLG GDKSNRLSKL YKIWKKEGVD CEEGIQQFCE AVKDKMGQIP IRNVLYKYLWQ FRETVSAEDF EAAAKANHLE EKISRVKAHP IVISNRYWAF GTSALVGNIM PADKRHQGEY AGQNFKMWLR AELHYDGKKA KHHLPPFYAR FFEVYCYHP SVAEITPFKT KQFGCEIGKD IPDYVSVALK DNPYKKATKR ILRAIYNPVA NTRTRVDKTTN CSFMIKREND EYKLVINRKI SRDRPKRIEV GRTIMGYDRN QTASDTYWIG RLVPPGTRGA YRIGESVQY IKSGPVLSTT QGVNNSTTDQ LVYNGMPSSS ERFKAWKKAR MAFIRKLIRQ LNDEGLESKG QDYIPENPSS FDVRGETLYV FNSNYLKALV SKHRKAKKPV EGILDEIEAW TSKDKDSCSL MRLSSSLSDAS MQGIASLKS LINSYFNKNGC KTIEDKEKFN PVLVYAKLVEV EQRRTNKRSE KVGRIAGSLE QLALLNGVEV VIGEADLGEV EKGKSKQNS RNMDWCAKQV AQRLEYKLAF HGIGYFGVNP MYTSHQDPFE HRRVADHIVM RARFEEVNVE NIAEWHVRNF SNYLRADSGT GLYYKQATMD FLKHYGLEEH AEGLENKKIK FYDFRKILED KNLTSVIIPK RGGRIYMATN PVTSDSTPIT YAGKTYNRCN ADEVAAANIV ISVLAPRSKK NREQDDIPLI TKKAESKSP KDRKRSKTSQ LPQK	Varia nt Cas12i4 B
4503	MSNKEKNASETRKAYTTKMIPRSHDRMKLLGNFMDYLMGTPIFF ELWNQFGGGIDRDIISGTANKDKISDLLLLAVNWFKVMPINSKPQ GVSPSNLANLFQQYSGSEPDIAQAEYFASNFDTEKHQWKDMRVEY ERLLAELQLSRSDMHDLKLMYKEKCIGLSLSTAHYITSVMFGTG AKNNRQTKHQFYSKVIQLLEESTQINSVEQLASIIKAGDCDSYR KLRIRCSRKGATPSILKIVQDYELGTNHDDEVNVP SLIANLKEKL GRFEYECEWKCMEKIKAFASKVGPYYLGSYSAMLENALSPIKGM TTKNCKFVLKQIDAKNDIKYENEPFGKIVEGFFDSPYFESDTNVK WVLPHPHHIGESNIKTWEDLNAIHISKYEEDIASLSEDKKEKRIKV YQGDVCQTINTYCEEVGKEAKTPLVQLLRYLYSRKDDIAVDKIID GITFLSKKHKVEKQKINPVIQKYP SFNFGNNSKLLGKIISPDKL KHNLKCNRNQVDNYIWIEIKVLNTKTMRWEKHHYALSSTRFLEEV YYPATSENPPDALAARFRTKTNGYEGKPALSAEQIEQIRSAPVGL RKVKKRQMRLEAARQQNLLPRYTGWKDFNINICKRGNNFEVTLAT KVKKKKEKNYKVVLGYDANIVRKNTYAAIEAHANGDGVIDYNDLP VKPIESGFVTVESQVRDKSYDQLSYNGVKLLYCKPHVESRRSFLE KYRNGTMKDNRGNNIQIDFMKDFEAIADDETSLYYFNMKYCKLLQ SSIRNHSSQAKEYREEIFELLRDGKLSVLKLSSLSNLSFVMFKVA KSLIGTYFGHLLKKPKNSKSDVKAPPITDEDKQKADPEMFALRLA LEEKRLNKVKSKEVIANKIVAKALELRDKYGPVLIKGENISDTT	Cas1 2i1 (SEQ ID NO: 3 of U.S. Patent No. 10,808,245)

SEQ ID NO:	Sequence	Description
	KKGKKSSTNSFLMDWLARGVANKVKEMVMMHQGLEFVEVNPNTS HQDPFVHKNPENTFRARYSRCTPSELTEKNRKEILSFLSDKPSKR PTNAYYNEGAMAFATYGLKKNDVLGVSLEKFKQIMANILHQRSE DQLLFPSRGGMFYLATYKLDADATSVNWNGKQFWVCNADLVAAYN VGLVDIQKDFKKK	
4504	MSISNNNILPYNPKLLPDDRKHKMLVDTFNQDLIRNNLHDMI IA LYGALKYDNIKQFASKEKPHISADALCSINWFRVLKTNERKPAIE SNQIISKFIQYSGHTPDKYALSHITGNHEPSHKWIDCREYAINYA RIMHLSFSQFQDLATACLNCKILILNGTLTSSWAWGANSALFGGS DKENFSVKAKILNSFIENLKDEMNTTKFQVVEKVCQQIGSSDAAD LFDLYRSTVKDGNRGPATGRNPKVMNLFSDGEISSEQREDFIES FQKVMQEKNSKQIIPHLDKLYHLVKQSGLYDIYSWAAAIAKNANS TIVASNSSNLNTILNKTEKQQTFEELRKDEKIVACSKILLSVNDT LPEDLHYNPSTSNLGKNLDVFFDLLNENSVHTIENKEEKNKIVKE CVNQYMEECKGLNKPPMPVLLTFISDYAHKHQAQDFLSAAKMNFI DLKIKSIKVPTVHGSSPYTWISNLSKKNKDGKMIRTPNSSLIGW IIPPEEIHQKFAGQNPIIWAVLRVYCENKWEHMFPSDSRFFT EVYAYKPNLPYLPGENRSKRFGYRHSTNLSNESRQILLDKSKYA KANKSVLRCMENMTHNVFDPKTSNIRIKTDKNNSPVLDKGRRI TFVMQINHRILEKYNNTKIEIGDRILAYDQNSNHTYAILQRTE EGSHAHQFNGWYVRVLETGKVTSIVQGLSGPIDQLNYDGMPTSH KFNCWQADRSFVSQFASLKISETETFEAYQAINAQGAYTWNLF YLRILRKALRVCHMENINQFREEILAIKSNRLSPMSLGSLSQNSL KMIRAFKSIINCYMSRMSFVDELQKKEGDLELHTIMRLTDNKLND KRVEKINRASSFLTNKAHSMGCKMIVGESDLPVADSKTSKKQNV RMDWCARALSHKVEYACKLMGLAYRGIPAYMSSHQDPLVHLVESK RSVLRPRFVADKSDVKQHHLNLRMLNSKTKVGTAVYYREAVE LMCEELGIHKTDMAKGVSLSDFVDKFIGEKAIFPQRGGRFYMST KRLTTGAKLICYSGSDVWLSDADEIAAINIGMFVVCQTGAFFKKK KKEKLDDEECDILPFRPM	Cas1 2i3 (SEQ ID NO: 14 of U.S. Patent No. 10,808,245)
454	AGTCTTCTCTCTCGCTCTCTCCGCTGCTGTAGCCGGACCCCTTGC CTTCGCCACTGCTCAGCGTCTGCACATCCCTACAATGGCTAAAAC AGCAATGGGTAAGGCACTGCGCCTCGTTCTCCGTCGGCTCTACCT GGAGCCACCTCTCACCTCCTCTCTTGAGCTCTAGAAGCATTAG AGATATTTTATAAAGAAAAAGATGTTAATGGTAACACAGGACCAG GAAGGACAGGGCAGTTCTGGGGGAGGTGGGAGGGCAGAGAAGAGG TCTATGGAAATCTAAAGCGAAGAATTTCTTTTAAAGGTAGAAGC GGGTAAGTTGCCCTCCTATGGGTAGAGAATTTATTCTGTTTCCAT ATTTAAATTAGGACTCAATCGTGAGGGGAGGAAGCTACCTTAAC TGTTTGCCTTAAATGGGCTTAAGGGACATTTTGGAAAGTGCTTTA TAACGACCTTTTTTTTTTTTTTTTATTCTTCTCTAGTTTAAAGAAA ATAGGAAAAGGGTAAAGGGAAGGTGGGAGAAAGGAAAAAGAAAAT TGCAAAGTCAAAGCGGTCCCATCCCGCTGTTTGAAAGATGGGTGG AGACGGGGGGAGGGGATGGAGAGAACTGGGCACATTTTACGGTAT TGTCTCGTCGAAGAAACCGCTAGTCCTGGGGTGCGGTGCAGGGAG GTAAGACGGCGGGGGACAGGGTGGGGGTAGGACCTCCGCTCCTTT GTTTTAGGGCAAGGGAGGGGAAGGAGAGAGGAAGTCGCGGAGGGC GTGGAGGGCGCGGGTGGGCAGCTGCAGGGGCGGGGAAGCGCGCGG CAGGGAGGGGTGGAGGGACAGCGGCTTCGAAGGCGCTGGGGTGGG GTTTTCTTGTGTGCGGACCAGCGGTCCCGGGGGGAGGCACCTGCA GCGCTGGGCGCACAAATGCGGACAGCCCCACCCAGTGCGGAACCGC	STM N2

SEQ ID NO:	Sequence	Description
	GCAGCCCCGCCCCCGCCCGGTGCTGCATCTTCATTTCGAAAGGG GGTTCGGGTGGGGAGCGCAGCGTGACACCCAGGAGCCCAACCCTGC GGGGACAGCGGCGCCACGCCCCGCGCTCCCCGCTCCCGACTCCCC GCCGCGGCTTCCAAGAGAGACCTGACCACTGACCCCGCCCTCCCC ACGCTGGCCTCATTGTTCTGCTTTTAAAGAGAGATGGGAAAAGTGG GTTAACATTTTTCTTTTCGGAAGCAAATTACATAGAGTGTTTAGA CATAGACACAGATAAAGGGTTCTTTGAAGACCTTTGATCGTTTGC GGGAAAAGCTTCTAGAACCTAGACATGTGTATGTATAATAATAGA GATGACATGAAATCGTATATAAAGCAAAGAGGTCAAAGTCTTAA GTTAAGCCACGCGAAATTTCCGTTTTGTGGGTGAGACAGTGCCAA ATATCGGCAATTTCTAAGCTCAGAGAGACAAGACAGTGGAGACA CAGGATGACCGGAAAAGATTCTGGATTACAGGGCCTTCATCCGCAA TTGGTCTTGTGCCTTGAGTGCCACGGTTCTGGCGCTCAGTGGCC CCGGGGTGAAAAGGCAGGGTGGGGCCTGGGGTCTGTGGCAGCTG GAAGCACGTGTCCCCGGGACTTGGTTGCAGGATGCGGAGACAGG GAAAGCTGCCGAAAGGACTCCATCTGCGCGGCTCCGCCCTGCCCT ACCCTCCCCGCGGAGCCGGGGAGACCTCAGGCTCCGAGACTGGCG GGGAAGAGGAATATGGGAGGGGCAGTTGAGCTGTATGCAGTCCTG GAACCTCTTTTTTCAGCCCCGAGTCCACAACGGCCCGAGCACCC CTTGATGTGCGCAGACCCCGGCGTGGCTCTCAGCCCCAGCACCG AGCCCCCTCCAGCCAAGCGGGTGGCTCTGCAGAAAAGCTGGCTCG AGCCCCGCCCCGCCACACAAAGGCGCGGCCCCACCCAGCCGGGC GCGAGACCGCAGAGGTGACCCCTTCCCAGGGATTACAGGGAGGGC TGTCTCTTCTCGCCCCACCCACGGTCCGCGGAGCTCGGGGCTTTTT TTCCCCAGCCCAAGCCCCCGCCACCCTCTGTTCTCTATGATT TTCCAGAATGGAGACCCCGCGAGGGGCTTCTCTAAGGGAGACCCT CGCTCCTCCAGCGGGGCGCGGCTCGGCCCCACCCCTCCAGCTGA GGCCAGAGCCGCCTACCGCTGGCCGGGTGGGGGCGCACGTGGCG ACTGGGTGTGTGGAGCGCAGCCAGCCCTGCAGAGCCCCGCGCCGC GCCCTGCGCTCCCCCTCCCCGGAGTTGGGCGCTCGCCCCGCGGTG CAGCCGGGGAGACCGTTTTCTGCGCAGTGTCTTGAGCTACCCCCG CTTTCCACAATTTCGAGTTCACTCGCACGTCCAGAAAAGGTTCTGA GAATGGGTGGTGGGGGCGATCTCGCCTCGCTTTCTGCACCCCTCA GAAAGGTTTCCGCTGCAGGCTAGTGGCTGCAAATCATCGTCATC ATCAGTATTATTATCATTTCAAATCGTTGTTATTATTTAATGATT CAGTAGCCTTGTGTTCTCATTTGTTCAAAGGGACGTGGATTG CTCTTGGTTAAGGATTAACCCCTGTTGCGTTGCTTTGCTTCCTC CTAATTGCCCTCATCCCTTTCCCCCACAAAAGGTAAATTTGTCT CCAGTTGTTCAATTTAAGTTATAAAGCAAATATATTTTGTCTCC TGCCAGGATTATGTATGTTTATGTGGCTAAGATACATGTGCAAGT GCTTGCTAAGAGCAGGGTTTGTGTGCCAACGATTGCTGGAAAATT CTCTGCAAAGAATTGTTTGTGGCTGCAATGGGTGAGAATACACAT ATATAATTGAGATGATCTTCAACATAAGGTTATATCTATAAATAT ATAAATATAGTTTATGCACAAAATTTTAAAGTTTTTCCCTGAAA CTGTTCTTCCAACCTGCTGATTCTTGATACAGCCTCAATCCTACAC AGATACATGGATCGTGAAATGGTAGCCGCCATCCAAATAAAAATC CCACCCCAAATATGACAAACGCAAGCATCCTTTCTGGCCATAATT TAACTGCATTTGCAAATCATGAAAAAAACACTACTTCTGCAGTAT TAAAATAATAGATTTTGAAATTAATTCCAATTTCAAAGATAATTA ATTATCAGGGCGAGTGCTTTTTTCTGATTCAATTAACAATTATG TATTCAGCATGATTGTAAGAGGTGCATATAATATTCCCCATTATC	

SEQ ID NO:	Sequence	Description
	TTTTCTAATGAAGTGGGCACCTTCTGAATGGATATATAAGTAACT AGAAATGAAAAGCTGAGGATTTGGTCAGAATTTTCAGGATAAACT GAAAGAAATGGCAGTAGTTTATCAATTAATCTCATGTATTTAGTT TATACCAGGTGAGTAAGCTGAGCCTGCAATAAACACTCTCTGTCC CAGTGTAACACGTCGCAGGTAGCTAGAATGATAGGATAAAATTAAT AGACCTTGTGGTGTGTTGTCTATGCACGTTAAAATTCTCTGAGAGA AAGTATATTTTAAAATGATAATTAAGATTGGACATTTGTGCTATT AAAATCTACAACCTTTAGTCAAAAATTCACAATGGTTTTTTTTTACA ATAATGTGACTTACAGATTTGTAGTAAATTATTCTATTCTAAAAG AGAAATGAGTGTTTTTATTGTTACAGCTATTACCTCATTAATATT TTTAGCAAACTTTTATTTGTTGCATTGAAAGCAGTTTTAATTACT TTGGGTTTTTATTTTTCAAATTACTAATGGATAGATGGTGGAATA AGCATTTAATCATTGTCACAAATATGACTTCCATCAAATAGCTCA TTCTCAGTGATTAAAAAATGCTACAAGAGGCTACAATTTACTCAG ATTCAGGAAATGTCCTTTTCAGAGTGCCATAAGGCTGATTCATATA ATAAAAATAGTTTTCTTCCCTATAATTTAAGATCAAATAGTTACTT AGTTCTGTGAATACCTAGCAGTAGCTATCAAACAGAATTTTAAAG TTAAATCTGTACAATAACAATGAAGTGGAGGATGAATCGATACA TATTGAATGGAAGACTTTGTGATTGATAAATTCAGGCCATCTTTA GGAAATTTCCGGATTTATCAATCACCATTATTTTTTACTTCAACT GAGTGTGACTGATCACATGCTCAGGCTACCTTGGTAGCTCATTGC TCACAGGAGGCTGAAAAAGCTGGCCTCCGAGCAGGAGGAAGCTC AGAGCACAAACCTAGGCCTGGGCGTGGCCACTGGGAGCTGCTGAT AGCGAACCCAGCTCACACCAGTTTCTTTTTTGGTCTGTGGGAAGA AAAACACATATTATCCTGTTGTCACAAGATCTGTGACCTTATATG AAAAAATGCTAGAATTTTTTCATTAAAAAAGAAAATACTGAACATA GCCAGTGACCCAGATGTTTTTCAGAACCTAGACTGGTTCTGTCCAT TGGAAAACCTCGGTGTCTGCATTAACTTTTACCACACTAGAGGG CAATCATGTTCTCTAAAAAAGCAGATGATTGATGTAAACCTAGTT CCAAATATTAAGTGTTTAATAAAATCTTTTCTTTTACCAGGAACA TTCAAGTGTTTATTCAATAAGCTGATGCCATGCTTTACCCTAGTG GATGAACAGAGCTTGTACAATTTTCAAGGAGACAGGATGAAATGA GTGGTCATAATCTGAAAGTAGATACACGCCCTGGTTAATTATTCC CTGATGGTTTTACTTCTCAGTTTTATTACATTGTTATTATAATAC CATTTATGTTACTTCTGAGATTTTGTAGTGGATAAATAGTAGAAA AATGTCAGTAGTAATAGCAAAGTTATTTAGCAGCCGAATATTTTA ATGCTTAAAAATAAAGGAATAAATTAAAGAAAATCATTGTTTACT TCTTCATCGATTGAAATGTGCCCCCTGTTTCAGAGCACATCTGAAT ATCAGAGTCTCCACCTGCAGAGAACATGCAGCTTAGCGAGTAAAA CAGGCAGGTATGTGATACTGAGGAGGTGTACCAAAAACCTGACTGC TGTTATTTTTCCCATCTTCTAAGTCTGTCTTTCTTTTCCATTTAA AGATACCTTTTTTAAATCTAATCCAATGTGATTTCAATCTAGTTTT ATCAGATTTCAACAATTATTGAGCATCTCCTTGTAGTGGTTTTCT GTTTATTAGAAAATCGATGTAAATTTTAAACGAAGTAAGAAGAAAT ATATAAGTATAAACTAATTTTGGGTATCATCAAAAGTGGATTTTT TAAATATGCATTGATAGAATTATTTTTTGATTACATTTTATGTAA TTCTAATCCAGCTATAAAATATTTAATAGTGTATATTACTGTGT TCCTCAAACTTTGATGTGCATATGAATTACCTTTGATTTTCATTA AAATGCAAATTCTGATTCAATACATCTGGCTTGAGGCAGACATTC TGTCTTCCGAACAAGCTCCAGATGATGCTGATTCTGACCACTAA ACACATCAGTTTTAGGGATATTAACCTGTAATATACAGGTATCCC	

SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
	ACTGCTGGATCATCTAGTAGTTTTATTTTTTTTTATTTTTTATTT TTTTTATTTTGAGACAGAGCCTTGCTATGTCGCCCAGGCTGGAGT ACAGTGGTGCCATCTAGGCTCACTGCAATCTCTGCCTCCTGGGTT CAAGCAATTTTCCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAG GCACGCACCACCATGCCCCGGCTAATTTTTGTATGTTTAGTAGAGA CGGGGTTTTACCATGTCTCGAACTCCTGTCTTCAAGTGATCCGTC CACCTCAGACTCCCAAAGTGCTGCGATTACAGGTGTGAGCCACCA CGCCTGGCCTAGTAGTTCTGTTTTTAATTTTTTGAGGAGCCTCCA TACTGCTTTCCATAATGGCTCTAGGAATTTACATTCCACCAGCAG TGCACAAGGATTGCTTTTCTCCACATTCTGGCTAACCAGTCTCCT GTCTTTTTTGAGAACAGACATTTCAACACGTGTGAGATAATATCTC ATTGTGGTTTTGATTTGCATTTCCCTGATGATTAGTGATCTTGTG CCTTTTTTCATATAACTGCTGGACATTAATATGCCTTCCTTTGAG AACTGTGTATACAGGAGAAAATAATCACTTCTCAGAGGAGCTTTC ATTTCAAAATATCCGGGAAAAAATAGAAAAATGGAAAAATTTAT CCTAGAGTAAGTTGTCTTTTATATTTTGACCCTGTTTGTGACATA AACTGGATGATACAAAAGTGAATGCAAAGGCTTTAGGAGGATTA CTTACTTACTTGTATATTGCTTTAGGTTGTTTGCAGAAAATTATA CTAATTGAAGTTCAGGCTATGATGTGATAAAATCTATGTCAGGAG ATGAGTCTACATGCAAAGTTTGAGGAAGTGACATTTGAGTTTCAA AACAAAAAGCAATTTTCAATGTCATATCTAGGTTAACCCAAAAG ATTTCTTTCACCCTATTTAGCTGCCTCTAAGATGGATGCTGAGGA TAATTACACTGTAGAACAATAGGACGATGCTTCACACTCACCTCA CAGGCTCTGTTATTCCCACATACTGCCAGAGATACTCCAAAATAA AATCACTGCAACATCAGGCAGTTATAAACCTCAACGGTATTATTT TCTATTTATATACAGTATATTTTATATTTTACAAGTATAAAATAG AATATATTTATTCTATTCTCTTTGACACAAAGTGACCATAAGACA TATTACTTAAGTATGACTAGCAAAGTCATGGGGCTTGTCAATTCAG GAGGAACTCTTAATACTGTTTCAAGTTTTTGTTCCTGACCAT TTACATAAGCCAACTAATGCTTCACACTGTGCAAAACAATGCAC AGTGTGTGAATGAATGGCTAAAATAAACTCTAATGAGTGGGGT TTGAAAAATGCACTTTAGAAAAGTGTGAGAAAATGTTGCACAC TGCGCATTTTACAAAATTTGTTGAAGGACACTGGATATTCTTTT TAGGATTATGGAGGGAAGCAAAATTTTGGCTCCTACATGCAGTTT TTGTGGCCTTTGCCTGAAATAGTCATCTCCCATTAATTATTTAGA TATCATTCAATTTCTAAGACAACATTTAGGGAGACTGCCTTAAGT ACAATTTGTACACTACCCAGATAAGAATTTCTTTTGGTGAAACAT CGATAAATATTACTTGGCAGTAACACCAAGTTAAAATATTTGTTT CACAGTCGACGTTAATAACTATTATAGATAAAGTGAATTTTATAA GACATACTCAGATCTAAAACAGCAATATGGAGCTCTTCAAATCCA TTGAAACTTCATACCAGCCTACGGAAGTAGAGGTTTTTATGCAAA CTCTTCAAGAAATATGCTCTGAACTTTTAATTCCTTAGATTGATA GAGGAATTAAATCATGATATAACTAATAGGTTTGTGGTACAAATT GCTGCTGCTTAATCTGACTCTGTGTCTTCCAGTGTTCTATATGA ATTAGATATTCCATTATCTAAAGACAATCAACCCCATCCCACGGT GATAGCTCTAGGACTCCCTTTGAGTTCATTAAATCTGTATTCTCA GTCTCCAACTTCTGGTTAATTCAAACAGAAAAGTCAACTGGCCC ATGAACTAAAATAAAGTCATCTGAATTTTTTTTTTATTTTGCAGT GTGATAAAAGTCTCGCACTTTTTATTTCTGAAAGTTTCTGCTTTC ACTGAGAGCATAATAGGCTATCCACCCTTATGCAATCTTACATAC AAAGTCATAGTCAGGCTAAATTCAAAAACACATGTGAGATAGAAG	

SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
	CATTTCCTTAATTTATTAATTTTACTAATTGCATAATTAACAAA AGTAAGAAGATTTTACCTCCTTATCCCCATCTGGTAGTTTGCAGA TACTTGGCCTGATGACAACTGACAGTGATGAGATACTCACCAAGT TTACCAGGGCAGGAGGCTTCTAGAGAAAAAATGAGAAAAATGAAA TGGGGAAGGGGAGTGAAGGATTGAGGAGGTGACAATCTGGACTCT TGCAACTGCATGGCAAGGTTGGCACACAAGCTGGGTTGCAACGGA GGGAAAGGAGATCCTTATCAGATGTAATCAGAGCTCAGATCGAGGG CTTTGGTGTGTGTAGAAAGAGGGAGAGACAAAGAACTTAAAACAG AGCTGCCATTTGACCTTGCAATCCCATTACTTGGTGTATACCCAA AGGAGAATAAATCATTCTATTAAAAAGACACATGTGCTTGTATGT TCATGGCAGCACTATTACAAATAGCTAAGACATGGAATCAAACATA GGTGTCCATCTATGGCAGATTGGATAAAGAAAAATGGGGTAAATAT AAAGCATGCAATACAACATGGCCATAAGAAAAAATGAAATCATGT CCTTTGCTGCAACATGGATGCAGTTGGGACCCATAATCCTAAGTG AATTAACACAGGAACAGAAAACCAAATACAGCATGTTCTCACTTA TAAGTGGGAGCTAAACACTGAGCACACATGGACATAAATATGAGA ACAATAAACTGTGGACTACTAGAGGGGGGAAGGAGAGAGGTTT GTAAACTACCTATCAGGTGCTATGCTCAATACCTGGGTGATGGG ATTTACACCCCAAACATCAGCATCATTTAATATTCCCATGTAAAA AGACTGCACATATACCCCTTGTATCTAAAATAAACTTGAAATTA AAAAAAAAAAGAAAGAAAGAAAGAGGCTGGAAATAGAGGCTCACAC CTGTAATCCCAGCACTTTGGGTGGCCAAGGTGGGTGGATTGCTTG AGCCCGGAATTCAAGACCAGCCTGAGAAACCTGGTGAACTCTG TCTGTACAAAAAATACAAAAATTATCCAGGCATGGTGGAGCGCAC CTGTAGTCCCAGCTAATGGGGAGGCTGAGGGGGGAACATCACTTG AGCCAGGAGGTGGAGGTTGCAGTGAGCTGGGATCACACCACTGC ACTACAGCCTGGGTAACAGAGCAACTCTGTCTCAAAGAGAGAGAG GAAAGAAAAAAGAAAAGATGGACAGATAAGAAAATGCACTTGGAG ATTAAGAGAAAGCAGCAACATAGGACCCTGGATAATGTGTTTGCT TAATAACTATCCTGATGAGTTATCTGACTATTCCCAAATGAGTAC GTGGCAATTCAGGCTGAACCATCAGAGTAGCCCTCCGGAATCTTA CTTATGTACAATAGACCTGCATGCACATTTACTAGAATGAGCCTC TCTCTCTGGTAATCATGTCTGCTTCCACTAATTCCATCTGTTTCC TCTCTCTCCCTCCTATCCTGCTAGATCTTAATTCCTTCGACCTTC CTTTGTCTTTTCTAACTCCCTTTCTTTCTCTTGTTATTTAACCTGC TATACTATGCAATTGATCTCCTCTGCACTAAGGAACATGCACTTC AGAATTCTGTTGACATCTTGCAATTCCTTTATATTTAGTGAAAGAA TGCAAAGGAGTCTACCTGGCAATATTCCTCTGCAGGAGGCAATA ATTATTATTCAAATTAAGGAAGCAGTAAAGAGAAATTCAGAAAA AATGAAATATACTAATCTTCAGCTTTTTCATTTTCAGCCTACAAGGA AAAAATGAAGGAGCTGTCCATGCTGTCACTGATCTGCTCTTGCTT TTACCCGGAACCTCGCAACATCAACATCTATACTTACGATGGTGA GTAACCTAGGATAGACATAACCCCTGCTAGCTAGATCATTGGA GGTTGACATATATTTGTTTCTTACAGCTCCTGATATAATTACATC AATATTTTGTAGCTCTCACTATTGACTTGCCGTGTCTAGCTATTA TGTCCAATTGATTACCTATTGCTGAAAACAGTTTGAATTTGGTGC TAATAACAACACATCAATGTCTGTAAAGAAATGTGGATGGATTCT TATTAACAGCCACATCCAGCATATCAACATCCACAATATGTCTAA GGTCTTTCTTTGCAAATAATTTAATAGGCTAAGCCATAATTGGAG TAGATCATAATTTGTAAGAAAATGCTTTTATACTTAGAAAACTCAA GAGAAAGAATCAACAACCATAATTGTTTTTGCTTTATTGTAGTCT	

SEQ ID NO:	Sequence	Description
	TTATAAAGTTTCTATACTTTGTATATACATGTCAACCAGCTAATG ATAATAATAATTGGCTCAATAAAATAAACTGACTTACGACTGAGG CCCTAGATAAAGAGGGTCTGAAAAGAAAAGCCTAAAGAATTAGCA TGGCAATTAACATGATTGAGGTGCAACTCTTTAGGTTTGATTTAT CCTGATTCATTTTGCTTACTTTGGCTCTGCCACAATCCACATGAT CTTGGTCAAATAGATACTTGGATTCTCTAAGTCTCATTTAACCTCT AGCATCTTCCTCTTGGAGTTGTTGTGAGGTTTAAACGGTTTAATG TAAGTCAAATATGCAAACCAAGCCTAGCTCATTATATCACTCTA CAATGATAGCTATCATTATCAACATCATCCTTACCTAATTCAGTC AATTTAACTAAAATATTTTATACAGTTCTATGTATCCTAGATATC CCTAAGGCATATTTTACTAACTCTCAGGCTCACAAATATTTTTCT TTTCCATATATGTAAAGAAAGACATTAATGACAAAACAACTGAC CTTGTGGCAGTTAACCCCTTCTGCACCTTTAAAGCCTATTCAAGG ACTCAAAGGCATTTACCTTCCAAAGTTATTCTATCGTAGCACAAA AATCATAAATGCTAATTAAGTGTCCATAAGGAAATGTCTCCAT GTGAAAGGAATTCTGTCTCCAAACAAAACATTTCATTAGAATGCAG GGCCAATGCCTACTTTGTACAAATTCATTGGTTCAGCAAATAAAT TAGACAGACCTTTATTATTTGCTAGATGTAGCTGTGAAGAAGGAT CCAGCTATGTTTCTTATGAGACTAATGTCGAACTATGGGTTGTCA CTGAGGATCCAGAGTTCCATAGGGCGTAGTCCTCACCTTCAAAGA ATTTCAGGGCTTAGTAGAAGAGTCTTACACAAATGACTAGAATGTA GAACACAGAGTGGTTAGGACAAAGGAGCCAGGGATGGTTTTTGCT GGGTTAGGGAATGAAAAAGGGGAAGAAAATATGTGAAGTTATGT GTGAGCTGATTCTTGAAATAAGCTGTTTTTATTTGCCTGCGTTCT CTTATAATCCTTTTCCATAGGCTTCCATAATTTTTATTGAGCTGT ATTTAAAGTTGAATAGATAATTCAACATTTCTCGTAAACTGTGCT TCCTAAAAGAGTCCGTAGAGAATTTCAAATTTCTGCAGTCTTTAA CTTGACCTGGTATTTCTATGTTAGATAATAACGTGACTTGTTTTAT TGCAGGCAAACATTATAACAATAAATTATTATTATTGTTTACATT TGTAAGCACTAAGTATATGGCTTGTGCTTTGCATTTCAGCATCCTT TATCATTTAATCTTCACAACCACCTTAGAAGGAAGGTACTCTTTT TATTTCCATCTTTTAAATGAGGAAATAAAAGCATAAAGAAGTTAA TTAACTTACCTAGTGTACACAGCTATTAAGAGGGGCTTACTATT TGGATGCAAATATAGGCAGTTCTAATTCCAGAGCCTCTAATCTAA GGCATTTTAAACCCCATCACCTTATCAAATAAGCTGTTTTTATTT GCCCCGTGTTCTCTTATAATCCTTATCCATAGGTTTCCATAATTTT TATAAAATTGTATTTAAATTTAAGTATAATCTTGGATGCCATCA GGAAATGAAAAACATTTTTACATTTGTGAAGGAAAAAGCCCACA TCATTTCCAATATAGTTATTGAGTTAGTATTATCTAGACTATCTA TTAGCAGCTAAGGATCTGAGGTCAAGGCCTGCCAGCCTGGCATT TACTTGACCACAACCTCCATGTGCACTAACCAGGCTGCTAAAAGA ACATTAACGGGAACATAACCTGCTGGCTTGGTTGCCACAATTTTA AAAAGACGTTAATAAATTAGAGAGCACTTAGAGGTTAGGAAATAA TATGGTGGTAAAGATCTAGAAACAGTGTCAATTCTGGGGCACTTGA AGATGTTTAGCCTGGGGGAACAACCTGAAATGGAACATAACTGTT TTCAAATACTTGAAAAATGGTGGTGCACCACAGAGAATGGCCTAA TCATGGGTAGCTTCAGACTTCAAACAAGGATCAGTGGGCTAAAAC CAGAGAGATGGAGTTTGGGACTCAAAGAATGCTCATCTGAAATTG AGGGCTGACCAGCGAGGTTCTTTTAAAAATCATTGCATTTTACTA AATTGTGAGTTCTGTAATTATAAATGTCCTAGCAGGTGCTAGCTG TCATCTTTTCTATTATAAATTATACTATTTTATGTTATAATTTGT	

SEQ ID NO:	Sequence	Description
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SEQ ID NO:	Sequence	Description
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455	TAGCCGGACCCTTTGCCTTCGCCACTGCTCAGCGTCTGCACATCC CTACAATGGCTAAACAGCAATGGGTAAGGCACTGCGCCTCGTTC TCCGTCCGCTCTACCTGGAGCCCACCTCT	STM N2 Exon 1
456	AATCTTTCAAAACCTCCCTGGCTTAGAAAACCAAATTTTTGTAGA GAGAGATGGGTAGAATCTAATTTTATTCTAAAGCAATTAGCATTA CATCATCACAGCAG	STM N2 Exon 2

SEQ ID NO:	Sequence	Description
457	GAGAAATTCAGAAAAAATGAAATATACTAATCTTCAGCTTTTCAT TTCAGCCTACAAGGAAAAAATGAAGGAGCTGTCCATGCTGTCAC GATCTGCTCTTGCTTTTACCCGGAACCTCGCAACATCAACATCTA TACTTACGATGGTGAGTAACCTAGGATAGACATAACCCCTGCTAGC TAGATCATTGGAAG	STM N2 Exon 3
458	CCATGCTGCAAGCTTTGTATGCTTAACATTCTCAAATGTTCACTT TTCAGATATGGAAGTGAAGCAAATCAACAAACGTGCCTCTGGCCA GGCTTTTGTAGCTGATCTTGAAGCCACCATCTCCTATCTCAGAAGC CCCACGAACTTTAGCTTCTCCAAAGAAGAAAGACCTGTCCCTGGA GGAGATCCAGAAGAACTGGAGGCTGCAGAGGAAAGAAGAAAGGT AACTTTTTCATAGGTTTTCTTCTCTCTCTCCCTCCCCTGCTCC TCC	STM N2 Exon 4
459	CTAGGTTTGTGTTTGGATAATTATAAGATGGCTATGTTTTTCTTC CCCAGTCTCAGGAGGCCAGGTGCTGAAACAATTGGCAGAGAAGA GGGAACACGAGCGAGAAGTCCCTTCAGAAGGCTTTGGAGGAGAACA ACAACCTTCAGCAAGATGGCGGAGGAAAAGCTGATCCTGAAAATGG AACAAATTAAGGAAAACCGTGAGGCTAATCTAGCTGCTATTATTG AACGTCTGCAGGAAAAGGTAATCTCAGCAGAGTCCTGAGCAGATG GATATATTCATATGCAGCACAG	STM N2 Exon 5
460	TGTAGACTCCTTGAGATTAATAGAGTTTAAACGATAAGTTTTACTT TATAGCTGGTCAAGTTTATTTCTTCTGAACTAAAAGAATCTATAG AGTCTCAATTTCTGGAGCTTCAGAGGGAAGGAGAGAAGCAATGTA AGCAACATTCTACAGAAATATAAATAATACTACTAATAATTAGCA TC	STM N2 Exon 6
461	ACCAGACAAAAAGGGCCTGTGACATTTCTTCTTCTTTTGTGTTT TTTAGGAGAGGCATGCTGCGGAGGTGCGCAGGAACAAGGAACTCC AGGTTGAACTGTCTGGCTGAAGCAAGGGAGGGTCTGGCACGCCCC ACCAATAGTAAATCCCCCTGCCTAT	STM N2 Exon 7

In some embodiments, the gene editing system disclosed herein may comprise a Cas12i polypeptide as disclosed herein. In other embodiments, the gene editing system may comprise a nucleic acid encoding the Cas12i polypeptide. For example, the gene editing system may

5 comprise a vector (*e.g.*, a viral vector such as an AAV vector, such as AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11 and AAV12) encoding the Cas12i polypeptide. Alternatively, the gene editing system may comprise a mRNA molecule encoding the Cas12i polypeptide. In some instances, the mRNA molecule may be codon-

optimized.

10

II. Preparation of Gene Editing System Components

The present disclosure provides methods for production of components of the gene editing systems disclosed herein, *e.g.*, the RNA guide, methods for production of the Cas12i polypeptide, and methods for complexing the RNA guide and Cas12i polypeptide.

15

A. RNA Guide

In some embodiments, the RNA guide is made by in vitro transcription of a DNA molecule. Thus, for example, in some embodiments, the RNA guide is generated by in vitro transcription of a DNA molecule encoding the RNA guide using an upstream promoter sequence
5 (e.g., a T7 polymerase promoter sequence).

In some embodiments, the DNA molecule encodes multiple RNA guides or the in vitro transcription reaction includes multiple different DNA molecules, each encoding a different RNA guide. In some embodiments, the RNA guide is made using chemical synthetic methods. In some embodiments, the RNA guide is made by expressing the RNA guide sequence in cells
10 transfected with a plasmid including sequences that encode the RNA guide. In some embodiments, the plasmid encodes multiple different RNA guides. In some embodiments, multiple different plasmids, each encoding a different RNA guide, are transfected into the cells. In some embodiments, the RNA guide is expressed from a plasmid that encodes the RNA guide and also encodes a Cas12i polypeptide. In some embodiments, the RNA guide is expressed from
15 a plasmid that expresses the RNA guide but not a Cas12i polypeptide. In some embodiments, the RNA guide is purchased from a commercial vendor. In some embodiments, the RNA guide is synthesized using one or more modified nucleotide, e.g., as described above.

B. Cas12i Polypeptide

In some embodiments, the Cas12i polypeptide of the present disclosure can be prepared
20 by (a) culturing bacteria which produce the Cas12i polypeptide of the present disclosure, isolating the Cas12i polypeptide, optionally, purifying the Cas12i polypeptide, and complexing the Cas12i polypeptide with an RNA guide. The Cas12i polypeptide can be also prepared by (b) a known genetic engineering technique, specifically, by isolating a gene encoding the Cas12i
25 polypeptide of the present disclosure from bacteria, constructing a recombinant expression vector, and then transferring the vector into an appropriate host cell that expresses the RNA guide for expression of a recombinant protein that complexes with the RNA guide in the host cell. Alternatively, the Cas12i polypeptide can be prepared by (c) an in vitro coupled transcription-translation system and then complexing with an RNA guide.

In some embodiments, a host cell is used to express the Cas12i polypeptide. The host cell
30 is not particularly limited, and various known cells can be preferably used. Specific examples of the host cell include bacteria such as E. coli, yeasts (budding yeast, *Saccharomyces cerevisiae*, and fission yeast, *Schizosaccharomyces pombe*), nematodes (*Caenorhabditis elegans*), *Xenopus laevis* oocytes, and animal cells (for example, CHO cells, COS cells and HEK293 cells). The
35 method for transferring the expression vector described above into host cells, i.e., the

transformation method, is not particularly limited, and known methods such as electroporation, the calcium phosphate method, the liposome method and the DEAE dextran method can be used.

After a host is transformed with the expression vector, the host cells may be cultured, cultivated or bred, for production of the Cas12i polypeptide. After expression of the Cas12i polypeptide, the host cells can be collected and Cas12i polypeptide purified from the cultures etc. according to conventional methods (for example, filtration, centrifugation, cell disruption, gel filtration chromatography, ion exchange chromatography, etc.).

In some embodiments, the methods for Cas12i polypeptide expression comprises translation of at least 5 amino acids, at least 10 amino acids, at least 15 amino acids, at least 20 amino acids, at least 50 amino acids, at least 100 amino acids, at least 150 amino acids, at least 200 amino acids, at least 250 amino acids, at least 300 amino acids, at least 400 amino acids, at least 500 amino acids, at least 600 amino acids, at least 700 amino acids, at least 800 amino acids, at least 900 amino acids, or at least 1000 amino acids of the Cas12i polypeptide. In some embodiments, the methods for protein expression comprises translation of about 5 amino acids, about 10 amino acids, about 15 amino acids, about 20 amino acids, about 50 amino acids, about 100 amino acids, about 150 amino acids, about 200 amino acids, about 250 amino acids, about 300 amino acids, about 400 amino acids, about 500 amino acids, about 600 amino acids, about 700 amino acids, about 800 amino acids, about 900 amino acids, about 1000 amino acids or more of the Cas12i polypeptide.

A variety of methods can be used to determine the level of production of a Cas12i polypeptide in a host cell. Such methods include, but are not limited to, for example, methods that utilize either polyclonal or monoclonal antibodies specific for the Cas12i polypeptide or a labeling tag as described elsewhere herein. Exemplary methods include, but are not limited to, enzyme-linked immunosorbent assays (ELISA), radioimmunoassays (MA), fluorescent immunoassays (FIA), and fluorescent activated cell sorting (FACS). These and other assays are well known in the art (See, e.g., Maddox et al., J. Exp. Med. 158:1211 [1983]).

The present disclosure provides methods of in vivo expression of the Cas12i polypeptide in a cell, comprising providing a polyribonucleotide encoding the Cas12i polypeptide to a host cell wherein the polyribonucleotide encodes the Cas12i polypeptide, expressing the Cas12i polypeptide in the cell, and obtaining the Cas12i polypeptide from the cell.

The present disclosure further provides methods of in vivo expression of a Cas12i polypeptide in a cell, comprising providing a polyribonucleotide encoding the Cas12i polypeptide to a host cell wherein the polyribonucleotide encodes the Cas12i polypeptide and expressing the Cas12i polypeptide in the cell. In some embodiments, the polyribonucleotide encoding the Cas12i polypeptide is delivered to the cell with an RNA guide and, once expressed

in the cell, the Cas12i polypeptide and the RNA guide form a complex. In some embodiments, the polyribonucleotide encoding the Cas12i polypeptide and the RNA guide are delivered to the cell within a single composition. In some embodiments, the polyribonucleotide encoding the Cas12i polypeptide and the RNA guide are comprised within separate compositions. In some
5 embodiments, the host cell is present in a subject, e.g., a human patient.

C. Complexes

In some embodiments, an RNA guide targeting STMN2 is complexed with a Cas12i polypeptide to form a ribonucleoprotein (RNP). In some embodiments, complexation of the
10 RNA guide and Cas12i polypeptide occurs at a temperature lower than about any one of 20°C, 21°C, 22°C, 23°C, 24°C, 25°C, 26°C, 27°C, 28°C, 29°C, 30°C, 31°C, 32°C, 33°C, 34°C, 35°C, 36°C, 37°C, 38°C, 39°C, 40°C, 41°C, 42°C, 43°C, 44°C, 45°C, 50°C, or 55°C. In some
embodiments, the RNA guide does not dissociate from the Cas12i polypeptide at about 37°C over an incubation period of at least about any one of 10mins, 15mins, 20mins, 25mins, 30mins,
15 35mins, 40mins, 45mins, 50mins, 55mins, 1hr, 2hr, 3hr, 4hr, or more hours.

In some embodiments, the RNA guide and Cas12i polypeptide are complexed in a complexation buffer. In some embodiments, the Cas12i polypeptide is stored in a buffer that is replaced with a complexation buffer to form a complex with the RNA guide. In some
embodiments, the Cas12i polypeptide is stored in a complexation buffer.

20 In some embodiments, the complexation buffer has a pH in a range of about 7.3 to 8.6. In one embodiment, the pH of the complexation buffer is about 7.3. In one embodiment, the pH of the complexation buffer is about 7.4. In one embodiment, the pH of the complexation buffer is about 7.5. In one embodiment, the pH of the complexation buffer is about 7.6. In one
embodiment, the pH of the complexation buffer is about 7.7. In one embodiment, the pH of the complexation buffer is about 7.8. In one embodiment, the pH of the complexation buffer is about
25 7.9. In one embodiment, the pH of the complexation buffer is about 8.0. In one embodiment, the pH of the complexation buffer is about 8.1. In one embodiment, the pH of the complexation
buffer is about 8.2. In one embodiment, the pH of the complexation buffer is about 8.3. In one embodiment, the pH of the complexation buffer is about 8.4. In one embodiment, the pH of the
30 complexation buffer is about 8.5. In one embodiment, the pH of the complexation buffer is about 8.6.

In some embodiments, the Cas12i polypeptide can be overexpressed and complexed with the RNA guide in a host cell prior to purification as described herein. In some embodiments, mRNA or DNA encoding the Cas12i polypeptide is introduced into a cell so that the Cas12i
35 polypeptide is expressed in the cell. In some embodiments, the RNA guide is also introduced

into the cell, whether simultaneously, separately, or sequentially from a single mRNA or DNA construct, such that the RNP complex is formed in the cell.

III. Genetic Editing Methods

5 The present disclosure also provides methods of modifying a target site within the STMN2 gene. In some embodiments, the methods comprise introducing a STMN2-targeting RNA guide and a Cas12i polypeptide into a cell. The STMN2-targeting RNA guide and Cas12i polypeptide can be introduced as a ribonucleoprotein complex into a cell. The STMN2-targeting RNA guide and Cas12i polypeptide can be introduced on a nucleic acid vector. The Cas12i
10 polypeptide can be introduced as an mRNA. The RNA guide and template DNA can be introduced directly into the cell. In some embodiments, the composition described herein is delivered to a cell/tissue/person to reduce STMN2 in the cell/tissue/person. In some embodiments, the composition described herein is delivered to a cell/tissue/person to reduce STMN2 production in the cell/tissue/person. In some embodiments, the composition described
15 herein is delivered to a cell/tissue/person to treat a neurodegenerative disease (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a cell/tissue/person. In some embodiments, the composition described herein is delivered to a person with a neurodegenerative disease (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)).

20 Any of the gene editing systems disclosed herein may be used to genetically engineered a STMN2 gene. The gene editing system may comprise a guide RNA, a Cas12i2 polypeptide, and a template DNA. The guide RNA comprises a spacer sequence specific to a target sequence in the STMN2 gene, e.g., specific to a region in exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene.

25

A. Target Sequences

In some embodiments, an RNA guide as disclosed herein is designed to be complementary to a target sequence that is adjacent to a 5'-TTN-3' PAM sequence or 5'-NTTN-3' PAM sequence.

30 In some embodiments, the target sequence is within a STMN2 gene or a locus of a STMN2 gene (e.g., exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron), to which the RNA guide can bind via base pairing. In some embodiments, a cell has only one copy of the target sequence. In some embodiments, a cell has more than one copy, such as at least about any one of 2, 3, 4, 5, 10, 100, or more copies of the target sequence.

In some embodiments, the STMN2 gene is a mammalian gene. In some embodiments, the STMN2 gene is a human gene. For example, in some embodiments, the target sequence is within the sequence of SEQ ID NO: 454, or the reverse complement thereof. In some embodiments, the target sequence is within an exon of the STMN2 gene set forth in SEQ ID NO: 454, or the reverse complement thereof, e.g., within a sequence of any one of SEQ ID NOs: 455-461 (or a reverse complement of any thereof). Target sequences within an exon region of the STMN2 gene of SEQ ID NO: 454 are set forth in Table 6. The exon sequences are set forth in Table 7. In some embodiments, the target sequence is within an intron of the STMN2 gene set forth in SEQ ID NO: 454, or the reverse complement thereof. In some embodiments, the target sequence is within a variant (e.g., a polymorphic variant) of the STMN2 gene sequence set forth in SEQ ID NO: 454, or the reverse complement thereof. In some embodiments, the STMN2 gene sequence is a homolog of the sequence set forth in SEQ ID NO: 454, or the reverse complement thereof. In some embodiments, the STMN2 gene sequence is a non-human STMN2 sequence.

In some embodiments, the target sequence is adjacent to a 5'-NTTN-3' PAM sequence, wherein N is any nucleotide. The 5'-NTTN-3' sequence may be immediately adjacent to the target sequence or, for example, within a small number (e.g., 1, 2, 3, 4, or 5) of nucleotides of the target sequence. In some embodiments the 5'-NTTN-3' sequence is 5'-NTTY-3', 5'-NTTC-3', 5'-NTTT-3', 5'-NTTA-3', 5'-NTTB-3', 5'-NTTG-3', 5'-CTTY-3', 5'-DTTR-3', 5'-CTTR-3', 5'-DTTT-3', 5'-ATTN-3', or 5'-GTTN-3', wherein Y is C or T, B is any nucleotide except for A, D is any nucleotide except for C, and R is A or G. In some embodiments, the 5'-NTTN-3' sequence is 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'. The PAM sequence may be 5' to the target sequence.

In some embodiments, the target sequence is single-stranded (e.g., single-stranded DNA). In some embodiments, the target sequence is double-stranded (e.g., double-stranded DNA). In some embodiments, the target sequence comprises both single-stranded and double-stranded regions. In some embodiments, the target sequence is linear. In some embodiments, the target sequence is circular. In some embodiments, the target sequence comprises one or more modified nucleotides, such as methylated nucleotides, damaged nucleotides, or nucleotides analogs. In some embodiments, the target sequence is not modified. In some embodiments, the RNA guide binds to a first strand of a double-stranded target sequence (e.g., the target strand or the spacer-complementary strand), and the 5'-NTTN-3' PAM sequence is present in the second, complementary strand (e.g., the non-target strand or the non-spacer-complementary strand). In some embodiments, the RNA guide binds adjacent to a 5'-NAAN-3' sequence on the target strand (e.g., the spacer-complementary strand).

The 5'-NTTN-3' sequence may be immediately adjacent to the target sequence or, for example, within a small number (e.g., 1, 2, 3, 4, or 5) of nucleotides of the target sequence. In some embodiments the 5'-NTTN-3' sequence is 5'-NTTY-3', 5'-NTTC-3', 5'-NTTT-3', 5'-NTTA-3', 5'-NTTB-3', 5'-NTTG-3', 5'-CTTY-3', 5'-DTTR-3', 5'-CTTR-3', 5'-DTTT-3', 5'-ATTN-3', or 5'-GTTN-3', wherein Y is C or T, B is any nucleotide except for A, D is any nucleotide except for C, and R is A or G. In some embodiments, the 5'-NTTN-3' sequence is 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'. In some embodiments, the RNA guide is designed to bind to a first strand of a double-stranded target nucleic acid (*i.e.*, the non-PAM strand), and the 5'-NTTN-3' PAM sequence is present in the second, complementary strand (*i.e.*, the PAM strand). In some embodiments, the RNA guide binds to a region on the non-PAM strand that is complementary to a target sequence on the PAM strand, which is adjacent to a 5'-NAAN-3' sequence.

In some embodiments, the target sequence is present in a cell. In some embodiments, the target sequence is present in the nucleus of the cell. In some embodiments, the target sequence is endogenous to the cell. In some embodiments, the target sequence is a genomic DNA. In some embodiments, the target sequence is a chromosomal DNA. In some embodiments, the target sequence is a protein-coding gene or a functional region thereof, such as a coding region, or a regulatory element, such as a promoter, enhancer, a 5' or 3' untranslated region, etc. In some embodiments, the target sequence is present in a readily accessible region of the target sequence. In some embodiments, the target sequence is in an exon of a target gene. In some embodiments, the target sequence is across an exon-intron junction of a target gene. In some embodiments, the target sequence is present in a non-coding region, such as a regulatory region of a gene.

25

B. Gene Editing

In some embodiments, the Cas12i polypeptide has enzymatic activity (e.g., nuclease activity). In some embodiments, the Cas12i polypeptide induces one or more DNA double-stranded breaks in the cell. In some embodiments, the Cas12i polypeptide induces one or more DNA single-stranded breaks in the cell. In some embodiments, the Cas12i polypeptide induces one or more DNA nicks in the cell. In some embodiments, DNA breaks and/or nicks result in formation of one or more indels (e.g., one or more deletions).

In some embodiments, an RNA guide disclosed herein forms a complex with the Cas12i polypeptide and directs the Cas12i polypeptide to a target sequence adjacent to a 5'-NTTN-3' sequence. In some embodiments, the complex induces a deletion (e.g., a nucleotide deletion or

35

DNA deletion) adjacent to the 5'-NTTN-3' sequence. In some embodiments, the complex induces a deletion adjacent to a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the
5 complex induces a deletion adjacent to a T/C-rich sequence.

In some embodiments, the deletion is downstream of a 5'-NTTN-3' sequence. In some embodiments, the deletion is downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In
10 some embodiments, the deletion is downstream of a T/C-rich sequence.

In some embodiments, the deletion alters expression of the STMN2 gene. In some embodiments, the deletion alters function of the STMN2 gene. In some embodiments, the deletion inactivates the STMN2 gene. In some embodiments, the deletion is a frameshifting deletion. In some embodiments, the deletion is a non-frameshifting deletion. In some
15 embodiments, the deletion leads to cell toxicity or cell death (e.g., apoptosis).

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of a 5'-ATTA-3', 5'-ATTT-
20 3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-
30 3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) of the 5'-NTTN-3' sequence. In some
35 embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7,

8, 9, 10, 11, or 12 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some
 5 8, 9, 10, 11, or 12 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-
 10 ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g.,
 15 about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some
 20 embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g.,
 25 about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence.

30 In some embodiments, the deletion ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-
 35 3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-

3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion ends within about 20 to about 30 nucleotides (e.g.,
5 about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream
of the 5'-NTTN-3' sequence. In some embodiments, the deletion ends within about 20 to about
30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33
nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-
3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3',
10 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the
deletion ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24,
25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of a T/C-rich sequence.

In some embodiments, the deletion ends within about 20 to about 25 nucleotides (e.g.,
about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of the 5'-NTTN-3' sequence.
15 In some embodiments, the deletion ends within about 20 to about 25 nucleotides (e.g., about 17,
18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-
ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-
GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'
sequence. In some embodiments, the deletion ends within about 20 to about 25 nucleotides (e.g.,
20 about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion ends within about 20 to about 25 nucleotides (e.g.,
about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-NTTN-
3' sequence. In some embodiments, the deletion ends within about 20 to about 25 nucleotides
(e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of a 5'-
25 ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-
TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-
CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion ends within about 20 to
about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides)
downstream of a T/C-rich sequence.

30 In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g.,
about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence.
In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g., about 22,
23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-
ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-
35 GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'

sequence. In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3',

5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-G TTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-G TTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-G TTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-G TTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15
 5 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the
 10 deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-
 15 NTTN-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-
 20 GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In
 25 some embodiments, the deletion starts within about 5 to about 15 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g.,
 30 about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30,
 35 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-

3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3',
5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the
deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12
nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22,
5 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g.,
about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of the 5'-NTTN-3' sequence and
ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,
27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some
10 embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7,
8, 9, 10, 11, or 12 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-
ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-
GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and
ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,
15 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-
ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-
GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'
sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g.,
about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a T/C-rich sequence and ends
20 within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28,
29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g.,
about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 20 to about 25
nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of the 5'-
25 NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10
nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 20 to
about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a
5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3',
5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3',
30 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5
to about 10 nucleotides and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19,
20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12
nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g.,
35 about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of the 5'-NTTN-3' sequence and

ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a T/C-rich sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 5 to about 10 nucleotides (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 nucleotides) downstream of a T/C-rich sequence and ends within about 25 to about 30 nucleotides (e.g., about

22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 20 to about 30 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15

nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 20 to about 25 nucleotides (e.g., about 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17

nucleotides) and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) of a T/C-rich sequence.

In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of the 5'-NTTN-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-NTTN-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3' sequence. In some embodiments, the deletion starts within about 10 to about 15 nucleotides (e.g., about 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides) downstream of a T/C-rich sequence and ends within about 25 to about 30 nucleotides (e.g., about 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 nucleotides) downstream of the T/C-rich sequence.

In some embodiments, the deletion is up to about 50 nucleotides in length (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, or 55 nucleotides). In some embodiments, the deletion is up to about 40 nucleotides in length (e.g., about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 nucleotides). In some embodiments, the deletion is between about 4 nucleotides and about 40 nucleotides in length (e.g., about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 nucleotides). In some embodiments, the deletion is between about 4 nucleotides and about 25 nucleotides in length (e.g., about 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, or 28 nucleotides). In some embodiments, the deletion is between about 10 nucleotides and about 25 nucleotides in length (e.g., about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, or 28 nucleotides). In some embodiments, the deletion is between about 10 nucleotides and about 15 nucleotides in length (e.g., about 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, or 17 nucleotides).

In some embodiments, two or more RNA guides described herein are used to introduce a deletion that has a length of greater than 40 nucleotides. In some embodiments, two or more RNA guides described herein are used to introduce a deletion of at least about 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 16, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, or 400 nucleotides. In some embodiments, two or more RNA guides described herein are used delete all or a portion of the STMN2 gene or SEQ ID NO: 454.

In some embodiments, the methods described herein are used to engineer a cell comprising a deletion as described herein in a STMN2 gene. In some embodiments, the methods are carried out using a complex comprising a Cas12i enzyme as described herein and an RNA guide comprising a direct repeat sequence and a spacer sequence as described herein.

In some embodiments, the RNA guide targeting STMN2 is encoded in a plasmid. In some embodiments, the RNA guide targeting STMN2 is synthetic or purified RNA. In some embodiments, the Cas12i polypeptide is encoded in a plasmid. In some embodiments, the Cas12i polypeptide is encoded by an RNA that is synthetic or purified.

C. Delivery

Components of any of the gene editing systems disclosed herein may be formulated, for example, including a carrier, such as a carrier and/or a polymeric carrier, e.g., a liposome, and delivered by known methods to a cell (e.g., a prokaryotic, eukaryotic, plant, mammalian, etc.). Such methods include, but not limited to, transfection (e.g., lipid-mediated, cationic polymers, calcium phosphate, dendrimers); electroporation or other methods of membrane disruption (e.g., nucleofection), viral delivery (e.g., lentivirus, retrovirus, adenovirus, adeno-associated virus (AAV)), microinjection, microprojectile bombardment ("gene gun"), fugene, direct sonic loading, cell squeezing, optical transfection, protoplast fusion, impalefection, magnetofection, exosome-mediated transfer, lipid nanoparticle-mediated transfer, and any combination thereof.

In some embodiments, the method comprises delivering one or more nucleic acids (e.g., nucleic acids encoding the Cas12i polypeptide, RNA guide, donor DNA, etc.), one or more transcripts thereof, and/or a pre-formed RNA guide/Cas12i polypeptide complex to a cell, where a ternary complex is formed. In some embodiments, an RNA guide and an RNA encoding a Cas12i polypeptide are delivered together in a single composition. In some embodiments, an RNA guide and an RNA encoding a Cas12i polypeptide are delivered in separate compositions. In some embodiments, an RNA guide and an RNA encoding a Cas12i polypeptide delivered in separate compositions are delivered using the same delivery technology. In some embodiments,

an RNA guide and an RNA encoding a Cas12i polypeptide delivered in separate compositions are delivered using different delivery technologies.

In some embodiments, the Cas12i component and the RNA guide component are delivered together. For example, the Cas12i component and the RNA guide component are packaged together in a single AAV particle. In another example, the Cas12i component and the RNA guide component are delivered together via lipid nanoparticles (LNPs). In some embodiments, the Cas12i component and the RNA guide component are delivered separately. For example, the Cas12i component and the RNA guide are packaged into separate AAV particles. In another example, the Cas12i component is delivered by a first delivery mechanism and the RNA guide is delivered by a second delivery mechanism.

Exemplary intracellular delivery methods, include, but are not limited to: viruses, such as AAV, or virus-like agents; chemical-based transfection methods, such as those using calcium phosphate, dendrimers, liposomes, or cationic polymers (e.g., DEAE-dextran or polyethylenimine); non-chemical methods, such as microinjection, electroporation, cell squeezing, sonoporation, optical transfection, impalefection, protoplast fusion, bacterial conjugation, delivery of plasmids or transposons; particle-based methods, such as using a gene gun, magnetofection or magnet assisted transfection, particle bombardment; and hybrid methods, such as nucleofection. In some embodiments, a lipid nanoparticle comprises an mRNA encoding a Cas12i polypeptide, an RNA guide, or an mRNA encoding a Cas12i polypeptide and an RNA guide. In some embodiments, the mRNA encoding the Cas12i polypeptide is a transcript of the nucleotide sequence set forth in SEQ ID NO: 447 or SEQ ID NO: 481 or a variant thereof. In some embodiments, the present application further provides cells produced by such methods, and organisms (such as animals, plants, or fungi) comprising or produced from such cells.

D. Genetically Modified Cells

Any of the gene editing systems disclosed herein can be delivered to a variety of cells. In some embodiments, the cell is an isolated cell. In some embodiments, the cell is in cell culture or a co-culture of two or more cell types. In some embodiments, the cell is ex vivo. In some embodiments, the cell is obtained from a living organism and maintained in a cell culture. In some embodiments, the cell is a single-cellular organism.

In some embodiments, the cell is a prokaryotic cell. In some embodiments, the cell is a bacterial cell or derived from a bacterial cell. In some embodiments, the cell is an archaeal cell or derived from an archaeal cell.

In some embodiments, the cell is a eukaryotic cell. In some embodiments, the cell is a plant cell or derived from a plant cell. In some embodiments, the cell is a fungal cell or derived from a fungal cell. In some embodiments, the cell is an animal cell or derived from an animal cell. In some embodiments, the cell is an invertebrate cell or derived from an invertebrate cell. In some embodiments, the cell is a vertebrate cell or derived from a vertebrate cell. In some
5 embodiments, the cell is a mammalian cell or derived from a mammalian cell. In some
embodiments, the cell is a human cell. In some embodiments, the cell is a zebra fish cell. In
some embodiments, the cell is a rodent cell. In some embodiments, the cell is synthetically made,
sometimes termed an artificial cell.

10 In some embodiments, the cell is derived from a cell line. A wide variety of cell lines for
tissue culture are known in the art. Examples of cell lines include, but are not limited to, 293T,
MF7, K562, HeLa, CHO, and transgenic varieties thereof. Cell lines are available from a variety
of sources known to those with skill in the art (see, e.g., the American Type Culture Collection
(ATCC) (Manassas, Va.)). In some embodiments, the cell is an immortal or immortalized cell.

15 In some embodiments, the cell is a primary cell. In some embodiments, the cell is a stem
cell such as a totipotent stem cell (e.g., omnipotent), a pluripotent stem cell, a multipotent stem
cell, an oligopotent stem cell, or an unipotent stem cell. In some embodiments, the cell is an
induced pluripotent stem cell (iPSC) or derived from an iPSC. In some embodiments, the cell is
a differentiated cell. For example, in some embodiments, the differentiated cell is a neural cell
20 (e.g., a glial cell, such as an astrocyte, an oligodendrocyte, a microglial cell, or an ependymal
cell, or a neuron), muscle cell (e.g., a myocyte), a fat cell (e.g., an adipocyte), a bone cell (e.g.,
an osteoblast, osteocyte, osteoclast), a blood cell (e.g., a monocyte, a lymphocyte, a neutrophil,
an eosinophil, a basophil, a macrophage, a erythrocyte, or a platelet), an epithelial cell, an
immune cell (e.g., a lymphocyte, a neutrophil, a monocyte, or a macrophage), a liver cell (e.g., a
25 hepatocyte), a fibroblast, or a sex cell. In some embodiments, the cell is a terminally
differentiated cell. For example, in some embodiments, the terminally differentiated cell is a
neuronal cell, an adipocyte, a cardiomyocyte, a skeletal muscle cell, an epidermal cell, or a gut
cell. In some embodiments, the cell is an immune cell. In some embodiments, the immune cell is
a T cell. In some embodiments, the immune cell is a B cell. In some embodiments, the immune
30 cell is a Natural Killer (NK) cell. In some embodiments, the immune cell is a Tumor Infiltrating
Lymphocyte (TIL). In some embodiments, the cell is a cancer cell (e.g., a colorectal cancer cell,
renal cell cancer cell, breast cancer cell, or glioma cell). In some embodiments, the cell is a
mammalian cell, e.g., a human cell or a murine cell. In some embodiments, the murine cell is
derived from a wild-type mouse, an immunosuppressed mouse, or a disease-specific mouse
35 model. In some embodiments, the cell is a cell within a living tissue, organ, or organism.

Any of the genetically modified cells produced using any of the gene editing system disclosed herein is also within the scope of the present disclosure. Such modified cells may comprise a disrupted STMN2 gene.

Any of the gene editing systems, compositions comprising such, vectors, nucleic acids, RNA guides and cells disclosed herein may be used in therapy. Gene editing systems, compositions, vectors, nucleic acids, RNA guides and cells disclosed herein may be used in methods of treating a disease or condition in a subject. Any suitable delivery or administration method known in the art may be used to deliver compositions, vectors, nucleic acids, RNA guides and cells disclosed herein. Such methods may involve contacting a target sequence with a composition, vector, nucleic acid, or RNA guide disclosed herein. Such methods may involve a method of editing a STMN2 sequence as disclosed herein. In some embodiments, a cell engineered using an RNA guide disclosed herein is used for *ex vivo* gene therapy.

IV. Therapeutic Applications

Any of the gene editing systems or modified cells generated using such a gene editing system as disclosed herein may be used for treating a disease that is associated with the STMN2 gene, for example, neurodegenerative diseases (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)). Any suitable delivery or administration method known in the art may be used to deliver compositions, vectors, nucleic acids, RNA guides and cells disclosed herein. Such methods may involve contacting a target sequence with a composition, vector, nucleic acid, or RNA guide disclosed herein. Such methods may involve a method of editing a STMN2 sequence as disclosed herein. In some embodiments, a cell engineered using an RNA guide disclosed herein is used for *ex vivo* gene therapy. In some embodiments, provided herein is a method for treating a target disease as disclosed herein (e.g., a neurodegenerative disease) comprising administering to a subject (e.g., a human patient) in need of the treatment any of the gene editing systems disclosed herein. The gene editing system may be delivered to a specific tissue or specific type of cells where the gene edit is needed. The gene editing system may comprise LNPs encompassing one or more of the components, one or more vectors (e.g., viral vectors) encoding one or more of the components, or a combination thereof. Components of the gene editing system may be formulated to form a pharmaceutical composition, which may further comprise one or more pharmaceutically acceptable carriers.

In some embodiments, modified cells produced using any of the gene editing systems disclosed herein may be administered to a subject (e.g., a human patient) in need of the treatment. The modified cells may comprise a substitution, insertion, and/or deletion described herein. In some examples, the modified cells may include a cell line modified by a CRISPR

nuclease, reverse transcriptase polypeptide, and editing template RNA (e.g., RNA guide and RT donor RNA). In some instances, the modified cells may be a heterogeneous population comprising cells with different types of gene edits. Alternatively, the modified cells may comprise a substantially homogeneous cell population (e.g., at least 80% of the cells in the whole population) comprising one particular gene edit in the STMN2 gene. In some examples, the cells can be suspended in a suitable media.

In some embodiments, provided herein is a composition comprising the gene editing system or components thereof. Such a composition can be a pharmaceutical composition. A pharmaceutical composition that is useful may be prepared, packaged, or sold in a formulation suitable for oral, rectal, vaginal, parenteral, topical, pulmonary, intranasal, intra-lesional, buccal, ophthalmic, intravenous, intra-organ or another route of administration. A pharmaceutical composition of the disclosure may be prepared, packaged, or sold in bulk, as a single unit dose, or as a plurality of single unit doses. As used herein, a "unit dose" is discrete amount of the pharmaceutical composition (e.g., the gene editing system or components thereof), which would be administered to a subject or a convenient fraction of such a dosage such as, for example, one-half or one-third of such a dosage.

A formulation of a pharmaceutical composition suitable for parenteral administration may comprise the active agent (e.g., the gene editing system or components thereof or the modified cells) combined with a pharmaceutically acceptable carrier, such as sterile water or sterile isotonic saline. Such a formulation may be prepared, packaged, or sold in a form suitable for bolus administration or for continuous administration. Some injectable formulations may be prepared, packaged, or sold in unit dosage form, such as in ampules or in multi-dose containers containing a preservative. Some formulations for parenteral administration include, but are not limited to, suspensions, solutions, emulsions in oily or aqueous vehicles, pastes, and implantable sustained-release or biodegradable formulations. Some formulations may further comprise one or more additional ingredients including, but not limited to, suspending, stabilizing, or dispersing agents.

The pharmaceutical composition may be in the form of a sterile injectable aqueous or oily suspension or solution. This suspension or solution may be formulated according to the known art, and may comprise, in addition to the cells, additional ingredients such as the dispersing agents, wetting agents, or suspending agents described herein. Such sterile injectable formulation may be prepared using a non-toxic parenterally-acceptable diluent or solvent, such as water or saline. Other acceptable diluents and solvents include, but are not limited to, Ringer's solution, isotonic sodium chloride solution, and fixed oils such as synthetic mono- or di-glycerides. Other parentally-administrable formulations which that are useful include those

which may comprise the cells in a packaged form, in a liposomal preparation, or as a component of a biodegradable polymer system. Some compositions for sustained release or implantation may comprise pharmaceutically acceptable polymeric or hydrophobic materials such as an emulsion, an ion exchange resin, a sparingly soluble polymer, or a sparingly soluble salt.

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V. Kits and Uses Thereof

The present disclosure also provides kits that can be used, for example, to carry out a method described herein for genetical modification of the STMN2 gene. In some embodiments, the kits include an RNA guide and a Cas12i polypeptide. In some embodiments, the kits include an RNA guide, a template DNA, and a Cas12i polypeptide. In some embodiments, the kits include a polynucleotide that encodes such a Cas12i polypeptide, and optionally the polynucleotide is comprised within a vector, e.g., as described herein. In some embodiments, the kits include a polynucleotide that encodes an RNA guide disclosed herein. The Cas12i polypeptide (or polynucleotide encoding the Cas12i polypeptide) and the RNA guide (e.g., as a ribonucleoprotein) can be packaged within the same or other vessel within a kit or can be packaged in separate vials or other vessels, the contents of which can be mixed prior to use.

The Cas12i polypeptide, the RNA guide, and the template DNA can be packaged within the same or other vessel within a kit or can be packaged in separate vials or other vessels, the contents of which can be mixed prior to use. The kits can additionally include, optionally, a buffer and/or instructions for use of the RNA guide, template DNA, and Cas12i polypeptide.

All references and publications cited herein are hereby incorporated by reference.

ADDITIONAL EMBODIMENTS

Provided below are additional embodiments, which are also within the scope of the present disclosure.

Embodiment 1: A composition comprising an RNA guide, wherein the RNA guide comprises (i) a spacer sequence that is substantially complementary or complete complementary to a region on a non-PAM strand (the complementary sequence of a target sequence) within an STMN2 gene and (ii) a direct repeat sequence; wherein the target sequence is adjacent to a protospacer adjacent motif (PAM) comprising the sequence 5'-NTTN-3'.

In Embodiment 1, the target sequence may be within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene. In some examples, the STMN2 gene comprises the sequence of SEQ ID NO: 454, the reverse complement of SEQ ID NO: 454, a variant of SEQ ID NO: 454, or the reverse complement of a variant of SEQ ID NO: 454.

In Embodiment 1, the spacer sequence may comprise: (a) nucleotide 1 through nucleotide 16 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through
5 nucleotide 18 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (e) nucleotide 1 through nucleotide 20 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of a sequence that is
10 at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (i) nucleotide 1 through nucleotide 24 of a sequence that is at least 90% identical to a
15 sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (j) nucleotide 1 through nucleotide 25 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (k) nucleotide 1 through nucleotide 26 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (l) nucleotide 1 through nucleotide 27 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID
20 NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; or (o) nucleotide 1 through nucleotide 30 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502.

25 In any of the compositions of Embodiment 1, the spacer sequence may comprise: (a) nucleotide 1 through nucleotide 16 of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through nucleotide 18 of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of any one of SEQ ID NOs: 229-446 or 2497-4502; (e)
30 nucleotide 1 through nucleotide 20 of any one of SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of any one of SEQ ID NOs: 229-446 or 2497-4502; (i) nucleotide 1 through nucleotide 24 of any one of SEQ ID NOs: 229-446 or 2497-4502; (j)
35 nucleotide 1 through nucleotide 25 of any one of SEQ ID NOs: 229-446 or 2497-4502; (k)

- nucleotide 1 through nucleotide 26 of any one of SEQ ID NOs: 229-446 or 2497-4502; (l) nucleotide 1 through nucleotide 27 of any one of SEQ ID NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of any one of SEQ ID NOs: 229-446 or 2497-4502; or (o)
- 5 nucleotide 1 through nucleotide 30 of any one of SEQ ID NOs: 229-446 or 2497-4502.

- In any of the compositions of Embodiment 1, the direct repeat sequence may comprise:
- (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through
- 10 nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of
- 15 SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (n) nucleotide 14
- 25 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (o) nucleotide 1 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (r) nucleotide 4
- 30 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (s) nucleotide 5 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (v) nucleotide 8 through
- 35 nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (w)

nucleotide 9 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (z) nucleotide 12 through
5 nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; or (aa) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (d)
10 nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of any
15 one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (o) nucleotide 1 through nucleotide 34 of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of
20 SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of SEQ ID NO: 9; (s) nucleotide 5 through nucleotide 34 of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of SEQ ID NO: 9; (w) nucleotide 9 through nucleotide 34 of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of SEQ ID NO:
25 9; (z) nucleotide 12 through nucleotide 34 of SEQ ID NO: 9; or (aa) SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical
30 to a sequence of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through
35 nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID

NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 462-479; or (o) SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; or (o) a sequence that is at least 90% identical to SEQ ID NO: 485 or a portion thereof.

least 90% identical to SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (l) nucleotide 12 through
5 nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

10 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36
15 of SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 485; or (o) SEQ ID NO: 486 or SEQ ID
20 NO: 487 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through
25 nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90%
30 identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
35 SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90%

identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through
 5 nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) a sequence that is at least 90% identical to a sequence of SEQ ID NO:
 10 490 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID
 15 NO: 489; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO:
 20 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) SEQ ID NO: 490 or a portion
 25 thereof.

In some examples, the spacer sequence is substantially complementary to the complement of a sequence of any one of SEQ ID NOs: 11-228 or 491-2496.

In any of the composition of Embodiment 1, the PAM may comprise the sequence 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'.

In some examples, the target sequence is immediately adjacent to the PAM sequence.

In some examples, the RNA guide has a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 4505-4562.

In some examples, the RNA guide has the sequence of any one of SEQ ID NOs: 4505-4562.

Embodiment 2: The composition of Embodiment 1 may further comprise a Cas12i polypeptide or a polyribonucleotide encoding a Cas12i polypeptide, which can be one of the following: (a) a Cas12i2 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453; (b) a Cas12i4 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 482, SEQ ID NO: 483, or SEQ ID NO: 484; (c) a Cas12i1 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 4503; or (d) a Cas12i3 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 4504.

In specific examples, the Cas12i polypeptide is: (a) a Cas12i2 polypeptide comprising a sequence of SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453; (b) a Cas12i4 polypeptide comprising a sequence of SEQ ID NO: 482, SEQ ID NO: 483, or SEQ ID NO: 484; (c) a Cas12i1 polypeptide comprising a sequence of SEQ ID NO: 4503; or (d) a Cas12i3 polypeptide comprising a sequence of SEQ ID NO: 4504.

In any of the compositions of Embodiment 2, the RNA guide and the Cas12i polypeptide may form a ribonucleoprotein complex. In some examples, the ribonucleoprotein complex binds a target nucleic acid. In some examples, the composition is present within a cell.

In any of the compositions of Embodiment 2, the RNA guide and the Cas12i polypeptide may be encoded in a vector, *e.g.*, expression vector. In some examples, the RNA guide and the Cas12i polypeptide are encoded in a single vector. In other examples, the RNA guide is encoded in a first vector and the Cas12i polypeptide is encoded in a second vector.

Embodiment 3: A vector system comprising one or more vectors encoding an RNA guide disclosed herein and a Cas12i polypeptide. In some examples, the vector system comprises a first vector encoding an RNA guide disclosed herein and a second vector encoding a Cas12i polypeptide. The vectors may be expression vectors.

Embodiment 4: A composition comprising an RNA guide and a Cas12i polypeptide, wherein the RNA guide comprises (i) a spacer sequence that is substantially complementary or completely complementary to a region on a non-PAM strand (the complementary sequence of a target sequence) within an STMN2 gene, and (ii) a direct repeat sequence.

In some examples, the target sequence is within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene, which may comprise the sequence of SEQ ID NO: 454, the reverse complement of SEQ ID NO: 454, a variant of the sequence of SEQ ID NO: 454, or the reverse complement of a variant of SEQ ID NO: 454.

In some examples, the spacer sequence comprises: (a) nucleotide 1 through nucleotide 16 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through
5 nucleotide 18 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (e) nucleotide 1 through nucleotide 20 of a sequence that is at least 90% identical to a sequence of any one of
10 SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or
15 2497-4502; (i) nucleotide 1 through nucleotide 24 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (j) nucleotide 1 through nucleotide 25 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (k) nucleotide 1 through nucleotide 26 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (l) nucleotide 1 through
20 nucleotide 27 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of a sequence that is at least 90% identical to a sequence of any one of
25 SEQ ID NOs: 229-446 or 2497-4502; or (o) nucleotide 1 through nucleotide 30 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502.

In some examples, the spacer sequence comprises: (a) nucleotide 1 through nucleotide 16 of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through nucleotide 18 of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of any one of SEQ ID NOs: 229-446 or 2497-4502; (e) nucleotide 1 through nucleotide 20 of any one of
30 SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of any one of SEQ ID NOs: 229-446 or 2497-4502; (i) nucleotide 1 through nucleotide 24 of any one of SEQ ID NOs: 229-446 or 2497-4502; (j) nucleotide 1 through nucleotide 25 of any one of SEQ ID NOs: 229-446 or
35 2497-4502; (k) nucleotide 1 through nucleotide 26 of any one of SEQ ID NOs: 229-446 or 2497-

4502; (l) nucleotide 1 through nucleotide 27 of any one of SEQ ID NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of any one of SEQ ID NOs: 229-446 or 2497-4502; or (o) nucleotide 1 through nucleotide 30 of any one of SEQ ID NOs: 229-446 or 2497-4502.

- 5 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (d) nucleotide 4
- 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of
- 15 any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of a sequence that is at
- 20 least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (o)
- 25 nucleotide 1 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (s) nucleotide 5
- 30 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (w) nucleotide 9 through
- 35 nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (x)

nucleotide 10 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (z) nucleotide 12 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; or (aa) a sequence that is at least
5 90% identical to a sequence of SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through
10 nucleotide 36 of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 1-
15 8; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (o) nucleotide 1 through nucleotide 34 of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of SEQ ID NO: 9; (s) nucleotide 5
20 through nucleotide 34 of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of SEQ ID NO: 9; (w) nucleotide 9 through nucleotide 34 of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of SEQ ID NO: 9; (z) nucleotide 12 through nucleotide 34 of SEQ ID NO: 9; or (aa) SEQ ID NO: 10 or a portion
25 thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of a
30 sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID
35 NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical

to a sequence of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 462-479; or (o) SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of a sequence that

is at least 90% identical to SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (m) nucleotide 13
5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through
10 nucleotide 36 of SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 485; (i) nucleotide 9
15 through nucleotide 36 of SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 485; or (o) SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

20 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
25 SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through
30 nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
35 identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through

nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 490 or a portion thereof.

10 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) SEQ ID NO: 490 or a portion thereof.

25 In any of the compositions of Embodiment 4, the spacer sequence may be substantially complementary to the complement of a sequence of any one of SEQ ID NOs: 11-228 or 491-2496.

In some examples, the target sequence is adjacent to a protospacer adjacent motif (PAM) comprising the sequence 5'-NTTN-3'. In some examples, the PAM comprises the sequence 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'.

In some examples, the target sequence is immediately adjacent to the PAM sequence. In some examples, the target sequence is within 1, 2, 3, 4, or 5 nucleotides of the PAM sequence.

In any of the compositions of Embodiment 4, the Cas12i polypeptide is: (a) a Cas12i2 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453; (b) a Cas12i4 polypeptide comprising a sequence that is at least 90% identical to the
5 sequence of SEQ ID NO: 482, SEQ ID NO: 483, or SEQ ID NO: 484; (c) a Cas12i1 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 4503; or (d) a Cas12i3 polypeptide comprising a sequence that is at least 90% identical to the sequence of SEQ ID NO: 4504.

In some examples, the Cas12i polypeptide is: (a) a Cas12i2 polypeptide comprising a
10 sequence of SEQ ID NO: 448, SEQ ID NO: 449, SEQ ID NO: 450, SEQ ID NO: 451, SEQ ID NO: 452, or SEQ ID NO: 453; (b) a Cas12i4 polypeptide comprising a sequence of SEQ ID NO: 482, SEQ ID NO: 483, or SEQ ID NO: 484; (c) a Cas12i1 polypeptide comprising a sequence of SEQ ID NO: 4503; or (d) a Cas12i3 polypeptide comprising a sequence of SEQ ID NO: 4504.

In any of the composition of Embodiment 4, the RNA guide and the Cas12i polypeptide
15 may form a ribonucleoprotein complex. In some examples, the ribonucleoprotein complex binds a target nucleic acid.

In any of the composition of Embodiment 4, the composition may be present within a cell.

In any of the composition of Embodiment 4, the RNA guide and the Cas12i polypeptide
20 may be encoded in a vector, *e.g.*, expression vector. In some examples, the RNA guide and the Cas12i polypeptide are encoded in a single vector. In other examples, the RNA guide is encoded in a first vector and the Cas12i polypeptide is encoded in a second vector.

Embodiment 5: A vector system comprising one or more vectors encoding an RNA guide disclosed herein and a Cas12i polypeptide. In some examples, the vector system comprises a
25 first vector encoding an RNA guide disclosed herein and a second vector encoding a Cas12i polypeptide. In some examples, the vectors are expression vectors.

Embodiment 6: An RNA guide comprising (i) a spacer sequence that is substantially complementary or completely complementary to a region on a non-PAM strand (the complementary sequence of a target sequence) within an STMN2 gene, and (ii) a direct repeat
30 sequence.

In some examples, the target sequence is within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene, which may comprise the sequence of SEQ ID NO: 454, the reverse complement of SEQ ID NO: 454, a variant of the sequence of SEQ ID NO: 454, or the reverse complement of a variant of SEQ ID NO: 454.

In some examples, the spacer sequence comprises: (a) nucleotide 1 through nucleotide 16 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through
5 nucleotide 18 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (e) nucleotide 1 through nucleotide 20 of a sequence that is at least 90% identical to a sequence of any one of
10 SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or
15 2497-4502; (i) nucleotide 1 through nucleotide 24 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (j) nucleotide 1 through nucleotide 25 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (k) nucleotide 1 through nucleotide 26 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (l) nucleotide 1 through
20 nucleotide 27 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of a sequence that is at least 90% identical to a sequence of any one of
25 SEQ ID NOs: 229-446 or 2497-4502; or (o) nucleotide 1 through nucleotide 30 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 229-446 or 2497-4502.

In some examples, the spacer sequence comprises: (a) nucleotide 1 through nucleotide 16 of any one of SEQ ID NOs: 229-446 or 2497-4502; (b) nucleotide 1 through nucleotide 17 of any one of SEQ ID NOs: 229-446 or 2497-4502; (c) nucleotide 1 through nucleotide 18 of any one of SEQ ID NOs: 229-446 or 2497-4502; (d) nucleotide 1 through nucleotide 19 of any one of SEQ ID NOs: 229-446 or 2497-4502; (e) nucleotide 1 through nucleotide 20 of any one of
30 SEQ ID NOs: 229-446 or 2497-4502; (f) nucleotide 1 through nucleotide 21 of any one of SEQ ID NOs: 229-446 or 2497-4502; (g) nucleotide 1 through nucleotide 22 of any one of SEQ ID NOs: 229-446 or 2497-4502; (h) nucleotide 1 through nucleotide 23 of any one of SEQ ID NOs: 229-446 or 2497-4502; (i) nucleotide 1 through nucleotide 24 of any one of SEQ ID NOs: 229-446 or 2497-4502; (j) nucleotide 1 through nucleotide 25 of any one of SEQ ID NOs: 229-446 or
35 2497-4502; (k) nucleotide 1 through nucleotide 26 of any one of SEQ ID NOs: 229-446 or 2497-

4502; (l) nucleotide 1 through nucleotide 27 of any one of SEQ ID NOs: 229-446 or 2497-4502; (m) nucleotide 1 through nucleotide 28 of any one of SEQ ID NOs: 229-446 or 2497-4502; (n) nucleotide 1 through nucleotide 29 of any one of SEQ ID NOs: 229-446 or 2497-4502; or (o) nucleotide 1 through nucleotide 30 of any one of SEQ ID NOs: 229-446 or 2497-4502.

- 5 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (d) nucleotide 4
- 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of
- 15 any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of a sequence that is at
- 20 least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (o)
- 25 nucleotide 1 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (s) nucleotide 5
- 30 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (w) nucleotide 9 through
- 35 nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (x)

nucleotide 10 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (z) nucleotide 12 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; or (aa) a sequence that is at least
5 90% identical to a sequence of SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through
10 nucleotide 36 of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 1-
15 8; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (o) nucleotide 1 through nucleotide 34 of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of SEQ ID NO: 9; (s) nucleotide 5
20 through nucleotide 34 of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of SEQ ID NO: 9; (w) nucleotide 9 through nucleotide 34 of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of SEQ ID NO: 9; (z) nucleotide 12 through nucleotide 34 of SEQ ID NO: 9; or (aa) SEQ ID NO: 10 or a portion
25 thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of a
30 sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID
35 NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical

to a sequence of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 462-479; or (o) SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of a sequence that

is at least 90% identical to SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (m) nucleotide 13
5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through
10 nucleotide 36 of SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 485; (i) nucleotide 9
15 through nucleotide 36 of SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 485; or (o) SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

20 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
25 SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through
30 nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90%
35 identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through

nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
 5 SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 490 or a portion thereof.

10 In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (f)
 15 nucleotide 6 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 488 or SEQ
 20 ID NO: 489; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) SEQ ID NO: 490 or a portion thereof.

25 In any of the RNA guide of Embodiment 6, the spacer sequence may be substantially complementary to the complement of a sequence of any one of SEQ ID NOs: 11-228 or 491-2496.

In any of the RNA guide of Embodiment 6, the target sequence may be adjacent to a protospacer adjacent motif (PAM) comprising the sequence 5'-NTTN-3', wherein N is any
 30 nucleotide. In some examples, the PAM comprises the sequence 5'-ATTA-3', 5'-ATTT-3', 5'-ATTG-3', 5'-ATTC-3', 5'-TTTA-3', 5'-TTTT-3', 5'-TTTG-3', 5'-TTTC-3', 5'-GTTA-3', 5'-GTTT-3', 5'-GTTG-3', 5'-GTTC-3', 5'-CTTA-3', 5'-CTTT-3', 5'-CTTG-3', or 5'-CTTC-3'.

In some examples, the target sequence is immediately adjacent to the PAM sequence. In other examples, the target sequence is within 1, 2, 3, 4, or 5 nucleotides of the PAM sequence.

In some examples, the RNA guide has a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 4505-4562. In specific examples, the RNA guide has the sequence of any one of SEQ ID NOs: 4505-4562.

Embodiment 7: A nucleic acid encoding an RNA guide as described herein.

5 Embodiment 8: A vector comprising such an RNA guide as described herein.

Embodiment 9: A cell comprising a composition, an RNA guide, a nucleic acid, or a vector as described herein. In some examples, the cell is a eukaryotic cell, an animal cell, a mammalian cell, a human cell, a primary cell, a cell line, a stem cell, a neuron, or a T cell.

10 Embodiment 10: A kit comprising a composition, an RNA guide, a nucleic acid, or a vector as described herein.

Embodiment 11: A method of editing an STMN2 sequence, the method comprising contacting an STMN2 sequence with a composition or an RNA guide as described herein. In some examples, the method is carried out *in vitro*. In other examples, the method is carried out *ex vivo*.

15 In some examples, the STMN2 sequence is in a cell.

In some examples, the composition or the RNA guide induces a deletion in the STMN2 sequence. In some examples, the deletion is adjacent to a 5'-NTTN-3' sequence, wherein N is any nucleotide. In some specific examples, the deletion is downstream of the 5'-NTTN-3' sequence. In some specific examples, the deletion is up to about 40 nucleotides in length. In
20 some instances, the deletion is from about 4 nucleotides to 40 nucleotides, about 4 nucleotides to 25 nucleotides, about 10 nucleotides to 25 nucleotides, or about 10 nucleotides to 15 nucleotides in length.

In some examples, the deletion starts within about 5 nucleotides to about 15 nucleotides, about 5 nucleotides to about 10 nucleotides, or about 10 nucleotides to about 15 nucleotides of
25 the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 15 nucleotides, about 5 nucleotides to about 10 nucleotides, or about 10 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion ends within about 20 nucleotides to about 30 nucleotides, about 20 nucleotides to about 25 nucleotides, or about 25 nucleotides to about 30 nucleotides of
30 the 5'-NTTN-3' sequence.

In some examples, the deletion ends within about 20 nucleotides to about 30 nucleotides, about 20 nucleotides to about 25 nucleotides, about 25 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 25 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 25 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 10 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 10 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 25 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 5 nucleotides to about 10 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 25 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 10 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 10 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 20 nucleotides to about 25 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the deletion starts within about 10 nucleotides to about 15 nucleotides downstream of the 5'-NTTN-3' sequence and ends within about 25 nucleotides to about 30 nucleotides downstream of the 5'-NTTN-3' sequence.

In some examples, the 5'-NTTN-3' sequence is 5'-CTTT-3', 5'-CTTC-3', 5'-GTTT-3', 5'-GTTC-3', 5'-TTTC-3', 5'-GTTA-3', or 5'-GTTG-3'.

In some examples, the deletion overlaps with a mutation in the STMN2 sequence. In some instances, the deletion overlaps with an insertion in the STMN2 sequence. In some instances, the deletion removes a repeat expansion of the STMN2 sequence or a portion thereof. In some instances, the deletion disrupts one or both alleles of the STMN2 sequence.

In any of the composition, RNA guide, nucleic acid, vector, cell, kit, or method of Embodiments 1-11 described herein, the RNA guide may comprise the sequence of any one of SEQ ID NOs: 4505-4562.

Embodiment 12: A method of treating neurodegenerative diseases (e.g., amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)) in a subject, the method comprising administering a composition, an RNA guide, or a cell described herein to the subject.

In any of the compositions, RNA guides, cells, kits, or methods described herein, the RNA guide and/or the polyribonucleotide encoding the Cas12i polypeptide are comprised within a lipid nanoparticle. In some examples, the RNA guide and the polyribonucleotide encoding the Cas12i polypeptide are comprised within the same lipid nanoparticle. In other examples, the RNA guide and the polyribonucleotide encoding the Cas12i polypeptide are comprised within separate lipid nanoparticles.

Embodiment 13: An RNA guide comprising (i) a spacer sequence that is complementary to a target site within an STMN2 gene (the target site being on the non-PAM strand and complementary to a target sequence), and (ii) a direct repeat sequence.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 1-8; (o)

nucleotide 1 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (s) nucleotide 5 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (w) nucleotide 9 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; (z) nucleotide 12 through nucleotide 34 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 9; or (aa) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (f) nucleotide 6 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (l) nucleotide 12 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (m) nucleotide 13 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 1-8; (o) nucleotide 1 through nucleotide 34 of SEQ ID NO: 9; (p) nucleotide 2 through nucleotide 34 of SEQ ID NO: 9; (q) nucleotide 3 through nucleotide 34 of SEQ ID NO: 9; (r) nucleotide 4 through nucleotide 34 of SEQ ID NO: 9; (s) nucleotide 5 through nucleotide 34 of SEQ ID NO: 9; (t) nucleotide 6 through nucleotide 34 of SEQ ID NO: 9; (u) nucleotide 7 through nucleotide 34 of SEQ ID NO: 9; (v) nucleotide 8 through nucleotide 34 of SEQ ID NO: 9; (w) nucleotide 9 through nucleotide 34 of SEQ ID NO: 9; (x) nucleotide 10 through nucleotide 34 of SEQ ID NO: 9; (y) nucleotide 11 through nucleotide 34 of SEQ ID NO:

9; (z) nucleotide 12 through nucleotide 34 of SEQ ID NO: 9; or (aa) SEQ ID NO: 10 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID
5 NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of a sequence that is at
10 least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of
15 SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of any one of SEQ ID NOs: 462-479; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (b) nucleotide 2 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (c) nucleotide 3 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (d) nucleotide 4 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (e) nucleotide 5 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (f) nucleotide 6 through
30 nucleotide 36 of any one of SEQ ID NOs: 462-479; (g) nucleotide 7 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (h) nucleotide 8 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (i) nucleotide 9 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (j) nucleotide 10 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (k) nucleotide 11 through nucleotide 36 of any one of SEQ ID NOs: 462-479; (l) nucleotide 12 through nucleotide
35 36 of any one of SEQ ID NOs: 462-479; (m) nucleotide 13 through nucleotide 36 of any one of

SEQ ID NOs: 462-479; (n) nucleotide 14 through nucleotide 36 of any one of SEQ ID NOs: 462-479; or (o) SEQ ID NO: 480 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to SEQ ID NO: 485; or (o) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 485; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 485; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO: 485; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 485; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 485; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 485; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 485; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 485; (i) nucleotide 9 through nucleotide 36 of SEQ ID NO: 485; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 485; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 485; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 485; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 485; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 485; or (o) SEQ ID NO: 486 or SEQ ID NO: 487 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through

nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
5 SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through
10 nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
15 SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of a sequence that is at least 90% identical to a sequence of SEQ ID NO: 488 or
20 SEQ ID NO: 489; or (p) a sequence that is at least 90% identical to a sequence of SEQ ID NO: 490 or a portion thereof.

In some examples, the direct repeat sequence comprises: (a) nucleotide 1 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (b) nucleotide 2 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (c) nucleotide 3 through nucleotide 36 of SEQ ID NO:
25 488 or SEQ ID NO: 489; (d) nucleotide 4 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (e) nucleotide 5 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (f) nucleotide 6 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (g) nucleotide 7 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (h) nucleotide 8 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (i) nucleotide 9 through nucleotide 36 of
30 SEQ ID NO: 488 or SEQ ID NO: 489; (j) nucleotide 10 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (k) nucleotide 11 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (l) nucleotide 12 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (m) nucleotide 13 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (n) nucleotide 14 through nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; (o) nucleotide 15 through

nucleotide 36 of SEQ ID NO: 488 or SEQ ID NO: 489; or (p) SEQ ID NO: 490 or a portion thereof.

In some examples, each of the first three nucleotides of the RNA guide comprises a 2'-O-methyl phosphorothioate modification.

5 In some examples, each of the last four nucleotides of the RNA guide comprises a 2'-O-methyl phosphorothioate modification.

In some examples, each of the first to last, second to last, and third to last nucleotides of the RNA guide comprises a 2'-O-methyl phosphorothioate modification, and wherein the last nucleotide of the RNA guide is unmodified.

10 Embodiment 14: A nucleic acid encoding an RNA guide as described herein.

Embodiment 15: A vector comprising the nucleic acid as described herein.

Embodiment 16: A vector system comprising one or more vectors encoding (i) the RNA guide of Embodiment 13 as described herein and (ii) a Cas12i polypeptide. In some examples, the vector system comprises a first vector encoding the RNA guide and a second vector encoding
15 the Cas12i polypeptide.

Embodiment 17: A cell comprising the RNA guide, the nucleic acid, the vector, or the vector system of Embodiments 13-16 as described herein. In some examples, the cell is a eukaryotic cell, an animal cell, a mammalian cell, a human cell, a primary cell, a cell line, a stem cell, a neuron, or a T cell.

20 Embodiment 18: A kit comprising the RNA guide, the nucleic acid, the vector, or the vector system of Embodiments 13-16 as described herein.

Embodiment 19: A method of editing an STMN2 sequence, the method comprising contacting an STMN2 sequence with an RNA guide of Embodiment 13 as described herein. In some examples, the STMN2 sequence is in a cell.

25 In some examples, the RNA guide induces an indel (*e.g.*, an insertion or deletion) in the STMN2 sequence.

Embodiment 20: A method of treating neurodegenerative diseases (*e.g.*, amyotrophic lateral sclerosis (ALS) or frontotemporal dementia (FTD)), in a subject, the method comprising administering the RNA guide of Embodiment 13 as described herein to the subject.

30

General techniques

The practice of the present disclosure will employ, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry, and immunology, which are within the skill of the
35 art. Such techniques are explained fully in the literature, such as *Molecular Cloning: A*

- Laboratory Manual*, second edition (Sambrook, et al., 1989) Cold Spring Harbor Press;
Oligonucleotide Synthesis (M. J. Gait, ed. 1984); *Methods in Molecular Biology*, Humana
 Press; *Cell Biology: A Laboratory Notebook* (J. E. Cellis, ed., 1989) Academic Press; *Animal*
Cell Culture (R. I. Freshney, ed. 1987); *Introduction to Cell and Tissue Culture* (J. P. Mather
 5 and P. E. Roberts, 1998) Plenum Press; *Cell and Tissue Culture: Laboratory Procedures* (A.
 Doyle, J. B. Griffiths, and D. G. Newell, eds. 1993-8) J. Wiley and Sons; *Methods in*
Enzymology (Academic Press, Inc.); *Handbook of Experimental Immunology* (D. M. Weir
 and C. C. Blackwell, eds.): *Gene Transfer Vectors for Mammalian Cells* (J. M. Miller and M.
 P. Calos, eds., 1987); *Current Protocols in Molecular Biology* (F. M. Ausubel, et al. eds.
 10 1987); *PCR: The Polymerase Chain Reaction*, (Mullis, et al., eds. 1994); *Current Protocols in*
Immunology (J. E. Coligan et al., eds., 1991); *Short Protocols in Molecular Biology* (Wiley
 and Sons, 1999); *Immunobiology* (C. A. Janeway and P. Travers, 1997); *Antibodies* (P.
 Finch, 1997); *Antibodies: a practice approach* (D. Catty., ed., IRL Press, 1988-1989);
Monoclonal antibodies: a practical approach (P. Shepherd and C. Dean, eds., Oxford
 15 University Press, 2000); *Using antibodies: a laboratory manual* (E. Harlow and D. Lane (Cold
 Spring Harbor Laboratory Press, 1999); *The Antibodies* (M. Zanetti and J. D. Capra, eds.
 Harwood Academic Publishers, 1995); *DNA Cloning: A practical Approach*, Volumes I and
 II (D.N. Glover ed. 1985); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins
 eds.(1985»; *Transcription and Translation* (B.D. Hames & S.J. Higgins, eds. (1984»; *Animal*
 20 *Cell Culture* (R.I. Freshney, ed. (1986»; *Immobilized Cells and Enzymes* (IRL Press, (1986»;
 and B. Perbal, *A practical Guide To Molecular Cloning* (1984); F.M. Ausubel *et al.* (eds.).

Without further elaboration, it is believed that one skilled in the art can, based on the
 above description, utilize the present disclosure to its fullest extent. The following specific
 embodiments are, therefore, to be construed as merely illustrative, and not limitative of the
 25 remainder of the present disclosure in any way whatsoever. All publications cited herein are
 incorporated by reference for the purposes or subject matter referenced herein.

EXAMPLES

The following examples are provided to further illustrate some embodiments of the
 30 present disclosure but are not intended to limit the scope of the present disclosure; it will be
 understood by their exemplary nature that other procedures, methodologies, or techniques known
 to those skilled in the art may alternatively be used.

Example 1 – Targeting of STMN2 Intron 1 by Variant Cas12i2

This Example describes indel assessment on multiple targets at the *STMN2* gene in cells after transfection with plasmids coding for variant Cas12i2 (SEQ ID NO: 450) and RNA guides.

The variant Cas12i2 polypeptide was cloned into a plasmid comprising a CMV promoter.

- 5 Fragments coding for RNA guides targeting the *STMN2* intron 1 gene were cloned into a pUC19 backbone (New England Biolabs). The plasmids were then maxi-prepped and diluted. The crRNA, target, and PAM sequences are listed in Table 6.

Table 6. Mammalian targets and corresponding crRNAs.

Target identifier	SEQ ID NO	crRNA sequence	SEQ ID NO	Target sequence	PAM sequence
1 or IIT1	4505	AGAAAUCCGUCUUUCAUU GACGGUGCCCCAUCACUCU CUCUUA	4563	TGCCCCATCACTCTCTCT TA	TTC
2 or IIT2	4506	AGAAAUCCGUCUUUCAUU GACGGAUUGGAUUUUUAA AAUUAUA	4564	ATTGGATTTTAAAATTA TA	TTA
3 or IIT3	4507	AGAAAUCCGUCUUUCAUU GACGGGAUUUUUAAAAUU AUAUUA	4565	GATTTTAAAATTATATT CA	TTG
4 or IIT4	4508	AGAAAUCCGUCUUUCAUU GACGGUAAAAUUAUUAU CAUAUUG	4566	TTAAAATTATATTCATAT TG	TTT
5 or IIT5	4509	AGAAAUCCGUCUUUCAUU GACGGUAAAAUUAUUAUC AUAUUGC	4567	TAAAATTATATTCATATT GC	TTT
6 or IIT6	4510	AGAAAUCCGUCUUUCAUU GACGGAAAAUUAUUAUCA UAUUGCA	4568	AAAATTATATTCATATTG CA	TTT
7 or IIT7	4511	AGAAAUCCGUCUUUCAUU GACGGAAAUUAUUAUUAU AUUGCAG	4569	AAATTATATTCATATTGC AG	TTA
8 or IIT8	4512	AGAAAUCCGUCUUUCAUU GACGGUAUUAUUAUUGCA GGACUCG	4570	TATTCATATTGCAGGACT CG	TTA
9 or IIT9	4513	AGAAAUCCGUCUUUCAUU GACGGAUUAUUGCAGGACU CGGCAGA	4571	ATATTGCAGGACTCGGC AGA	TTC
10 or IIT10	4514	AGAAAUCCGUCUUUCAUU GACGGCAGGACUCGGCAG AAGACCU	4572	CAGGACTCGGCAGAAGA CCT	TTG
11 or IIT11	4515	AGAAAUCCGUCUUUCAUU GACGGGAGAGAAAGGUAG AAAAUAA	4573	GAGAGAAAGGTAGAAA ATAA	TTC
12 or IIT12	4516	AGAAAUCCGUCUUUCAUU GACGGGGCUCUCUGUGUG AGCAUGU	4574	GGCTCTCTGTGTGAGCA TGT	TTT
13 or IIT13	4517	AGAAAUCCGUCUUUCAUU GACGGGCUCUCUGUGUGA GCAUGUG	4575	GCTCTCTGTGTGAGCAT GTG	TTG

14 or IIT14	4518	AGAAAUCCGUCUUUCAUU GACGGUGGCACAGUUGAC AAGGAUG	4576	TGGCACAGTTGACAAGG ATG	TTG
15 or IIT15	4519	AGAAAUCCGUCUUUCAUU GACGGACAAGGAUGAUAA AUCAAUA	4577	ACAAGGATGATAAATCA ATA	TTG
16 or IIT16	4520	AGAAAUCCGUCUUUCAUU GACGGCUAUCAUUUAUGA AUAGCAA	4578	CTATCATTTATGAATAGC AA	TTA
17 or IIT17	4521	AGAAAUCCGUCUUUCAUU GACGGAUGAAUAGCAAUA CUGAAGA	4579	ATGAATAGCAATACTGA AGA	TTT
18 or IIT18	4522	AGAAAUCCGUCUUUCAUU GACGGUGAAUAGCAAUAC UGAAGAA	4580	TGAATAGCAATACTGAA GAA	TTA
19 or IIT19	4523	AGAAAUCCGUCUUUCAUU GACGGAAACAAAAGAUUG CUGUCUC	4581	AAACAAAAGATTGCTGT CTC	TTA
20 or IIT20	4524	AGAAAUCCGUCUUUCAUU GACGGCUGUCUCAAUAUA UCUUAUA	4582	CTGTCTCAATATATCTTA TA	TTG
21 or IIT21	4525	AGAAAUCCGUCUUUCAUU GACGGUAUUUAUUUUUA CCAAAUU	4583	TATTTATTATTTACCAAA TT	TTA
22 or IIT22	4526	AGAAAUCCGUCUUUCAUU GACGGAGGAAGAAAUACU CUUAGAA	4584	AGGAAGAAATACTCTTA GAA	TTC
23 or IIT23	4527	AGAAAUCCGUCUUUCAUU GACGGGAAUAAUUUGGUA AAUAAUA	4585	GAATAATTTGGTAAATA ATA	TTA
24 or IIT24	4528	AGAAAUCCGUCUUUCAUU GACGGGGUAAAUAUAAA UAUAAGA	4586	GGTAAATAATAAATATA AGA	TTT
25 or IIT25	4529	AGAAAUCCGUCUUUCAUU GACGGGUAAAUAUAAAU AUAAGAU	4587	GTAAATAATAAATATAA GAT	TTG
26 or IIT26	4530	AGAAAUCCGUCUUUCAUU GACGGAGACAGCAAUCUU UUGUUUU	4588	AGACAGCAATCTTTTGTT TT	TTG
27 or IIT27	4531	AGAAAUCCGUCUUUCAUU GACGGUGUUUUAAUUUCU UCAGUAU	4589	TGTTTTAATTTCTTCAGT AT	TTT
28 or IIT28	4532	AGAAAUCCGUCUUUCAUU GACGGGUUUUAAUUUCUU CAGUAUU	4590	GTTTTAATTTCTTCAGTA TT	TTT
29 or IIT29	4533	AGAAAUCCGUCUUUCAUU GACGGUUUUAAUUUCUUC AGUAUUG	4591	TTTTAATTTCTTCAGTAT TG	TTG
30 or IIT30	4534	AGAAAUCCGUCUUUCAUU GACGGUAAUUUCUUCAGU AUUGCUA	4592	TAATTTCTTCAGTATTGC TA	TTT
31 or IIT31	4535	AGAAAUCCGUCUUUCAUU GACGGAAUUUCUUCAGUA UUGCUAU	4593	AATTTCTTCAGTATTGCT AT	TTT

32 or IIT32	4536	AGAAAUCCGUCUUUCAUU GACGGAUUUUCUUCAGUAU UGCUAUU	4594	ATTTCTTCAGTATTGCTA TT	TTA
33 or IIT33	4537	AGAAAUCCGUCUUUCAUU GACGGCUUCAGUAUUGCU AUUCAUA	4595	CTTCAGTATTGCTATTCA TA	TTT
34 or IIT34	4538	AGAAAUCCGUCUUUCAUU GACGGUUCAGUAUUGCUA UUCAUAA	4596	TTCAGTATTGCTATTTCAT AA	TTC
35 or IIT35	4539	AGAAAUCCGUCUUUCAUU GACGGAGUAUUGCUAUUC AUAAGAUG	4597	AGTATTGCTATTCATAA ATG	TTC
36 or IIT36	4540	AGAAAUCCGUCUUUCAUU GACGGCUAUUCAUAAAUG AUAGUAA	4598	CTATTCATAAATGATAG TAA	TTG
37 or IIT37	4541	AGAAAUCCGUCUUUCAUU GACGGAUAAAUGAUAGUA AGCUUGC	4599	ATAAATGATAGTAAGCT TGC	TTC
38 or IIT38	4542	AGAAAUCCGUCUUUCAUU GACGGCAUUAUUGAUUUA UCAUCCU	4600	CATTATTGATTTATCATC CT	TTG
39 or IIT39	4543	AGAAAUCCGUCUUUCAUU GACGGUUGAUUUAUCAUC CUUGUCA	4601	TTGATTTATCATCCTTGT CA	TTA
40 or IIT40	4544	AGAAAUCCGUCUUUCAUU GACGGAUUUAUCAUCCUU GUCAACU	4602	ATTTATCATCCTTGTCAA CT	TTG
41 or IIT41	4545	AGAAAUCCGUCUUUCAUU GACGGAUCAUCCUUGUCA ACUGUGC	4603	ATCATCCTTGTCAACTGT GC	TTT
42 or IIT42	4546	AGAAAUCCGUCUUUCAUU GACGGUCAUCCUUGUCAA CUGUGCC	4604	TCATCCTTGTCAACTGTG CC	TTA
43 or IIT43	4547	AGAAAUCCGUCUUUCAUU GACGGUCAACUGUGCCAC AAGCCGC	4605	TCAACTGTGCCACAAGC CGC	TTG
44 or IIT44	4548	AGAAAUCCGUCUUUCAUU GACGGACAUUCAUUCUU CUUAGGC	4606	ACATTCATTTCTTCTTAG GC	TTC
45 or IIT45	4549	AGAAAUCCGUCUUUCAUU GACGGAUUUUCUUCUAGG CAGGCUG	4607	ATTTCTTCTTAGGCAGGC TG	TTC
46 or IIT46	4550	AGAAAUCCGUCUUUCAUU GACGGCUUCUUAAGGCAGG CUGUCUG	4608	CTTCTTAGGCAGGCTGTC TG	TTT
47 or IIT47	4551	AGAAAUCCGUCUUUCAUU GACGGUUCUUAAGGCAGGC UGUCUGU	4609	TTCTTAGGCAGGCTGTCT GT	TTC
48 or IIT48	4552	AGAAAUCCGUCUUUCAUU GACGGUUAAGGCAGGCUGU CUGUCUC	4610	TTAGGCAGGCTGTCTGT CTC	TTC
49 or IIT49	4553	AGAAAUCCGUCUUUCAUU GACGGGGCAGGCUGUCUG UCUCUCU	4611	GGCAGGCTGTCTGTCTCT CT	TTA

50 or IIT50	4554	AGAAAUCCGUCUUUCAUU GACGGUUAUUUUCUACCU UUCUCUC	4612	TTATTTTCTACCTTTCTC TC	TTC
51 or IIT51	4555	AGAAAUCCGUCUUUCAUU GACGGUUUUCUACCUUUC UCUCGAA	4613	TTTTCTACCTTTCTCTCG AA	TTA
52 or IIT52	4556	AGAAAUCCGUCUUUCAUU GACGGUCUACCUUUCUCUC GAAGGU	4614	TCTACCTTTCTCTCGAAG GT	TTT
53 or IIT53	4557	AGAAAUCCGUCUUUCAUU GACGGCUACCUUUCUCUCG AAGGUC	4615	CTACCTTTCTCTCGAAGG TC	TTT
54 or IIT54	4558	AGAAAUCCGUCUUUCAUU GACGGUACCUUUCUCUCG AAGGUCU	4616	TACCTTTCTCTCGAAGGT CT	TTC
55 or IIT55	4559	AGAAAUCCGUCUUUCAUU GACGGCUCUCGAAGGUCU UCUGCCG	4617	CTCTCGAAGGTCTTCTGC CG	TTT
56 or IIT56	4560	AGAAAUCCGUCUUUCAUU GACGGUCUCGAAGGUCUU CUGCCGA	4618	TCTCGAAGGTCTTCTGCC GA	TTC
57 or IIT57	4561	AGAAAUCCGUCUUUCAUU GACGGUGCCGAGUCCUGC AAUAUGA	4619	TGCCGAGTCCTGCAATA TGA	TTC
58 or IIT58	4562	AGAAAUCCGUCUUUCAUU GACGGUAAAAAUCCAAUU AAGAGAG	4620	TAAAAATCCAATTAAGA GAG	TTT

Approximately 16 hours prior to transfection, 25,000 HEK293T cells in DMEM/10%FBS+Pen/Strep (D10 media) were plated into each well of a 96-well plate. On the day of transfection, the cells were 70-90% confluent. For each well to be transfected, a mixture of LIPOFECTAMINE® 2000 transfection reagent (ThermoFisher) and Opti-MEM® reduced serum medium (ThermoFisher) was prepared and incubated at room temperature for 5 minutes (Solution 1). After incubation, the LIPOFECTAMINE® 2000:Opti-MEM® (transfection reagent (ThermoFisher):reduced serum medium (ThermoFisher)) mixture was added to a separate mixture containing nuclease plasmid, RNA guide plasmid, and Opti-MEM® reduced serum medium (ThermoFisher) (Solution 2). In the case of negative controls, the RNA guide plasmid was not included in Solution 2. Solution 1 and 2 were pipette mixed 8 times, then incubated at room temperature for 25 minutes. Following incubation, the Solution 1 and 2 mixture was added dropwise to each well of a 96-well plate containing the cells. 72 hours post transfection, cells were trypsinized by adding TRYPLE™ (recombinant cell-dissociation enzymes; ThermoFisher) to the center of each well and incubating at 37°C for approximately 5 minutes. D10 media was then added to each well and mixed to resuspend cells. The resuspended cells were centrifuged at 500 x g for 10 minutes to obtain a pellet, and the supernatant was discarded. QUICKEXTRACT™ (DNA

extraction solution; Lucigen) extraction reagent was added to each well to lyse pelleted cells. Cells were incubated at 65°C for 15 minutes, 68°C for 15 minutes, and 98°C for 10 minutes.

Samples for NGS were prepared by two rounds of PCR. The first round (PCR1) was used to amplify specific genomic regions depending on the target. Round 2 PCR (PCR2) was performed to add Illumina adapters and indices. Reactions were then pooled and purified by column purification. Sequencing runs were done with a 300 Cycle NEXTSEQ™ (Illumina) 500/550 High Output v2.5 Kit.

As shown in **FIG. 1**, RNA guides 1, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, and 58 all resulted in measurable indel activity, defined as >1% and >0.2% above the background rate for the no-RNA guide control.

RNA guides 4, 8, 55, and 57 resulted in >15% disruption of the cryptic splice site in intron 1 (**FIG. 2A**), where disruption is defined as an insertion or deletion at one or more bases of the cryptic splice site. 97% of the indels generated by RNA guide 4 resulted in disruption of the cryptic splice site in intron 1, where disruption is defined as an insertion or deletion at one or more bases of the cryptic splice site.

RNA guides 12, 46, 47, 48, and 49 resulted in >15% disruption of at least one of 3 TDP-43 binding motifs in intron 1 (**FIG. 2B**), where disruption is defined as an insertion or deletion at one or more bases of a TDP-43 binding motif. 97% of the indels generated by RNA guide 12 resulted in disruption of at least one of 3 TDP-43 binding motifs in intron 1, where disruption is defined as an insertion or deletion at one or more bases of a TDP-43 binding motif.

RNA guides 17 and 18 resulted in >15% disruption of the premature polyadenylation signal in intron 1 (**FIG. 2C**), where disruption is defined as an insertion or deletion at one or more bases of the polyadenylation signal. 88% of the indels generated by RNA guide 17 resulted in disruption of the premature polyadenylation signal at intron 1, where disruption is defined as an insertion or deletion at one or more bases of the premature polyadenylation site. 93% of the indels generated by RNA guide 18 resulted in disruption of the premature polyadenylation signal at intron 1, where disruption is defined as an insertion or deletion at one or more bases of the premature polyadenylation site.

FIG. 3 depicts the positions where each of the RNA guides binds intron 1 of STMN2 relative to the positions of the cryptic splice site, the TDP-43 binding motifs, and the premature polyadenylation signal. The darker grey reflects RNA guides demonstrating indels in greater than 30% of NGS reads, and the lighter grey reflects RNA guides demonstrating indels in less than 30% of NGS read. This Example thus shows that Cas12i2 guides edited intron 1 of STMN2 and were able to disrupt the cryptic splice site, TDP-43 binding motifs, and premature polyadenylation signals.

Example 2 – Targeting of STMN2 Intron 1 by Variant Cas12i2 in SH-SY5Y Cells

This Example describes indel assessment on multiple targets at the *STMN2* gene in a neuroblastoma cell line after transfection with plasmids coding for variant Cas12i2 (SEQ ID NO: 450) and RNA guides targeting the cryptic splice site of intron 1.

The variant Cas12i2 polypeptide and RNA guides 4, 5, 8, 9, 55, 56, 57, and 58 of Table 6 were cloned, purified, and diluted as described in Example 1. Approximately 16 hours prior to transfection, 25,000 SH-SY5Y cells in EMEM:F12/10%FBS+Pen/Strep (EF12-10 media) were plated into each well of a 96-well plate. On the day of transfection, the cells were 70-90% confluent. For each well to be transfected, a mixture of LIPOFECTAMINE® 2000 transfection reagent (ThermoFisher) and Opti-MEM® reduced serum medium (ThermoFisher) was prepared and incubated at room temperature for 5 minutes (Solution 1). After incubation, the LIPOFECTAMINE® 2000:Opti-MEM® (transfection reagent (ThermoFisher):reduced serum medium (ThermoFisher)) mixture was added to a separate mixture containing nuclease plasmid, RNA guide plasmid, and Opti-MEM® reduced serum medium (ThermoFisher) (Solution 2). In the case of negative controls, the RNA guide plasmid was not included in Solution 2. Solution 1 and 2 were pipette mixed 8 times, then incubated at room temperature for 25 minutes. Following incubation, the Solution 1 and 2 mixture was added dropwise to each well of a 96-well plate containing the cells. 72 hours post transfection, cells were trypsinized by adding TRYPLE™ (recombinant cell-dissociation enzymes; ThermoFisher) to the center of each well and incubating at 37°C for approximately 5 minutes. EF12-10 media was then added to each well and mixed to resuspend cells. The resuspended cells were centrifuged at 500 x g for 10 minutes to obtain a pellet, and the supernatant was discarded. QUICKEXTRACT™ (DNA extraction solution; Lucigen) extraction reagent was added to each well to lyse pelleted cells. Cells were incubated at 65°C for 15 minutes, 68°C for 15 minutes, and 98°C for 10 minutes.

Samples for NGS were prepared by two rounds of PCR. The first round (PCR1) was used to amplify specific genomic regions depending on the target. Round 2 PCR (PCR2) was performed to add Illumina adapters and indices. Reactions were then pooled and purified by column purification. Sequencing runs were done with a 300 Cycle NEXTSEQ™ (Illumina) 500/550 High Output v2.5 Kit.

FIG. 4 shows indel activity of the tested RNA guides in SH-SY5Y cells. Guide 4 showed 0.56% splice site motif disruption and 2.0% overall editing; greater than 25% of total edits disrupted the splice site. Guide 5 showed 0.12% splice site motif disruption and 1.5% overall editing; less than 10% of total edits disrupted the splice site. Guide 8 showed 0.62% splice site motif disruption and 2.4% overall editing; greater than 25% of total edits disrupted the splice site. Guide 9 showed 0.34% splice site motif disruption and 3.8% overall editing; less than 10% of total edits disrupted the splice site. Guide 55 showed 2.2% splice site motif disruption and 4.9% overall editing; greater than 40% of total edits disrupted the splice site. Guide 56 showed 2.3% splice site motif disruption and 4.9% overall editing; greater than 45% of total edits disrupted the splice site. Guide 57 showed 0% splice site motif disruption

and 1.6% overall editing. Guide 58 showed 0.49% splice site motif disruption and 3.3% overall editing; greater than 10% of total edits disrupted the splice site.

FIG. 5A is a plot comparing indel activity (% indels) demonstrated in HEK293T cells and SH-SY5Y cells from Example 1 and Example 2, respectively. **FIG. 5B** is a plot comparing splice site motif disruption demonstrated in HEK293T cells and SH-SY5Y cells from Example 1 and Example 2, respectively. As shown in **FIG. 5A**, Guide 55 and Guide 9 demonstrated the highest % indels across the two cell types. Guide 56 demonstrated the highest % indels in SH-SY5Y cells but low % indels in HEK293T cells. Guide 55 resulted in the highest splice site motif disruption in the two cell types as well (**FIG. 5B**).

This Example thus shows that the cryptic splice site of intron 1 of *STMN2* is capable of being targeted by Cas12i2 and multiple RNA guides in multiple cell types.

OTHER EMBODIMENTS

All of the features disclosed in this specification may be combined in any combination. Each feature disclosed in this specification may be replaced by an alternative feature serving the same, equivalent, or similar purpose. Thus, unless expressly stated otherwise, each feature disclosed is only an example of a generic series of equivalent or similar features.

From the above description, one skilled in the art can easily ascertain the essential characteristics of the present disclosure, and without departing from the spirit and scope thereof, can make various changes and modifications of the present disclosure to adapt it to various usages and conditions. Thus, other embodiments are also within the claims.

EQUIVALENTS

While several inventive embodiments have been described and illustrated herein, those of ordinary skill in the art will readily envision a variety of other means and/or structures for performing the function and/or obtaining the results and/or one or more of the advantages described herein, and each of such variations and/or modifications is deemed to be within the scope of the inventive embodiments described herein. More generally, those skilled in the art will readily appreciate that all parameters, dimensions, materials, and configurations described herein are meant to be exemplary and that the actual parameters, dimensions, materials, and/or configurations will depend upon the specific application or applications for which the inventive teachings is/are used. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific inventive embodiments described herein. It is, therefore, to be understood that the foregoing embodiments are presented by way of example only and that, within the scope of the appended claims and equivalents

thereto, inventive embodiments may be practiced otherwise than as specifically described and claimed. Inventive embodiments of the present disclosure are directed to each individual feature, system, article, material, kit, and/or method described herein. In addition, any combination of two or more such features, systems, articles, materials, kits, and/or methods, if such features,
5 systems, articles, materials, kits, and/or methods are not mutually inconsistent, is included within the inventive scope of the present disclosure.

All definitions, as defined and used herein, should be understood to control over dictionary definitions, definitions in documents incorporated by reference, and/or ordinary meanings of the defined terms.

10 All references, patents and patent applications disclosed herein are incorporated by reference with respect to the subject matter for which each is cited, which in some cases may encompass the entirety of the document.

The indefinite articles “a” and “an,” as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to mean “at least one.”

15 The phrase “and/or,” as used herein in the specification and in the claims, should be understood to mean “either or both” of the elements so conjoined, *i.e.*, elements that are conjunctively present in some cases and disjunctively present in other cases. Multiple elements listed with “and/or” should be construed in the same fashion, *i.e.*, “one or more” of the elements so conjoined. Other elements may optionally be present other than the elements specifically
20 identified by the “and/or” clause, whether related or unrelated to those elements specifically identified. Thus, as a non-limiting example, a reference to “A and/or B”, when used in conjunction with open-ended language such as “comprising” can refer, in one embodiment, to A only (optionally including elements other than B); in another embodiment, to B only (optionally including elements other than A); in yet another embodiment, to both A and B (optionally
25 including other elements); etc.

As used herein in the specification and in the claims, “or” should be understood to have the same meaning as “and/or” as defined above. For example, when separating items in a list, “or” or “and/or” shall be interpreted as being inclusive, *i.e.*, the inclusion of at least one, but also including more than one, of a number or list of elements, and, optionally, additional unlisted
30 items. Only terms clearly indicated to the contrary, such as “only one of” or “exactly one of,” or, when used in the claims, “consisting of,” will refer to the inclusion of exactly one element of a number or list of elements. In general, the term “or” as used herein shall only be interpreted as indicating exclusive alternatives (*i.e.* “one or the other but not both”) when preceded by terms of exclusivity, such as “either,” “one of,” “only one of,” or “exactly one of.” “Consisting

essentially of,” when used in the claims, shall have its ordinary meaning as used in the field of patent law.

As used herein in the specification and in the claims, the phrase “at least one,” in reference to a list of one or more elements, should be understood to mean at least one element
5 selected from any one or more of the elements in the list of elements, but not necessarily including at least one of each and every element specifically listed within the list of elements and not excluding any combinations of elements in the list of elements. This definition also allows that elements may optionally be present other than the elements specifically identified within the list of elements to which the phrase “at least one” refers, whether related or unrelated to those
10 elements specifically identified. Thus, as a non-limiting example, “at least one of A and B” (or, equivalently, “at least one of A or B,” or, equivalently “at least one of A and/or B”) can refer, in one embodiment, to at least one, optionally including more than one, A, with no B present (and optionally including elements other than B); in another embodiment, to at least one, optionally including more than one, B, with no A present (and optionally including elements other than A);
15 in yet another embodiment, to at least one, optionally including more than one, A, and at least one, optionally including more than one, B (and optionally including other elements); etc.

It should also be understood that, unless clearly indicated to the contrary, in any methods claimed herein that include more than one step or act, the order of the steps or acts of the method is not necessarily limited to the order in which the steps or acts of the method are recited.

WHAT IS CLAIMED IS:

1. A gene editing system for genetic editing of a stathmin 2 (STMN2) gene,
comprising
 - (i) a Cas12i2 polypeptide or a first nucleic acid encoding the Cas12i2 polypeptide,
wherein the Cas12i2 polypeptide comprises an amino acid sequence at least 95% identical to
SEQ ID NO: 448 and comprises one or more mutations relative to SEQ ID NO: 448; and
 - (ii) an RNA guide or a second nucleic acid encoding the RNA guide, wherein the
RNA guide comprises a spacer sequence specific to a target sequence within an STMN2 gene,
the target sequence being adjacent to a protospacer adjacent motif (PAM) comprising the motif
of 5'-TTN-3', which is located 5' to the target sequence.
2. The gene editing system of claim 1, wherein the one or more mutations in the
Cas12i2 polypeptide are at positions D581, G624, F626, P868, I926, V1030, E1035, and/or
S1046 of SEQ ID NO: 448.
3. The gene editing system of claim 1 or claim 2, wherein the one or more mutations
are amino acid substitutions, which optionally is D581R, G624R, F626R, P868T, I926R,
V1030G, E1035R, S1046G, or a combination thereof.
4. The gene editing system of claim 3, wherein the Cas12i2 polypeptide comprises:
 - (i) mutations at positions D581, D911, I926, and V1030, which optionally are
amino acid substitutions of D581R, D911R, I926R, and V1030G;
 - (ii) mutations at positions D581, I926, and V1030, which optionally are amino
acid substitutions of D581R, I926R, and V1030G;
 - (iii) mutations at positions D581, I926, V1030, and S1046, which optionally are
amino acid substitutions of D581R, I926R, V1030G, and S1046G;
 - (iv) mutations at positions D581, G624, F626, I926, V1030, E1035, and S1046,
which optionally are amino acid substitutions of D581R, G624R, F626R, I926R, V1030G,
E1035R, and S1046G; or
 - (v) mutations at positions D581, G624, F626, P868, I926, V1030, E1035, and
S1046, which optionally are amino acid substitutions of D581R, G624R, F626R, P868T, I926R,
V1030G, E1035R, and S1046G.

5. The gene editing system of claim 1, wherein the Cas12i2 polypeptide comprises the amino acid sequence of SEQ ID NO: 449, 450, 451, 452, or 453, optionally wherein the Cas12i2 polypeptide comprises the amino acid sequence of SEQ ID NO: 450 or 453.
- 5 6. The gene editing system of any one of claims 1-5, which comprises the first nucleic acid encoding the Cas12i2 polypeptide.
7. The gene editing system of claim 6, wherein the first nucleic acid is a messenger RNA (mRNA).
- 10 8. The gene editing system of claim 6, wherein the first nucleic acid is included in a viral vector, which optionally is an adeno-associated viral (AAV) vector.
9. The gene editing system of any one of claims 1-8, wherein the target sequence is
15 within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene.
10. The gene editing system of any one of claims 1-9, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4508, 4512, 4559, and 4561, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4508, 4512, 4559, and
20 4561.
11. The gene editing system of any one of claims 1-9, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562, or the
25 second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.
12. The gene editing system of any one of claims 1-11, wherein the spacer sequence
30 is 20-30-nucleotides in length, optionally wherein the spacer sequence is 20-nucleotides in length.
13. The gene editing system of any one of claims 1-12, wherein the RNA guide comprises the spacer sequence and a direct repeat sequence.
- 35

14. The gene editing system of claim 13, wherein the direct repeat sequence is 23-36-nucleotides in length.

15. The gene editing system of claim 14, wherein the direct repeat sequence is at least 90% identical to any one of SEQ ID NOs: 1-10 or a fragment thereof that is at least 23-nucleotides in length.

16. The gene editing system of claim 15, wherein the direct repeat sequence is any one of SEQ ID NOs: 1-10, or a fragment thereof that is at least 23-nucleotides in length.

17. The gene editing system of claim 16, wherein the direct repeat sequence is 5'-AGAAAUCCGUCUUUCAUUGACGG-3' (SEQ ID NO: 10).

18. The gene editing system of any one of claims 1-17, wherein the system comprises the second nucleic acid encoding the RNA guide.

19. The gene editing system of claim 18, wherein the second nucleic acid encoding the RNA guide is located in a viral vector.

20. The gene editing system of any one of claims 8-19, wherein the viral vector comprises the both the first nucleic acid encoding the Cas12i2 polypeptide and the second nucleic acid encoding the RNA guide.

21. The gene editing system of any one of claims 1-19, wherein the system comprises the first nucleic acid encoding the Cas12i2 polypeptide, which is located on a first vector, and wherein the system comprises the second nucleic acid encoding the RNA guide, which is located on a second vector.

22. The gene editing system of claim 21, wherein the first and second vector are the same vector.

23. The gene editing system of any one of claims 1-22, wherein the system comprises one or more lipid nanoparticles (LNPs), which encompass (i), (ii), or both.

24. The gene editing system of claim 23, wherein the system comprises the LNP, which encompass (i), and wherein the system comprises a viral vector comprising the second nucleic acid encoding the RNA guide; optionally wherein the viral vector is an AAV vector.
- 5 25. The gene editing system of claim 23, wherein the system comprises the LNP, which encompass (ii), and wherein the system comprises a viral vector comprising the first nucleic acid encoding Cas12i2 polypeptide; optionally wherein the viral vector is an AAV vector.
- 10 26. A gene editing system for genetic editing of a stathmin 2 (STMN2) gene, comprising
- (i) a Cas12i polypeptide or a first nucleic acid encoding the Cas12i polypeptide, optionally wherein the Cas12i polypeptide is a Cas12i2 polypeptide; and
- (ii) an RNA guide or a second nucleic acid encoding the RNA guide, wherein the
- 15 RNA guide comprises a spacer sequence specific to a target sequence within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of a STMN2 gene, the target sequence being adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3', which is located 5' to the target sequence.
- 20 27. The gene editing system of 26, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4508, 4512, 4559, and 4561, or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4508, 4512, 4559, and 4561.
- 25 28. The gene editing system of claim 26, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562 or the second nucleic acid encodes an RNA guide comprising any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512, 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.
- 30 29. The gene editing system of any one of claims 26-28, which comprises the first nucleic acid encoding the Cas12i polypeptide.
- 35 30. The gene editing system of claim 29, wherein the first nucleic acid is a messenger RNA (mRNA).

31. The gene editing system of claim 29, wherein the first nucleic acid is included in a viral vector, which optionally is an adeno-associated viral (AAV) vector.
32. The gene editing system of any one of claims 26-31, wherein the spacer sequence is 20-30-nucleotides in length, optionally wherein the spacer sequence is 20-nucleotides in length.
33. The gene editing system of any one of claims 26-32, wherein the RNA guide comprises the spacer sequence and a direct repeat sequence.
34. The gene editing system of claim 33, wherein the direct repeat sequence is 23-36-nucleotides in length.
35. The gene editing system of claim 34, wherein the direct repeat sequence is at least 90% identical to any one of SEQ ID NOs: 1-10 or a fragment thereof that is at least 23-nucleotides in length.
36. The gene editing system of claim 35, wherein the direct repeat sequence is any one of SEQ ID NOs: 1-10, or a fragment thereof that is at least 23-nucleotides in length.
37. The gene editing system of claim 36, wherein the direct repeat sequence is 5'-AGAAAUCCGUCUUUCAUUGACGG-3' (SEQ ID NO: 10).
38. The gene editing system of any one of claims 26-37, wherein the system comprises the second nucleic acid encoding the RNA guide.
39. The gene editing system of claim 38, wherein the second nucleic acid encoding the RNA guide is located in a viral vector.
40. The gene editing system of any one of claims 31-39, wherein the viral vector comprises the both the first nucleic acid encoding the Cas12i polypeptide and the second nucleic acid encoding the RNA guide.
41. The gene editing system of any one of claims 26-40, wherein the system comprises the first nucleic acid encoding the Cas12i polypeptide, which is located on a first

vector, and wherein the system comprises the second nucleic acid encoding the RNA guide, which is located on a second vector.

42. The gene editing system of any one of claims 26-41, wherein the system
5 comprises one or more lipid nanoparticles (LNPs), which encompass (i), (ii), or both.

43. The gene editing system of claim 42, wherein the system comprises the LNP,
which encompass (i), and wherein the system comprises a viral vector comprising the second
nucleic acid encoding the RNA guide; optionally wherein the viral vector is an AAV vector.
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44. The gene editing system of claim 42, wherein the system comprises the LNP,
which encompass (ii), and wherein the system comprises a viral vector comprising the first
nucleic acid encoding Cas12i polypeptide; optionally wherein the viral vector is an AAV vector.

45. A pharmaceutical composition comprising the gene editing system set forth in any
15 one of claims 1-44.

46. A kit comprising the elements (i) and (ii) of the gene editing system set forth in
any one of claims 1-44.
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47. A method for editing a stathmin 2 (STMN2) gene in a cell, the method
comprising contacting a host cell with the gene editing system for editing the STMN2 gene set
forth in any one of claims 1-44 to genetically edit the STMN2 gene in the host cell.

48. The method of claim 47, wherein the host cell is cultured *in vitro*.
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49. The method of claim 47, wherein contacting step is performed by administering
the gene editing system for editing the STMN2 gene to a subject comprising the host cell.

50. A cell comprising a disrupted stathmin 2 (STMN2) gene, wherein the cell
optionally is produced by contacting a host cell with the gene editing system of any one of
claims 1-44 to genetically edit the STMN2 gene in the host cell, thereby disrupting the STMN2
gene.
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51. A method for treating neurodegenerative diseases in a subject, comprising administering to a subject in need thereof a gene editing system for editing a stathmin 2 (STMN2) gene set forth in any one of claims 1-44 or the cell of claim 50.

5 52. The method of claim 51, wherein the subject is a human patient having the neurodegenerative disease, which optionally is amyotrophic lateral sclerosis (ALS).

53. The method of claim 51, wherein the subject is a human patient having the neurodegenerative disease, which optionally is frontotemporal dementia (FTD).

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54. An RNA guide, comprising (i) a spacer sequence that is specific to a target sequence in a stathmin 2 (STMN2) gene, wherein the target sequence is adjacent to a protospacer adjacent motif (PAM) comprising the motif of 5'-TTN-3', which is located 5' to the target sequence; and (ii) a direct repeat sequence.

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55. The RNA guide of claim 54, wherein the spacer sequence is 20-30-nucleotides in length, optionally 20-nucleotides in length.

56. The RNA guide of claim 54 or claim 55, wherein the direct repeat sequence is 23-
20 36-nucleotides in length, optionally 23-nucleotides in length.

57. The RNA guide of any one of claims 54-56, wherein the target sequence is within exon 1, exon 2, exon 3, exon 4, exon 5, exon 6, exon 7, or an intron of the STMN2 gene.

25 58. The RNA guide of any one of claims 54-57, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4508, 4512, 4559, and 4561.

59. The RNA guide of any one of claims 54-57, wherein the RNA guide comprises the sequence of any one of SEQ ID NOs: 4505, 4506, 4507, 4508, 4509, 4510, 4511, 4512,
30 4513, 4514, 4515, 4554, 4555, 4556, 4557, 4558, 4559, 4560, 4561, and 4562.

60. The RNA guide of any one of claims 54-59, wherein the direct repeat sequence is at least 90% identical to any one of SEQ ID NOs: 1-10 or a fragment thereof that is at least 23-nucleotides in length.

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61. The RNA guide of claim 60, wherein the direct repeat sequence is any one of SEQ ID NOs: 1-10, or a fragment thereof that is at least 23-nucleotides in length.

62. The RNA guide of claim 61, wherein the direct repeat sequence is 5'-
5 AGAAAUCCGUCUUUCAUUGACGG-3' (SEQ ID NO: 10).