EXCISION OF EXON 53 FOR TREATMENT OF DUCHENNE MUSCULAR DYSTROPHY

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of priority of US Provisional Patent Application No. 63/559,662 filed February 29, 2024, and U.S. Provisional Patent Application No. 63/750,143 filed January 27, 2025, both of which are incorporated by reference herein in their entireties for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on February 21, 2024, is named 01245-0061-60US.xml and is 4,327,739 bytes in size.

INTRODUCTION AND SUMMARY

[0003] Muscular dystrophies (MD) are a group of more than 30 genetic diseases characterized by progressive weakness and degeneration of the skeletal muscles that control movement. Duchenne muscular dystrophy (DMD) is one of the most severe forms of MD that affects approximately 1 in 5000 boys and is characterized by progressive muscle weakness and premature death. Cardiomyopathy and heart failure are common, incurable and lethal features of DMD. The disease is caused by mutations in the gene encoding dystrophin (*DMD*), which result in loss of expression of dystrophin, causing muscle membrane fragility and progressive muscle wasting.

[0004] CRISPR-based genome editing can provide sequence-specific cleavage of genomic DNA using a Cas9 and a guide RNA. For example, a nucleic acid encoding the Cas9 enzyme and a nucleic acid encoding for the appropriate guide RNA can be provided on separate vectors or together on a single vector and administered *in vivo* or *in vitro* to knockout or correct a genetic mutation, for example. The approximately 20 nucleotides at the 5′ end of the guide RNA serves as the guide or spacer sequence that can be any sequence complementary to one strand of a genomic target location that has an adjacent protospacer adjacent motif (PAM). The PAM sequence is a short sequence adjacent to the Cas9 nuclease cut site that the Cas9 molecule requires for appropriate binding. The nucleotides 3’ of the guide or spacer sequence of the guide RNA serve as a scaffold sequence for interacting with Cas9. When a guide RNA and a Cas9 are expressed, the guide RNA will bind to Cas9 and direct it to the sequence complementary to the guide sequence, where it will then initiate a double-stranded break (DSB). To repair these breaks, cells typically use the mechanism of non-homologous end joining (NHEJ). *See*, e.g., Kumar et al. (2018) Front. Mol. Neurosci. Vol. 11, Article 413.

[0005] While gene editing strategies using systems (e.g., CRISPR) for treating DMD have been previously explored, these strategies have focused primarily on either: a) cutting at multiple different sites to excise large portions (e.g., one or more exons) of the dystrophin gene (see, e.g., Ousterout et

al., 2015, Nat Commun. 6:6244) using *Streptococcus pyogenes* Cas9 protein; or b) cutting in a single site to introduce indels that either result in a frame-shifting mutation and/or that destroy a splice acceptor/donor site in the dystrophin gene (see, e.g., Amoassi et al., 2018, Science, 362(6410):86-91). However, there remains a need for additional and alternative effective gene editing strategies for treating diseases like DMD.

[0006] Provided herein are compositions and methods for treating DMD utilizing Cas proteins such as *Staphylococcus aureus* (SaCas9) and *Staphylococcus lugdunensis* (SluCas9). In some embodiments, pairs of guide RNAs that excise all or a portion of exon 53 of the DMD gene are provided. In some embodiments, such a pair of guide RNAs is encoded on a single nucleic acid molecule.

[0007] Accordingly, the following non-limiting embodiments are provided.

[0008] Embodiment 1 is a composition comprising one or more guide RNAs or a nucleic acid encoding one or more guide RNAs, wherein the one or more guide RNAs comprise i) a guide sequence of any one of the guide sequences shown in **Tables 1A or 1C**; ii) at least 16, 17, 18, 19, or 20 contiguous nucleotides of any one of the guide sequences shown in **Tables 1A or 1C**; iii) a guide sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of the guide sequences shown in **Tables 1A or 1C**; or iv) a pair of guide RNAs comprising any of the guide sequence pairs shown in **Table 1D**, optionally further comprising a *Staphylococcus lugdunensis* Cas9 (SluCas9) or a nucleic acid encoding a SluCas9.

[0009] Embodiment 2 is a composition comprising a first guide RNA and a second guide RNA, wherein

a. the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and

b. the second guide RNA is selected from any one of SEQ ID NOs: 88-143.

[0010] Embodiment 3 is a composition comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprise or consist of a first and a second guide sequence selected from any of the following pairs of first and second guide sequences:

a. SEQ ID NOs: 88 and 1; 88 and 2; 88 and 3; 88 and 4; 88 and 5; 88 and 6; 88 and 7; 88 and 8; 88 and 9; 88 and 10; 88 and 11; 88 and 12; 88 and 13; 88 and 14; 88 and 15; 88 and 16; 88 and 17; 88 and 18; 88 and 19; 88 and 20; 88 and 21; 88 and 22; 88 and 23; 88 and 24; 88 and 25; 88 and 26; 88 and 27; 88 and 28; 88 and 29; 88 and 30; 88 and 31; 88 and 32; 88 and 33; 88 and 34; 88 and 35; 88 and 36; 88 and 37; 88 and 38; 88 and 39; 88 and 40; 88 and 41; 88 and 42; 88 and 43; 88 and 44; 88 and 45; 88 and 46; 88 and 47; 88 and 48; 88 and 49; 88 and 50; 88 and 51; 88 and 52; 88 and 53; 88 and 54; 88 and 55; 88 and 56; 88 and 57; 88 and 58; 88 and 59; 88 and 60; 88 and 61; 88 and 62; 88 and 63; 88 and 64; 89 and 1; 89 and 2; 89 and 3; 89 and 4; 89 and 5; 89 and 6; 89 and 7; 89 and 8; 89 and 9; 89 and 10; 89 and 11; 89 and 12; 89 and 13; 89 and 14; 89 and 15; 89 and 16; 89 and 17; 89

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b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

[0011] Embodiment 4 is a composition comprising one or more nucleic acid molecules encoding:

a. a *Staphylococcus lugdunensis* Cas9 (SluCas9); and

b. at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first guide sequence and a second guide sequence selected from any of the pairs of guide sequences shown in Table 1D.

[0012] Embodiment 5 is a composition comprising:

a. a single nucleic acid molecule comprising:

i. a nucleic acid encoding *Staphylococcus lugdunensis* (SluCas9) and at least one, at least two, or at least three guide RNAs; or

ii. a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

iii. a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Table 1D**, and further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence; or

b. two nucleic acid molecules comprising:

i. a first nucleic acid encoding SluCas9; and a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. from one to six guide RNAs;

ii. a first nucleic acid encoding SluCas9 and

1. at least one, at least two, or at least three guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. from one to six guide RNAs;

iii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

iv. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from the pairs of guide sequences shown in **Table 1D**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

[0013] Embodiment 6 is a composition comprising a single nucleic acid molecule encoding at least one pair of guide RNAs and a Cas9, wherein the single nucleic acid molecule comprises:

a. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences shown in Table 1D; and a second nucleic acid encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9); or

b. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42; and a second nucleic acid encoding a SluCas9.

[0014] Embodiment 7 is a composition comprising a first and a second nucleic acid molecule, wherein the first nucleic acid molecule encodes a *Staphylococcus lugdunensis* (SluCas9) endonuclease and optionally a first or a first and second guide RNA, and the second nucleic acid molecule comprises a first or a first and second guide RNA, wherein the first guide RNA comprises a first guide sequence and the second guide RNA comprises a second guide sequence selected from any one the following pairs of first and second guide sequences:

a. any one of the pairs of first and second guide sequences shown in Table 1D; or

b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

[0015] Embodiment 8 is a composition comprising one or more nucleic acid molecules encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9) and at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide RNA, and wherein the first guide RNA targets a sequence in intron 53 of a DMD gene and the second guide RNA targets a sequence in intron 52 of the DMD gene.

[0016] Embodiment 9 is the composition of any one of embodiments 1-8, comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising at least a portion of exon 53 of the DMD gene.

[0017] Embodiment 10 is the composition of any one of embodiments 1-9, comprising at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first

and a second guide sequence selected from any one of the following pairs of first and second guide sequences:

a. any one of the pairs of first and second guide sequences shown in Table 1D; or

b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

[0018] Embodiment 11 is the composition of any one of embodiments 1-10, wherein:

i) the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 2;

ii) the first guide RNA comprises the sequence of SEQ ID NO: 115, and the second guide RNA comprises the sequence of SEQ ID NO: 3; or

iii) the first guide RNA comprises the sequence of SEQ ID NO: 113, and the second guide RNA comprises the sequence of SEQ ID NO: 3.

[0019] Embodiment 12 is a composition comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of exon 53 of the DMD gene, and wherein

i. the fragment comprises a splice donor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice donor site, and a second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice donor site; or

ii. the fragment comprises a splice acceptor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice acceptor site, and a

second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice acceptor site.

[0020] Embodiment 13 is the composition of embodiment 12, wherein

i. the first guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice acceptor site, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice acceptor site; or

ii. the first guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice donor site, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice donor site.

[0021] Embodiment 14 is the composition of embodiment 12 or embodiment 13, wherein

a. the fragment of the DMD gene comprises a splice donor site and further comprises a portion of intron 53 and an adjoining portion of exon 53 of the DMD gene; or

b. the fragment of the DMD gene comprises a splice acceptor site and further comprises a portion of exon 53 and an adjoining portion of intron 52 of the DMD gene.

[0022] Embodiment 15 is the composition of any one of embodiments 12-14, wherein

a. the first guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 1-200 of SEQ ID NO: 144, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 201-400 of SEQ ID NO: 144; or

b. the first guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 1-200 of SEQ ID NO: 145, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 201-400 of SEQ ID NO: 145.

[0023] Embodiment 16 is the composition of any one of embodiments 12-15, further comprising a SluCas9 or a nucleic acid encoding a SluCas9.

[0024] Embodiment 17 is a composition comprising one or more guide RNAs or a nucleic acid encoding one or more guide RNAs, wherein the one or more guide RNAs comprise i) a guide sequence of any one of the guide sequences shown in **Tables 1A-1C**; ii) at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of any one of the guide sequences shown in **Tables 1A-1C**; iii) a guide sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of the guide sequences shown in **Tables 1A-1C**; or iv) a pair of guide RNAs comprising any two of the guide sequence pairs shown in **Tables 1E or 1F**; optionally further comprising a SluCas9 or a nucleic acid encoding a SluCas9.

[0025] Embodiment 18 is a composition comprising a first guide RNA and a second guide RNA, wherein

a. the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and the second guide RNA is selected from any one of SEQ ID NOs: 65-87; or

b. the first guide RNA is selected from any one of SEQ ID NOs: 65-87; and the second guide RNA is selected from any one of SEQ ID NOs: 88-143.

[0026] Embodiment 19 is a composition comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprise or consist of a first and a second guide sequence selected from any of the following pairs of first and second guide sequences:

a. SEQ ID NOs: 1 and 65; 1 and 66; 1 and 67; 1 and 68; 1 and 69; 1 and 70; 1 and 71; 1 and 72; 1 and 73; 1 and 74; 1 and 75; 1 and 76; 1 and 77; 1 and 78; 1 and 79; 1 and 80; 1 and 81; 1 and 82; 1 and 83; 1 and 84; 1 and 85; 1 and 86; 1 and 87; 2 and 65; 2 and 66; 2 and 67; 2 and 68; 2 and 69; 2 and 70; 2 and 71; 2 and 72; 2 and 73; 2 and 74; 2 and 75; 2 and 76; 2 and 77; 2 and 78; 2 and 79; 2 and 80; 2 and 81; 2 and 82; 2 and 83; 2 and 84; 2 and 85; 2 and 86; 2 and 87; 3 and 65; 3 and 66; 3 and 67; 3 and 68; 3 and 69; 3 and 70; 3 and 71; 3 and 72; 3 and 73; 3 and 74; 3 and 75; 3 and 76; 3 and 77; 3 and 78; 3 and 79; 3 and 80; 3 and 81; 3 and 82; 3 and 83; 3 and 84; 3 and 85; 3 and 86; 3 and 87; 4 and 65; 4 and 66; 4 and 67; 4 and 68; 4 and 69; 4 and 70; 4 and 71; 4 and 72; 4 and 73; 4 and 74; 4 and 75; 4 and 76; 4 and 77; 4 and 78; 4 and 79; 4 and 80; 4 and 81; 4 and 82; 4 and 83; 4 and 84; 4 and 85; 4 and 86; 4 and 87; 5 and 65; 5 and 66; 5 and 67; 5 and 68; 5 and 69; 5 and 70; 5 and 71; 5 and 72; 5 and 73; 5 and 74; 5 and 75; 5 and 76; 5 and 77; 5 and 78; 5 and 79; 5 and 80; 5 and 81; 5 and 82; 5 and 83; 5 and 84; 5 and 85; 5 and 86; 5 and 87; 6 and 65; 6 and 66; 6 and 67; 6 and 68; 6 and 69; 6 and 70; 6 and 71; 6 and 72; 6 and 73; 6 and 74; 6 and 75; 6 and 76; 6 and 77; 6 and 78; 6 and 79; 6 and 80; 6 and 81; 6 and 82; 6 and 83; 6 and 84; 6 and 85; 6 and 86; 6 and 87; 7 and 65; 7 and 66; 7 and 67; 7 and 68; 7 and 69; 7 and 70; 7 and 71; 7 and 72; 7 and 73; 7 and 74; 7 and 75; 7 and 76; 7 and 77; 7 and 78; 7 and 79; 7 and 80; 7 and 81; 7 and 82; 7 and 83; 7 and 84; 7 and 85; 7 and 86; 7 and 87; 8 and 65; 8 and 66; 8 and 67; 8 and 68; 8 and 69; 8 and 70; 8 and 71; 8 and 72; 8 and 73; 8 and 74; 8 and 75; 8 and 76; 8 and 77; 8 and 78; 8 and 79; 8 and 80; 8 and 81; 8 and 82; 8 and 83; 8 and 84; 8 and 85; 8 and 86; 8 and 87; 9 and 65; 9 and 66; 9 and 67; 9 and 68; 9 and 69; 9 and 70; 9 and 71; 9 and 72; 9 and 73; 9 and 74; 9 and 75; 9 and 76; 9 and 77; 9 and 78; 9 and 79; 9 and 80; 9 and 81; 9 and 82; 9 and 83; 9 and 84; 9 and 85; 9 and 86; 9 and 87; 10 and 65; 10 and 66; 10 and 67; 10 and 68; 10 and 69; 10 and 70; 10 and 71; 10 and 72; 10 and 73; 10 and 74; 10 and 75; 10 and 76; 10 and 77; 10 and 78; 10 and 79; 10 and 80; 10 and 81; 10 and 82; 10 and 83; 10 and 84; 10 and 85; 10 and 86; 10 and 87; 11 and 65; 11 and 66; 11 and 67; 11 and 68; 11 and 69; 11 and 70; 11 and 71; 11 and 72; 11 and 73; 11 and 74; 11 and 75; 11 and 76; 11 and 77; 11 and 78; 11 and 79; 11 and 80; 11 and 81; 11 and 82; 11 and 83; 11 and 84; 11 and 85; 11 and 86; 11 and 87; 12 and 65; 12 and 66; 12 and 67; 12 and 68; 12 and 69; 12 and 70; 12 and 71; 12 and 72; 12 and 73; 12 and 74; 12 and 75; 12 and 76; 12 and 77; 12 and 78; 12 and 79; 12 and 80; 12 and 81; 12 and 82; 12 and 83; 12 and 84; 12 and 85; 12 and 86; 12 and 87; 13 and 65; 13 and 66; 13 and 67; 13 and 68; 13

and 69; 13 and 70; 13 and 71; 13 and 72; 13 and 73; 13 and 74; 13 and 75; 13 and 76; 13 and 77; 13 and 78; 13 and 79; 13 and 80; 13 and 81; 13 and 82; 13 and 83; 13 and 84; 13 and 85; 13 and 86; 13 and 87; 14 and 65; 14 and 66; 14 and 67; 14 and 68; 14 and 69; 14 and 70; 14 and 71; 14 and 72; 14 and 73; 14 and 74; 14 and 75; 14 and 76; 14 and 77; 14 and 78; 14 and 79; 14 and 80; 14 and 81; 14 and 82; 14 and 83; 14 and 84; 14 and 85; 14 and 86; 14 and 87; 15 and 65; 15 and 66; 15 and 67; 15 and 68; 15 and 69; 15 and 70; 15 and 71; 15 and 72; 15 and 73; 15 and 74; 15 and 75; 15 and 76; 15 and 77; 15 and 78; 15 and 79; 15 and 80; 15 and 81; 15 and 82; 15 and 83; 15 and 84; 15 and 85; 15 and 86; 15 and 87; 16 and 65; 16 and 66; 16 and 67; 16 and 68; 16 and 69; 16 and 70; 16 and 71; 16 and 72; 16 and 73; 16 and 74; 16 and 75; 16 and 76; 16 and 77; 16 and 78; 16 and 79; 16 and 80; 16 and 81; 16 and 82; 16 and 83; 16 and 84; 16 and 85; 16 and 86; 16 and 87; 17 and 65; 17 and 66; 17 and 67; 17 and 68; 17 and 69; 17 and 70; 17 and 71; 17 and 72; 17 and 73; 17 and 74; 17 and 75; 17 and 76; 17 and 77; 17 and 78; 17 and 79; 17 and 80; 17 and 81; 17 and 82; 17 and 83; 17 and 84; 17 and 85; 17 and 86; 17 and 87; 18 and 65; 18 and 66; 18 and 67; 18 and 68; 18 and 69; 18 and 70; 18 and 71; 18 and 72; 18 and 73; 18 and 74; 18 and 75; 18 and 76; 18 and 77; 18 and 78; 18 and 79; 18 and 80; 18 and 81; 18 and 82; 18 and 83; 18 and 84; 18 and 85; 18 and 86; 18 and 87; 19 and 65; 19 and 66; 19 and 67; 19 and 68; 19 and 69; 19 and 70; 19 and 71; 19 and 72; 19 and 73; 19 and 74; 19 and 75; 19 and 76; 19 and 77; 19 and 78; 19 and 79; 19 and 80; 19 and 81; 19 and 82; 19 and 83; 19 and 84; 19 and 85; 19 and 86; 19 and 87; 20 and 65; 20 and 66; 20 and 67; 20 and 68; 20 and 69; 20 and 70; 20 and 71; 20 and 72; 20 and 73; 20 and 74; 20 and 75; 20 and 76; 20 and 77; 20 and 78; 20 and 79; 20 and 80; 20 and 81; 20 and 82; 20 and 83; 20 and 84; 20 and 85; 20 and 86; 20 and 87; 21 and 65; 21 and 66; 21 and 67; 21 and 68; 21 and 69; 21 and 70; 21 and 71; 21 and 72; 21 and 73; 21 and 74; 21 and 75; 21 and 76; 21 and 77; 21 and 78; 21 and 79; 21 and 80; 21 and 81; 21 and 82; 21 and 83; 21 and 84; 21 and 85; 21 and 86; 21 and 87; 22 and 65; 22 and 66; 22 and 67; 22 and 68; 22 and 69; 22 and 70; 22 and 71; 22 and 72; 22 and 73; 22 and 74; 22 and 75; 22 and 76; 22 and 77; 22 and 78; 22 and 79; 22 and 80; 22 and 81; 22 and 82; 22 and 83; 22 and 84; 22 and 85; 22 and 86; 22 and 87; 23 and 65; 23 and 66; 23 and 67; 23 and 68; 23 and 69; 23 and 70; 23 and 71; 23 and 72; 23 and 73; 23 and 74; 23 and 75; 23 and 76; 23 and 77; 23 and 78; 23 and 79; 23 and 80; 23 and 81; 23 and 82; 23 and 83; 23 and 84; 23 and 85; 23 and 86; 23 and 87; 24 and 65; 24 and 66; 24 and 67; 24 and 68; 24 and 69; 24 and 70; 24 and 71; 24 and 72; 24 and 73; 24 and 74; 24 and 75; 24 and 76; 24 and 77; 24 and 78; 24 and 79; 24 and 80; 24 and 81; 24 and 82; 24 and 83; 24 and 84; 24 and 85; 24 and 86; 24 and 87; 25 and 65; 25 and 66; 25 and 67; 25 and 68; 25 and 69; 25 and 70; 25 and 71; 25 and 72; 25 and 73; 25 and 74; 25 and 75; 25 and 76; 25 and 77; 25 and 78; 25 and 79; 25 and 80; 25 and 81; 25 and 82; 25 and 83; 25 and 84; 25 and 85; 25 and 86; 25 and 87; 26 and 65; 26 and 66; 26 and 67; 26 and 68; 26 and 69; 26 and 70; 26 and 71; 26 and 72; 26 and 73; 26 and 74; 26 and 75; 26 and 76; 26 and 77; 26 and 78; 26 and 79; 26 and 80; 26 and 81; 26 and 82; 26 and 83; 26 and 84; 26 and 85; 26 and 86; 26 and 87; 27 and 65; 27 and 66; 27 and 67; 27 and 68; 27 and 69; 27 and 70; 27 and 71; 27 and 72; 27 and 73; 27 and 74; 27 and 75; 27 and 76; 27 and 77; 27 and 78; 27 and 79; 27

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c. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35

and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

d. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

[0027] Embodiment 20 is a composition comprising one or more nucleic acid molecules encoding

a. a *Staphylococcus lugdunensis* Cas9 (SluCas9); and

b. at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first guide sequence and a second guide sequence selected from any of the pairs of guide sequences shown in Tables 1E or 1F.

[0028] Embodiment 21 is a composition comprising:

a. a single nucleic acid molecule comprising:

i. a nucleic acid encoding *Staphylococcus lugdunensis* (SluCas9) and at least one, at least two, or at least three guide RNAs; or

ii. a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

iii. a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Tables 1E or 1F**, and further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence; or

b. two nucleic acid molecules comprising:

i. a first nucleic acid encoding SluCas9; and a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. from one to six guide RNAs;

ii. a first nucleic acid encoding SluCas9 and

1. at least one, at least two, or at least three guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or

2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or

3. from one to six guide RNAs;

iii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

iv. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a guide sequence selected from the pairs of guide sequences shown in **Tables 1E or 1F**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

[0029] Embodiment 22 is a composition comprising a single nucleic acid molecule encoding at least one pair of guide RNAs and a Cas9, wherein the single nucleic acid molecule comprises:

a. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences shown in Table 1E or 1F; and a second nucleic acid encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9);

b. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; and a second nucleic acid encoding a SluCas9; or

c. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and

85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81; and a second nucleic acid encoding a SluCas9.

[0030] Embodiment 23 is a composition comprising a first and a second nucleic acid molecule, wherein the first nucleic acid molecule encodes a *Staphylococcus lugdunensis* Cas9 (SluCas9) and optionally a first or a first and second guide RNA, and the second nucleic acid molecule comprises a first or a first and second guide RNA, wherein the first guide RNA comprises a first guide sequence and the second guide RNA comprises a second guide sequence selected from any one the following pairs of first and second guide sequences:

a. any one of the pairs of first and second guide sequences shown in Tables 1E or 1F;

b. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

c. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and

84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

[0031] Embodiment 24 is a composition comprising one or more nucleic acid molecules encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9) and at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide RNA, wherein the first guide RNA targets a sequence in intron 53 of a DMD gene and the second guide RNA targets a sequence in exon 53 of the DMD gene, or the first guide RNA targets a sequence in exon 53 of a DMD gene and the second guide RNA targets a sequence in intron 52 of the DMD gene.

[0032] Embodiment 25 is the composition of any one of embodiments 12-24, comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of the DMD gene, wherein the fragment comprises a splice donor site or a splice acceptor site, and optionally wherein the fragment is between 5 and 400 nucleotides in length.

[0033] Embodiment 26 is the composition of any one of embodiments 12-15 or 25, wherein the excised fragment of the DMD gene does not comprise an entire exon of the DMD gene.

[0034] Embodiment 27 is the composition of any one of embodiments 12-26, comprising at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first and a second guide sequence selected from any one of the following pairs of first and second guide sequences:

a. any one of the pairs of first and second guide sequences shown in Tables 1E or 1F;

b. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35

and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

c. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

[0035] Embodiment 28 is the composition of any one of embodiments 12-26, wherein:

i) the first guide RNA comprises the sequence of SEQ ID NO: 70 and the second guide RNA comprises the sequence of SEQ ID NO: 2;

ii) the first guide RNA comprises the sequence of SEQ ID NO: 76, and the second guide RNA comprises the sequence of SEQ ID NO: 2; or

iii) the first guide RNA comprises the sequence of SEQ ID NO: 115, and the second guide RNA comprises the sequence of SEQ ID NO: 70.

[0036] Embodiment 29 is the composition of any one of the preceding embodiments, comprising at least one pair of guide RNAs, wherein once expressed in vitro or in vivo in combination with a SluCas9 endonuclease, the at least one pair of guide RNAs (i) excises exon 53 of a DMD gene, (ii) excises a fragment of the DMD gene comprising a portion of intron 53 and an adjoining portion of exon 53, wherein the excised fragment of the DMD gene comprises a splice donor site, or (iii) excises a fragment of the DMD gene comprising a portion of exon 53 and an adjoining portion of intron 52,

wherein the excised fragment of the DMD gene comprises a splice acceptor site; wherein the size of the excised fragment of the DMD gene is between 5 and 400 nucleotides in length.

[0037] Embodiment 30 is the composition of any one of embodiments 12-15 or 25-29, wherein the size of the excised fragment of the DMD gene is between 5 and 400, 5 and 375, 5 and 350, 5 and 325, 5 and 300, 5 and 275, 5 and 250, 5 and 225, 5 and 200, 5 and 175, 5 and 150, 5 and 125, 5 and 100, 20 and 400, 20 and 375, 20 and 350, 20 and 325, 20 and 300, 20 and 275, 20 and 250, 20 and 225, 20 and 200, 20 and 175, 20 and 150, 20 and 125, 20 and 100, 50 and 400, 50 and 375, 50 and 350, 50 and 325, 50 and 300, 50 and 275, 50 and 250, 50 and 225, 50 and 200, 50 and 175, 50 and 150, 50 and 125, or 50 and 100 nucleotides in length.

[0038] Embodiment 31 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs is an sgRNA, the first and/or second guide RNA is an sgRNA, or the at least one pair of guide RNAs is a pair of sgRNAs.

[0039] Embodiment 32 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs is modified, the first and/or second guide RNA is modified, or the at least one pair of guide RNAs is a pair of modified guide RNAs.

[0040] Embodiment 33 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs, the first and/or second guide RNA, the at least one pair of guide RNAs, or the nucleic acid is in a vector.

[0041] Embodiment 34 is the composition of embodiment 33, wherein the vector is a lipid nanoparticle or a liposome.

[0042] Embodiment 35 is the composition of embodiment 33, wherein the vector is a viral vector.

[0043] Embodiment 36 is the composition of embodiment 35, wherein the viral vector is an AAV vector.

[0044] Embodiment 37 is the composition of embodiment 36, wherein the AAV vector is an AAV9 vector.

[0045] Embodiment 38 is the composition of any one of the preceding embodiments, wherein a promoter for the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs is hU6c.

[0046] Embodiment 39 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs is a guide RNA for SluCas9, the first and/or second guide RNA is a guide RNA for SluCas9, or the at least one pair of guide RNAs is a pair of guide RNAs for SluCas9; and the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs comprise a scaffold comprising the sequence of any one of SEQ ID NOs: 600, 601, or 900-917.

[0047] Embodiment 40 is the composition of the immediately preceding embodiment, wherein the scaffold comprises the sequence of SEQ ID NO: 901.

[0048] Embodiment 41 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs is in an AAV vector, wherein the vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first guide RNA scaffold sequence; the reverse complement of a nucleic acid encoding a first guide RNA sequence; the reverse complement of a promoter for expression of the nucleic acid encoding the first guide RNA sequence; a promoter for expression of a nucleic acid encoding SluCas9; a nucleic acid encoding a SluCas9; a polyadenylation sequence; a promoter for expression of a second guide RNA sequence in the same direction as the promoter for SluCas9; a second RNA guide sequence; and a second guide RNA scaffold sequence.

[0049] Embodiment 42 is the composition of any one of the preceding embodiments, wherein the one or more guide RNAs, or the first and/or second guide RNA, is no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 nucleotides in length.

[0050] Embodiment 43 is a method of treating Duchenne Muscular Dystrophy (DMD), the method comprising delivering to a cell the composition of any one of embodiments 1-42.

[0051] Embodiment 44 is a method of excising a DMD gene or a fragment of the DMD gene, the method comprising delivering to a cell the composition of any one of embodiments 1-42, wherein the size of the excised portion of the DMD gene is less than about 400 nucleotides.

[0052] Embodiment 45 is a composition comprising:

a) a pair of guide RNA molecules or a nucleic acid encoding a pair of RNA molecules, wherein the first guide RNA targets a region upstream of a splice acceptor site or a splice donor site in a DMD gene and wherein the second guide RNA targets a region downstream of a splice acceptor site or a splice donor site in the DMD gene; and

b) an endonuclease or a nucleic acid encoding an endonuclease, optionally wherein the endonuclease is a *Staphylococcus lugdunensis* Cas9 (SluCas9).

[0053] Embodiment 46 is the composition of embodiment 45, wherein the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an exon of the DMD gene.

[0054] Embodiment 47 is the composition of embodiment 45, wherein the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an intron of the DMD gene.

[0055] Embodiment 48 is the composition of embodiment 45, wherein the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an exon of the DMD gene.

[0056] Embodiment 49 is the composition of embodiment 45, wherein the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an intron of the DMD gene.

[0057] Embodiment 50 is the composition of any one of embodiments 45-49, wherein the splice acceptor site or splice donor site is in intron 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, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, or 78 of the DMD gene.

[0058] Embodiment 51 is the composition of any one of embodiments 45-50, wherein the splice acceptor site or splice donor site is in intron 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 or 57 of the DMD gene.

[0059] Embodiment 52 is the composition of any one of embodiments 45-51, wherein the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides upstream of the splice acceptor or splice donor site.

[0060] Embodiment 53 is the composition of any one of embodiments 45-52, wherein the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides downstream of the splice acceptor or splice donor site.

[0061] Embodiment 54 is a method of excising a fragment of a DMD gene, the method comprising delivering to a cell the composition of any one of embodiments 45-53, wherein the pair of guide RNAs and the endonuclease excise a fragment of the DMD gene comprising the splice acceptor site or the splice donor site, wherein the fragment is between 3 and 400 nucleotides in length.

[0062] Embodiment 55 is the method of embodiment 54, wherein the excised fragment of the DMD gene comprises a splice acceptor site.

[0063] Embodiment 56 is the method of embodiment 54, wherein the excised fragment of the DMD gene comprises a splice donor site.

[0064] Embodiment 57 is the method of any one of embodiments 54-56, wherein the excised fragment is between 3-200, 3-150, 3-100, 3-50, 30-250, 30-200, 30-150, 30-100, 30-50, 75-250, 75-200, 75-150, 75-100, 100-250, 100-200, 100-150, 150-250, 150-200, 200-250, 250-400, 300-400, or 350-400 nucleotides in length.

DESCRIPTION OF FIGURES

[0065] **Figure 1** is a simplified schematic depicting the approximate excision fragment sizes for 24 tested guide pairs targeting intron 52 and intron 53 of the dystrophin gene, for excision of exon 53.

[0066] **Figure 2** shows the editing frequency of selected SluCas9 guide pairs targeting intron 52 and intron 53 of the dystrophin gene, for excision of exon 53 in immortalized HsMM ΔE52 cells. Each bar represents a sgRNA pair and the bar height depicts the average frequency of deletion of the sequence between the sgRNA pair targets, as determined by qPCR. Error bars denote the standard deviation for each sample group.

[0067] **Figures 3A and 3B** show dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected SluCas9 sgRNA pairs. **Figure 3A** shows detection of dystrophin restoration in treated samples using a Jess protein assay. **Figure 3B** shows dystrophin restoration in immortalized HsMM

ΔE52 cells treated with selected SluCas9 sgRNA pairs that result in either precise reframing deletion or deletion of the entire exon 53 of the dystrophin gene. Each bar represents a sgRNA pair and the bar height depicts normalized dystrophin protein signal of the sample as a percentage of normalized dystrophin expression in untreated WT13 cells. Error bars denote the standard deviation for each sample group. Samples treated with precise deletion or exon deletion pairs show approximately 30-50% deletion.

[0068] **Figure 4** is a set of three simplified schematics depicting guide pairing for three different editing goals: (top) exon deletion (e.g., deletion of exon 53 of the DMD gene using at least one guide pair selected from the guide pairs of **Table 1D**), (middle) splice acceptor deletion (e.g., skipping of exon 53 of the DMD gene using at least one guide pair selected from the guide pairs of **Table 1E**), and (bottom) splice donor deletion (e.g., skipping of exon 53 of the DMD gene using at least one guide pair selected from the guide pairs of **Table 1F**).

[0069] **Figure 5** shows dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected SluCas9 or sRGN sgRNA pairs that result in either precise reframing deletion, deletion of the entire exon 53 of the dystrophin gene, or skipping of exon 53. Each bar represents a sgRNA pair or triplet and the bar height depicts dystrophin protein signal normalized to the total protein signal, as determined by Jess protein assay. All guide pairs were tested with SluCas9 with the exception of "sRGN3.3_96-103", which was tested with sRGN3.3 and the E53SL96 and E53SL103 guides. Error bars denote the standard deviation for each sample group.

[0070] **Figure 6** shows dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected sgRNA pairs combined with SluCas9 or sRGN3.3 that result in either precise reframing deletion, deletion of the entire exon 53 of the dystrophin gene, or skipping of exon 53. Each bar represents a sgRNA pair and the bar height depicts dystrophin protein signal normalized to the total protein signal, as determined by Jess protein assay. All guide pairs were tested with SluCas9 with the exception of "[sRGN3.3]i52SL2_E53SL14", which was tested with sRGN3.3 and the i52SL2 and E53SL14 guides. Error bars denote the standard deviation for each sample group.

DETAILED DESCRIPTION

[0071] Reference will now be made in detail to certain embodiments of the invention, examples of which are illustrated in the accompanying drawings. While the invention is described in conjunction with the illustrated embodiments, it will be understood that they are not intended to limit the invention to those embodiments. On the contrary, the invention is intended to cover all alternatives, modifications, and equivalents, which may be included within the invention as defined by the appended claims and included embodiments.

[0072] Before describing the present teachings in detail, it is to be understood that the disclosure is not limited to specific compositions or process steps, as such may vary. It should be noted that, as used in this specification and the appended claims, the singular form "a", "an", and

"the" include plural references unless the context clearly dictates otherwise. Thus, for example, reference to "a guide" includes a plurality of guides and reference to "a cell" includes a plurality of cells and the like.

[0073] Numeric ranges are inclusive of the numbers defining the range. Measured and measurable values are understood to be approximate, taking into account significant digits and the error associated with the measurement. Also, the use of "comprise", "comprises", "comprising", "contain", "contains", "containing", "include", "includes", and "including" are not intended to be limiting. It is to be understood that both the foregoing general description and detailed description are exemplary and explanatory only and are not restrictive of the teachings.

[0074] Unless specifically noted in the specification, embodiments in the specification that recite "comprising" various components are also contemplated as "consisting of" or "consisting essentially of" the recited components; embodiments in the specification that recite "consisting of" various components are also contemplated as "comprising" or "consisting essentially of" the recited components; and embodiments in the specification that recite "consisting essentially of" various components are also contemplated as "consisting of" or "comprising" the recited components (this interchangeability does not apply to the use of these terms in the claims). The term "or" is used in an inclusive sense, i.e., equivalent to "and/or," unless the context clearly indicates otherwise.

[0075] The section headings used herein are for organizational purposes only and are not to be construed as limiting the desired subject matter in any way. In the event that any material incorporated by reference contradicts any term defined in this specification or any other express content of this specification, this specification controls. While the present teachings are described in conjunction with various embodiments, it is not intended that the present teachings be limited to such embodiments. On the contrary, the present teachings encompass various alternatives, modifications, and equivalents, as will be appreciated by those of skill in the art.

I. Definitions

[0076] Unless stated otherwise, the following terms and phrases as used herein are intended to have the following meanings:

[0077] "Polynucleotide," "nucleic acid," and "nucleic acid molecule," are used herein to refer to a multimeric compound comprising nucleosides or nucleoside analogs which have nitrogenous heterocyclic bases or base analogs linked together along a backbone, including conventional RNA, DNA, mixed RNA-DNA, and polymers that are analogs thereof. A nucleic acid "backbone" can be made up of a variety of linkages, including one or more of sugar-phosphodiester linkages, peptide-nucleic acid bonds ("peptide nucleic acids" or PNA; PCT No. WO 95/32305), phosphorothioate linkages, methylphosphonate linkages, or combinations thereof. Sugar moieties of a nucleic acid can be ribose, deoxyribose, or similar compounds with substitutions, e.g., 2' methoxy or 2' halide substitutions. Nitrogenous bases can be conventional bases (A, G, C, T, U), analogs thereof

(e.g., modified uridines such as 5-methoxyuridine, pseudouridine, or N1-methylpseudouridine, or others); inosine; derivatives of purines or pyrimidines (e.g., N^4-methyl deoxyguanosine, deaza- or aza-purines, deaza- or aza-pyrimidines, pyrimidine bases with substituent groups at the 5 or 6 position (e.g., 5-methylcytosine), purine bases with a substituent at the 2, 6, or 8 positions, 2-amino-6-methylaminopurine, O^6-methylguanine, 4-thio-pyrimidines, 4-amino-pyrimidines, 4-dimethylhydrazine-pyrimidines, and O^4-alkyl-pyrimidines; US Pat. No. 5,378,825 and PCT No. WO 93/13121). For general discussion see *The Biochemistry of the Nucleic Acids* 5-36, Adams et al., ed., 11th ed., 1992). Nucleic acids can include one or more "abasic" residues where the backbone includes no nitrogenous base for position(s) of the polymer (US Pat. No. 5,585,481). A nucleic acid can comprise only conventional RNA or DNA sugars, bases and linkages, or can include both conventional components and substitutions (e.g., conventional bases with 2' methoxy linkages, or polymers containing both conventional bases and one or more base analogs). Nucleic acid includes "locked nucleic acid" (LNA), an analogue containing one or more LNA nucleotide monomers with a bicyclic furanose unit locked in an RNA mimicking sugar conformation, which enhance hybridization affinity toward complementary RNA and DNA sequences (Vester and Wengel, 2004, *Biochemistry* 43(42):13233-41). RNA and DNA have different sugar moieties and can differ by the presence of uracil or analogs thereof in RNA and thymine or analogs thereof in DNA.

[0078] "Guide RNA" and simply "guide" are used herein interchangeably to refer to either a crRNA (also known as CRISPR RNA), or the combination of a crRNA and a trRNA (also known as tracrRNA). The crRNA and trRNA may be associated as a single RNA molecule (single guide RNA, sgRNA) or in two separate RNA molecules (dual guide RNA, dgRNA). "Guide RNA" refers to each type. The trRNA may be a naturally-occurring sequence, or a trRNA sequence with modifications or variations compared to naturally-occurring sequences. For clarity, the terms "guide RNA" or "guide" as used herein, and unless specifically stated otherwise, may refer to an RNA molecule (comprising A, C, G, and U nucleotides) or to a DNA molecule encoding such an RNA molecule (comprising A, C, G, and T nucleotides) or complementary sequences thereof. In general, in the case of a DNA nucleic acid construct encoding a guide RNA, the U residues in any of the RNA sequences described herein may be replaced with T residues, and in the case of a guide RNA construct encoded by any of the DNA sequences described herein, the T residues may be replaced with U residues.

[0079] As used herein, a "spacer sequence," sometimes also referred to herein and in the literature as a "spacer," "protospacer," "guide sequence," or "targeting sequence" refers to a sequence within a guide RNA that is complementary to a target sequence and functions to direct a guide RNA to a target sequence for cleavage by a Cas9. For clarity, the terms "spacer sequence", "spacer," "protospacer," "guide sequence," or "targeting sequence" as used herein, and unless specifically stated otherwise, may refer to an RNA molecule (comprising A, C, G, and U nucleotides) or to a DNA molecule encoding such an RNA molecule (comprising A, C, G, and T nucleotides) or complementary sequences thereof. A guide sequence can be 24, 23, 22, 21, 20 or fewer base pairs in

length, e.g., in the case of *Staphylococcus lugdunensis* (i.e., SluCas9) or *Staphylococcus aureus* (i.e., SaCas9) and related Cas9 homologs/orthologs. In preferred embodiments, a guide/spacer sequence in the case of SluCas9 or SaCas9 or sRGN is at least 20 base pairs in length, or more specifically, within 20-25 base pairs in length (*see, e.g.*, Schmidt et al., 2021, Nature Communications, "Improved CRISPR genome editing using small highly active and specific engineered RNA-guided nucleases"). Shorter or longer sequences can also be used as guides, e.g., 15-, 16-, 17-, 18-, 19-, 20-, 21-, 22-, 23-, 24-, or 25-nucleotides in length. For example, in some embodiments, the guide sequence comprises at least 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides of a sequence selected from SEQ ID NOs: 1-143. In some embodiments, the guide sequence comprises a sequence selected from SEQ ID NOs: 1-143. In some embodiments, the target sequence is in a gene or on a chromosome, for example, and is complementary to the guide sequence. In some embodiments, the degree of complementarity or identity between a guide sequence and its corresponding target sequence may be about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100%. For example, in some embodiments, the guide sequence comprises a sequence with about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to at least 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 contiguous nucleotides of a sequence selected from SEQ ID NOs: 1-143. In some embodiments, the guide sequence comprises a sequence with about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity to a sequence selected from SEQ ID NOs: 1-143. In preferred embodiments, a guide/spacer sequence in the case of SluCas9 or SaCas9 or a sRGN is at least 20 base pairs in length, or more specifically, within 20-25 base pairs in length (*see, e.g.*, Schmidt et al., 2021, Nature Communications, "Improved CRISPR genome editing using small highly active and specific engineered RNA-guided nucleases"). In some embodiments, the guide sequence and the target region may be 100% complementary or identical. In other embodiments, the guide sequence and the target region may contain at least one mismatch. For example, the guide sequence and the target sequence may contain 1, 2, 3, or 4 mismatches, where the total length of the target sequence is at least 16, 17, 18, 19, 20 or more base pairs. In some embodiments, the total length of the target sequence/guide is no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 22, no more than 23, or no more than 24 nucleotides in length. In some embodiments, the guide sequence and the target region may contain 1-4 mismatches where the guide sequence comprises at least 16, 17, 18, 19, 20 or more nucleotides. In some embodiments, the guide sequence and the target region may contain 1, 2, 3, or 4 mismatches where the guide sequence comprises 20 nucleotides. In some embodiments, the guide sequence and the target region do not contain any mismatches.

[0080] In some embodiments, the guide sequence comprises a sequence selected from SEQ ID NOs: 1-143, wherein if the 5' terminal nucleotide is not guanine, one or more guanine (g) is added to the sequence at its 5' end. In some embodiments, the 5' g or gg is included in some instances for transcription, for example, for expression by the RNA polymerase III-dependent U6 promoter or the

T7 promoter. In some embodiments, a 5' guanine is added to any one of the guide sequences or pairs of guide sequences disclosed herein.

[0081] Target sequences for Cas9s include both the positive and negative strands of genomic DNA (i.e., the sequence given and the sequence's reverse complement), as a nucleic acid substrate for a Cas9 is a double stranded nucleic acid. Accordingly, where a guide sequence is said to be "complementary to a target sequence", it is to be understood that the guide sequence may direct a guide RNA to bind to the reverse complement of a target sequence. Thus, in some embodiments, where the guide sequence binds the reverse complement of a target sequence, the guide sequence is identical to certain nucleotides of the target sequence (e.g., the target sequence not including the PAM) except for the substitution of U for T in the guide sequence.

[0082] As used herein, "ribonucleoprotein" (RNP) or "RNP complex" refers to a guide RNA together with a Cas9. In some embodiments, the guide RNA guides the Cas9, such as a SluCas9 or a SaCas9, to a target sequence, and the guide RNA hybridizes with and the agent binds to the target sequence, which can be followed by cleaving or nicking (in the context of a modified "nickase" Cas9).

[0083] As used herein, a first sequence is considered to "comprise a sequence with at least X% identity to" a second sequence if an alignment of the first sequence to the second sequence shows that X% or more of the positions of the second sequence in its entirety are matched by the first sequence. For example, the sequence AAGA comprises a sequence with 100% identity to the sequence AAG because an alignment would give 100% identity in that there are matches to all three positions of the second sequence. The differences between RNA and DNA (generally the exchange of uridine for thymidine or vice versa) and the presence of nucleoside analogs such as modified uridines do not contribute to differences in identity or complementarity among polynucleotides as long as the relevant nucleotides (such as thymidine, uridine, or modified uridine) have the same complement (e.g., adenosine for all of thymidine, uridine, or modified uridine; another example is cytosine and 5-methylcytosine, both of which have guanosine or modified guanosine as a complement). Thus, for example, the sequence 5'-AXG where X is any modified uridine, such as pseudouridine, N1-methyl pseudouridine, or 5-methoxyuridine, is considered 100% identical to AUG in that both are perfectly complementary to the same sequence (5'-CAU). Exemplary alignment algorithms are the Smith-Waterman and Needleman-Wunsch algorithms, which are well-known in the art. One skilled in the art will understand what choice of algorithm and parameter settings are appropriate for a given pair of sequences to be aligned; for sequences of generally similar length and expected identity >50% for amino acids or >75% for nucleotides, the Needleman-Wunsch algorithm with default settings of the Needleman-Wunsch algorithm interface provided by the EBI at the www.ebi.ac.uk web server is generally appropriate.

[0084] "mRNA" is used herein to refer to a polynucleotide that is not DNA and comprises an open reading frame that can be translated into a polypeptide (i.e., can serve as a substrate for

translation by a ribosome and amino-acylated tRNAs). mRNA can comprise a phosphate-sugar backbone including ribose residues or analogs thereof, e.g., 2'-methoxy ribose residues. In some embodiments, the sugars of an mRNA phosphate-sugar backbone consist essentially of ribose residues, 2'-methoxy ribose residues, or a combination thereof.

[0085] Guide sequences useful in the guide RNA compositions and methods described herein are shown, for example, in **Tables 1A-1F,** and throughout the specification.

[0086] As used herein, a "target sequence" refers to a sequence of nucleic acid in a target gene that has complementarity to at least a portion of the guide sequence of the guide RNA. The interaction of the target sequence and the guide sequence directs a Cas9 (such as a SluCas9) to bind, and potentially nick or cleave (depending on the activity of the agent), within or near the target sequence. A target sequence may be complementary to any of the guide RNA sequences disclosed herein (e.g., any of the guide RNA sequences disclosed in Tables 1A-1F).

[0087] As used herein, "treatment" refers to any administration or application of a therapeutic for disease or disorder in a subject, and includes inhibiting the disease or development of the disease (which may occur before or after the disease is formally diagnosed, e.g., in cases where a subject has a genotype that has the potential or is likely to result in development of the disease), arresting its development, relieving one or more symptoms of the disease, curing the disease, or preventing reoccurrence of one or more symptoms of the disease. For example, treatment of DMD may comprise alleviating symptoms of DMD.

[0088] As used herein, "ameliorating" refers to any beneficial effect on a phenotype or symptom, such as reducing its severity, slowing or delaying its development, arresting its development, or partially or completely reversing or eliminating it. In the case of quantitative phenotypes such as expression levels, ameliorating encompasses changing the expression level so that it is closer to the expression level seen in healthy or unaffected cells or individuals.

[0089] A "pharmaceutically acceptable excipient" refers to an agent that is included in a pharmaceutical formulation that is not the active ingredient. Pharmaceutically acceptable excipients may e.g., aid in drug delivery or support or enhance stability or bioavailability.

[0090] The term "about" or "approximately" means an acceptable error for a particular value as determined by one of ordinary skill in the art, which depends in part on how the value is measured or determined.

[0091] As used herein, "*Staphylococcus aureus* Cas9" may also be referred to as SaCas9, and includes wild type SaCas9 (e.g., SEQ ID NO: 711) and variants thereof. A variant of SaCas9 comprises one or more amino acid changes as compared to SEQ ID NO: 711, including insertion, deletion, or substitution of one or more amino acids, or a chemical modification to one or more amino acids. For clarity, SaCas9KKH is a SaCas9 variant.

[0092] As used herein, "*Staphylococcus lugdunensis* Cas9" may also be referred to as SluCas9, and includes wild type SluCas9 (e.g., SEQ ID NO: 712) and variants thereof. A variant of

SluCas9 comprises one or more amino acid changes as compared to SEQ ID NO: 712, including insertion, deletion, or substitution of one or more amino acids, or a chemical modification to one or more amino acids.

[0093] As used herein, "splice acceptor site" refers to a portion of a gene necessary for splicing that includes a 3' portion of an intron. Typically, a splice acceptor site comprises portion of a gene comprising at least the first two bases of a given exon (e.g., exon 53 of the dystrophin gene) and the last 26 bases of the upstream intron (e.g., intron 52 of the dystrophin gene). A sequence providing the dystrophin gene exon 53 splice acceptor site is provided in SEQ ID NO: 144, including nucleobases upstream and downstream of the splice acceptor site. In most mRNAs to be spliced, a splice acceptor site terminates an intron with an AG sequence.

[0094] As used herein, "splice donor site" refers to a portion of a gene necessary for splicing that includes a 5' portion of an intron. Typically, a splice donor site comprises at least the three terminal nucleotides of a given exon (e.g., exon 53 of the dystrophin gene) and the first seven bases of the downstream intron (e.g., intron 53 of the dystrophin gene). A sequence providing the dystrophin gene exon 53 splice donor site is provided in SEQ ID NO: 145, including nucleobases upstream and downstream of the splice acceptor site. In most mRNAs to be spliced, a splice donor site includes a GU sequence at the 5' end of the intron (a GT sequence within the gene itself), within a larger, less highly conserved region.

[0095] As used here, "DMD gene" refers to the human gene (represented by Genbank Accession No. NC_000023.11; SEQ ID NO: 146) encoding the dystrophin protein. Mutations (e.g., deletions, duplications, and/or point mutations) at the DMD gene locus have been associated with Duchenne muscular dystrophy (DMD), Becker muscular dystrophy (BMD), or cardiomyopathy.

II. Compositions

[0096] Provided herein are compositions comprising guide RNAs and pairs of guide RNAs useful for treating Duchenne Muscular Dystrophy (DMD). The provided pairs of guide RNAs, when used with the correct endonuclease, function to excise all or a portion of exon 53 of the DMD gene. **Tables 1A-1C** provide a listing of guide sequences of guide RNAs, and **Tables 1D-1F** provide exemplary guide pairs.

Guides and Guide Pairs

A. Table 1A. Intron 52 SluCas9 guides:

SEQ ID NO	Guide Name	Guide Sequence	Pam	Strand
1	i52SL1	TGAATTCTTTCAACTAGAATAA	AAGG	+
2	i52SL2	ATATATAGTAGTAAATGCTAGT	CTGG	+
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	GAGG	+
4	i52SL4	TTAAAAAATTATTCATTGTGTT	ATGG	+
5	i52SL5	AAATTATTCATTGTGTTATGGC	TAGG	+
6	i52SL6	TTATGGCTAGGATGATGAACAA	CAGG	+
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	ATGG	+

8	i52SL8	TTTCTGTTAAATTATTTTCCTG	AAGG	+
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	AAGG	+
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	CAGG	+
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	CAGG	+
12	i52SL12	CCATGTGACAGGCTAGACATAC	CAGG	+
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	GAGG	+
14	i52SL14	GCCTGTATATAATGACTAATTG	TAGG	+
15	i52SL15	ATATAATGACTAATTGTAGGAA	TTGG	+
16	i52SL16	TATAATGACTAATTGTAGGAAT	TGGG	+
17	i52SL17	GTTACACTAGCTCCCTTGATGC	TAGG	+
18	i52SL18	TTACACTAGCTCCCTTGATGCT	AGGG	+
19	i52SL19	TACACTAGCTCCCTTGATGCTA	GGGG	+
20	i52SL20	TGATGCTAGGGGAAATAACTCT	GAGG	+
21	i52SL21	AACTCTGAGGCATGTATTTTAC	AAGG	+
22	i52SL22	ACTCTGAGGCATGTATTTTACA	AGGG	+
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	AAGG	+
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	AGGG	+
25	i52SL25	CTCCAGTGACCCACAACAGCAG	CTGG	+
26	i52SL26	CTTGATAATGCACCACTCTTTA	CTGG	+
27	i52SL27	CAACATAAATGTGAGATAACGT	TTGG	–
28	i52SL28	TGTTGATGTTCTATGTCACCTT	CAGG	–
29	i52SL29	CAGATGATTCATATTTGGTTCT	AGGG	–
30	i52SL30	ACAGATGATTCATATTTGGTTC	TAGG	–
31	i52SL31	TTTTCTAACAGATGATTCATAT	TTGG	–
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	ATGG	–
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	GGGG	–
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	AGGG	–
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	GAGG	–
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	AAGG	–
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	GTGG	–
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	TGGG	–
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	ATGG	–
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	CAGG	–
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	TGGG	–
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	CTGG	–
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	CTGG	–
44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	CAGG	–
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	GTGG	–
46	i52SL46	GTATGTCTAGCCTGTCACATGG	ATGG	–
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	ATGG	–
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	CTGG	–
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	GAGG	–
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	GGGG	–
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	AGGG	–
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	GAGG	–
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	CTGG	–
54	i52SL54	GTCATTATATACAGGCTGCCTC	TGGG	–
55	i52SL55	AGTCATTATATACAGGCTGCCT	CTGG	–
56	i52SL56	TCCTACAATTAGTCATTATATA	CAGG	–
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	AGGG	–
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	AAGG	–
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	CTGG	–
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	TGGG	–
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	TTGG	–
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	CTGG	–
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	TGGG	–
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	GTGG	–

B. **Table 1B. Exon 53 SluCas9 guides:**

SEQ ID NO	Guide Name	Guide Sequence	Pam	Strand
65	E53SL29	CCTTGGTTTCTGTGATTTTCTT	TTGG	+
66	E53SL30	CTTTTGGATTGCATCTACTGTA	TAGG	+
67	E53SL31	TTTTGGATTGCATCTACTGTAT	AGGG	+
68	E53SL32	ACCCTCCTTCCATGACTCAAGC	TTGG	+
69	E53SL33	CTTCCATGACTCAAGCTTGGCT	CTGG	+
70	E53SL34	ACATTTCATTCAACTGTTGCCT	CCGG	+
71	E53SL35	TCAACTGTTGCCTCCGGTTCTG	AAGG	+
72	E53SL90	CCAAAAGAAAATCACAGAAACC	AAGG	-
73	E53SL91	GCCAAGCTTGAGTCATGGAAGG	AGGG	-
74	E53SL92	AGCCAAGCTTGAGTCATGGAAG	GAGG	-
75	E53SL93	CAGAGCCAAGCTTGAGTCATGG	AAGG	-
76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC	ATGG	-
77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA	CAGG	-
78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT	TAGG	-
79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG	CAGG	-
80	E53SL98	TTCAACACAATGGCTGGAAGCT	AAGG	-
81	E53SL99	GTTAAAGGATTCAACACAATGG	CTGG	-
82	E53SL100	AAATGTTAAAGGATTCAACACA	ATGG	-
83	E53SL101	GCAACAGTTGAATGAAATGTTA	AAGG	-
84	E53SL102	TACAAGAACACCTTCAGAACCG	GAGG	-
85	E53SL103	AAGTACAAGAACACCTTCAGAA	CCGG	-
86	E53SL104	AGTTGAAAGAATTCAGAATCAG	TGGG	-
87	E53SL105	TAGTTGAAAGAATTCAGAATCA	GTGG	-

C. **Table 1C. Intron 53 SluCas9 guides:**

SEQ ID NO	Guide Name	Guide Sequence	Pam	Strand
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	TAGG	+
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	AAGG	+
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	ATGG	+
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	ATGG	+
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	CTGG	+
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	TAGG	+
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	TTGG	+
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	TGGG	+
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	GAGG	+
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	AAGG	+
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	AAGG	+
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	GAGG	+
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	CAGG	+
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	GTGG	+
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	GTGG	+
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	CTGG	+
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	TAGG	+
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	AGGG	+
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	GAGG	+
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	GAGG	+
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	CAGG	+
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	GAGG	+
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	AAGG	+
111	i53SL26	GATTGTGCCACTGCACTTTAGC	CTGG	+
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	TGGG	+
113	i53SL28	AAACATCATTAAATTACAATCT	ATGG	+
114	i53SL29	GTAACCAGTATTTTATTTTAAA	AAGG	+

115	i53SL30	AAAGGTATCTTTGATACTAACC	TTGG	+
116	i53SL37	TTTCATATCTTATTTGGAGGCC	CTGG	–
117	i53SL38	CTACTCTTTCATATCTTATTTG	GAGG	–
118	i53SL39	GGTCTACTCTTTCATATCTTAT	TTGG	–
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	CAGG	–
120	i53SL41	TAGTTGCATGAAGTCAACCATT	CGGG	–
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	TCGG	–
122	i53SL43	CATCTTTAAGATCACTTCAAAA	TTGG	–
123	i53SL44	TTAGTAATCTGGATATAGTTGG	CTGG	–
124	i53SL45	TTGTTTAGTAATCTGGATATAG	TTGG	–
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	CTGG	–
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	GAGG	–
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	AAGG	–
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	CAGG	–
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	TAGG	–
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	TTGG	–
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	TTGG	–
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	TGGG	–
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	ATGG	–
134	i53SL55	AGCCAGGCGTGTACCACCACGC	CTGG	–
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	CAGG	–
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	TGGG	–
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	CTGG	–
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	GGGG	–
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	TGGG	–
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	CTGG	–
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	GTGG	–
142	i53SL63	GAGACAGAGTCTCACTGTCACC	CAGG	–
143	i53SL64	GATACCTTTTTAAAATAAAATA	CTGG	–

D. Table 1D. Intron 52-Intron 53 SluCas9 guide pairs:

Guide 1 SEQ ID NO	Guide 1 name	Guide 1 sequence	Guide 2 SEQ ID NO	Guide 2 name	Guide 2 sequence
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	5	i52SL5	AAATTATTCATTGTGTTATGGC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	6	i52SL6	TTATGGCTAGGATGATGAACAA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	12	i52SL12	CCATGTGACAGGCTAGACATAC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	14	i52SL14	GCCTGTATATAATGACTAATTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	15	i52SL15	ATATAATGACTAATTGTAGGAA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	16	i52SL16	TATAATGACTAATTGTAGGAAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA

88	i53SL3	AGAGTAGACCTGTTACTTTTTC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	26	i52SL26	CTTGATAATGCACCACTCTTTA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	27	i52SL27	CAACATAAATGTGAGATAACGT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	29	i52SL29	CAGATGATTCATATTTGGTTCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	30	i52SL30	ACAGATGATTCATATTTGGTTC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	31	i52SL31	TTTTCTAACAGATGATTCATAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	54	i52SL54	GTCATTATATACAGGCTGCCTC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	55	i52SL55	AGTCATTATATACAGGCTGCCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	56	i52SL56	TCCTACAATTAGTCATTATATA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	5	i52SL5	AAATTATTCATTGTGTTATGGC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	6	i52SL6	TTATGGCTAGGATGATGAACAA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	14	i52SL14	GCCTGTATATAATGACTAATTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	15	i52SL15	ATATAATGACTAATTGTAGGAA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	16	i52SL16	TATAATGACTAATTGTAGGAAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	18	i52SL18	TTACACTAGCTCCCTTGATGCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA

89	i53SL4	TAGACCTGTTACTTTTTCTAGG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	26	i52SL26	CTTGATAATGCACCACTCTTTA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	27	i52SL27	CAACATAAATGTGAGATAACGT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	30	i52SL30	ACAGATGATTCATATTTGGTTC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	31	i52SL31	TTTTCTAACAGATGATTCATAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	54	i52SL54	GTCATTATATACAGGCTGCCTC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	55	i52SL55	AGTCATTATATACAGGCTGCCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	56	i52SL56	TCCTACAATTAGTCATTATATA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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89	i53SL4	TAGACCTGTTACTTTTTCTAGG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	12	i52SL12	CCATGTGACAGGCTAGACATAC
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	15	i52SL15	ATATAATGACTAATTGTAGGAA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	26	i52SL26	CTTGATAATGCACCACTCTTTA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	30	i52SL30	ACAGATGATTCATATTTGGTTC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	54	i52SL54	GTCATTATATACAGGCTGCCTC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	56	i52SL56	TCCTACAATTAGTCATTATATA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	5	i52SL5	AAATTATTCATTGTGTTATGGC
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	54	i52SL54	GTCATTATATACAGGCTGCCTC
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	55	i52SL55	AGTCATTATATACAGGCTGCCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	56	i52SL56	TCCTACAATTAGTCATTATATA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG

92	i53SL7	TCTACCTTGACTCAAAAGTCTA	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	5	i52SL5	AAATTATTCATTGTGTTATGGC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	6	i52SL6	TTATGGCTAGGATGATGAACAA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	14	i52SL14	GCCTGTATATAATGACTAATTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	15	i52SL15	ATATAATGACTAATTGTAGGAA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	16	i52SL16	TATAATGACTAATTGTAGGAAT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	26	i52SL26	CTTGATAATGCACCACTCTTTA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	27	i52SL27	CAACATAAATGTGAGATAACGT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	30	i52SL30	ACAGATGATTCATATTTGGTTC
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC

93	i53SL8	CTTGACTCAAAAGTCTACTGGC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	5	i52SL5	AAATTATTCATTGTGTTATGGC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	12	i52SL12	CCATGTGACAGGCTAGACATAC
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	14	i52SL14	GCCTGTATATAATGACTAATTG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	15	i52SL15	ATATAATGACTAATTGTAGGAA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	16	i52SL16	TATAATGACTAATTGTAGGAAT
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	26	i52SL26	CTTGATAATGCACCACTCTTTA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	30	i52SL30	ACAGATGATTCATATTTGGTTC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	54	i52SL54	GTCATTATATACAGGCTGCCTC
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	56	i52SL56	TCCTACAATTAGTCATTATATA
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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95	i53SL10	CATGCCTGTAATCCTAGTGCTT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
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96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	5	i52SL5	AAATTATTCATTGTGTTATGGC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	6	i52SL6	TTATGGCTAGGATGATGAACAA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	14	i52SL14	GCCTGTATATAATGACTAATTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	15	i52SL15	ATATAATGACTAATTGTAGGAA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	16	i52SL16	TATAATGACTAATTGTAGGAAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	18	i52SL18	TTACACTAGCTCCCTTGATGCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	26	i52SL26	CTTGATAATGCACCACTCTTTA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	27	i52SL27	CAACATAAATGTGAGATAACGT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	30	i52SL30	ACAGATGATTCATATTTGGTTC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	31	i52SL31	TTTTCTAACAGATGATTCATAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG

96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	54	i52SL54	GTCATTATATACAGGCTGCCTC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	55	i52SL55	AGTCATTATATACAGGCTGCCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	56	i52SL56	TCCTACAATTAGTCATTATATA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	5	i52SL5	AAATTATTCATTGTGTTATGGC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	6	i52SL6	TTATGGCTAGGATGATGAACAA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	12	i52SL12	CCATGTGACAGGCTAGACATAC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	14	i52SL14	GCCTGTATATAATGACTAATTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	15	i52SL15	ATATAATGACTAATTGTAGGAA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	16	i52SL16	TATAATGACTAATTGTAGGAAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	26	i52SL26	CTTGATAATGCACCACTCTTTA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	27	i52SL27	CAACATAAATGTGAGATAACGT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	29	i52SL29	CAGATGATTCATATTTGGTTCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	30	i52SL30	ACAGATGATTCATATTTGGTTC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	31	i52SL31	TTTTCTAACAGATGATTCATAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA

97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	56	i52SL56	TCCTACAATTAGTCATTATATA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	14	i52SL14	GCCTGTATATAATGACTAATTG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	16	i52SL16	TATAATGACTAATTGTAGGAAT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	26	i52SL26	CTTGATAATGCACCACTCTTTA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	27	i52SL27	CAACATAAATGTGAGATAACGT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	30	i52SL30	ACAGATGATTCATATTTGGTTC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	31	i52SL31	TTTTCTAACAGATGATTCATAT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA

98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	54	i52SL54	GTCATTATATACAGGCTGCCTC
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	56	i52SL56	TCCTACAATTAGTCATTATATA
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	12	i52SL12	CCATGTGACAGGCTAGACATAC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	14	i52SL14	GCCTGTATATAATGACTAATTG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	15	i52SL15	ATATAATGACTAATTGTAGGAA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	16	i52SL16	TATAATGACTAATTGTAGGAAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	26	i52SL26	CTTGATAATGCACCACTCTTTA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	27	i52SL27	CAACATAAATGTGAGATAACGT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	28	i52SL28	TGTTGATGTTCTATGTCACCTT

99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	29	i52SL29	CAGATGATTCATATTTGGTTCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	30	i52SL30	ACAGATGATTCATATTTGGTTC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	31	i52SL31	TTTTCTAACAGATGATTCATAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	54	i52SL54	GTCATTATATACAGGCTGCCTC
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	56	i52SL56	TCCTACAATTAGTCATTATATA
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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100	i53SL15	CAAAAATTTTTAAAAAATTAGC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	14	i52SL14	GCCTGTATATAATGACTAATTG
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102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	5	i52SL5	AAATTATTCATTGTGTTATGGC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	6	i52SL6	TTATGGCTAGGATGATGAACAA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG

103	i53SL18	AGCCAGGCGTGGTGGTACACGC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	12	i52SL12	CCATGTGACAGGCTAGACATAC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	14	i52SL14	GCCTGTATATAATGACTAATTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	15	i52SL15	ATATAATGACTAATTGTAGGAA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	16	i52SL16	TATAATGACTAATTGTAGGAAT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	26	i52SL26	CTTGATAATGCACCACTCTTTA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	27	i52SL27	CAACATAAATGTGAGATAACGT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	29	i52SL29	CAGATGATTCATATTTGGTTCT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	30	i52SL30	ACAGATGATTCATATTTGGTTC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	31	i52SL31	TTTTCTAACAGATGATTCATAT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	56	i52SL56	TCCTACAATTAGTCATTATATA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
103	i53SL18	AGCCAGGCGTGGTGGTACACGC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG

104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	5	i52SL5	AAATTATTCATTGTGTTATGGC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	6	i52SL6	TTATGGCTAGGATGATGAACAA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	12	i52SL12	CCATGTGACAGGCTAGACATAC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	14	i52SL14	GCCTGTATATAATGACTAATTG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	15	i52SL15	ATATAATGACTAATTGTAGGAA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	16	i52SL16	TATAATGACTAATTGTAGGAAT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	26	i52SL26	CTTGATAATGCACCACTCTTTA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	27	i52SL27	CAACATAAATGTGAGATAACGT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	29	i52SL29	CAGATGATTCATATTTGGTTCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	30	i52SL30	ACAGATGATTCATATTTGGTTC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	31	i52SL31	TTTTCTAACAGATGATTCATAT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	54	i52SL54	GTCATTATATACAGGCTGCCTC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	55	i52SL55	AGTCATTATATACAGGCTGCCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	56	i52SL56	TCCTACAATTAGTCATTATATA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA

104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	5	i52SL5	AAATTATTCATTGTGTTATGGC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	6	i52SL6	TTATGGCTAGGATGATGAACAA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	12	i52SL12	CCATGTGACAGGCTAGACATAC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	14	i52SL14	GCCTGTATATAATGACTAATTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	15	i52SL15	ATATAATGACTAATTGTAGGAA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	16	i52SL16	TATAATGACTAATTGTAGGAAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	26	i52SL26	CTTGATAATGCACCACTCTTTA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	27	i52SL27	CAACATAAATGTGAGATAACGT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	29	i52SL29	CAGATGATTCATATTTGGTTCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	30	i52SL30	ACAGATGATTCATATTTGGTTC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	31	i52SL31	TTTTCTAACAGATGATTCATAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	54	i52SL54	GTCATTATATACAGGCTGCCTC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	55	i52SL55	AGTCATTATATACAGGCTGCCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	56	i52SL56	TCCTACAATTAGTCATTATATA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA

105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	5	i52SL5	AAATTATTCATTGTGTTATGGC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	6	i52SL6	TTATGGCTAGGATGATGAACAA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	14	i52SL14	GCCTGTATATAATGACTAATTG
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	16	i52SL16	TATAATGACTAATTGTAGGAAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	26	i52SL26	CTTGATAATGCACCACTCTTTA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	27	i52SL27	CAACATAAATGTGAGATAACGT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	30	i52SL30	ACAGATGATTCATATTTGGTTC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	31	i52SL31	TTTTCTAACAGATGATTCATAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG

106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	54	i52SL54	GTCATTATATACAGGCTGCCTC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	55	i52SL55	AGTCATTATATACAGGCTGCCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	56	i52SL56	TCCTACAATTAGTCATTATATA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	5	i52SL5	AAATTATTCATTGTGTTATGGC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	6	i52SL6	TTATGGCTAGGATGATGAACAA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	12	i52SL12	CCATGTGACAGGCTAGACATAC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	14	i52SL14	GCCTGTATATAATGACTAATTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	15	i52SL15	ATATAATGACTAATTGTAGGAA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	16	i52SL16	TATAATGACTAATTGTAGGAAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	26	i52SL26	CTTGATAATGCACCACTCTTTA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	27	i52SL27	CAACATAAATGTGAGATAACGT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	29	i52SL29	CAGATGATTCATATTTGGTTCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	30	i52SL30	ACAGATGATTCATATTTGGTTC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	31	i52SL31	TTTTCTAACAGATGATTCATAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC

107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	54	i52SL54	GTCATTATATACAGGCTGCCTC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	55	i52SL55	AGTCATTATATACAGGCTGCCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	56	i52SL56	TCCTACAATTAGTCATTATATA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	5	i52SL5	AAATTATTCATTGTGTTATGGC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	14	i52SL14	GCCTGTATATAATGACTAATTG
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	26	i52SL26	CTTGATAATGCACCACTCTTTA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	27	i52SL27	CAACATAAATGTGAGATAACGT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
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108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	14	i52SL14	GCCTGTATATAATGACTAATTG
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	26	i52SL26	CTTGATAATGCACCACTCTTTA
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	30	i52SL30	ACAGATGATTCATATTTGGTTC
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA

109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	54	i52SL54	GTCATTATATACAGGCTGCCTC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	55	i52SL55	AGTCATTATATACAGGCTGCCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	56	i52SL56	TCCTACAATTAGTCATTATATA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	5	i52SL5	AAATTATTCATTGTGTTATGGC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	6	i52SL6	TTATGGCTAGGATGATGAACAA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	14	i52SL14	GCCTGTATATAATGACTAATTG
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	16	i52SL16	TATAATGACTAATTGTAGGAAT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	26	i52SL26	CTTGATAATGCACCACTCTTTA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	27	i52SL27	CAACATAAATGTGAGATAACGT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	31	i52SL31	TTTTCTAACAGATGATTCATAT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT

110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	56	i52SL56	TCCTACAATTAGTCATTATATA
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	5	i52SL5	AAATTATTCATTGTGTTATGGC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	14	i52SL14	GCCTGTATATAATGACTAATTG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	15	i52SL15	ATATAATGACTAATTGTAGGAA
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
111	i53SL26	GATTGTGCCACTGCACTTTAGC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	26	i52SL26	CTTGATAATGCACCACTCTTTA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	27	i52SL27	CAACATAAATGTGAGATAACGT

111	i53SL26	GATTGTGCCACTGCACTTTAGC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	29	i52SL29	CAGATGATTCATATTTGGTTCT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	30	i52SL30	ACAGATGATTCATATTTGGTTC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	56	i52SL56	TCCTACAATTAGTCATTATATA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	26	i52SL26	CTTGATAATGCACCACTCTTTA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	27	i52SL27	CAACATAAATGTGAGATAACGT
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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113	i53SL28	AAACATCATTAAATTACAATCT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
113	i53SL28	AAACATCATTAAATTACAATCT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
113	i53SL28	AAACATCATTAAATTACAATCT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
113	i53SL28	AAACATCATTAAATTACAATCT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
113	i53SL28	AAACATCATTAAATTACAATCT	5	i52SL5	AAATTATTCATTGTGTTATGGC
113	i53SL28	AAACATCATTAAATTACAATCT	6	i52SL6	TTATGGCTAGGATGATGAACAA
113	i53SL28	AAACATCATTAAATTACAATCT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
113	i53SL28	AAACATCATTAAATTACAATCT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
113	i53SL28	AAACATCATTAAATTACAATCT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
113	i53SL28	AAACATCATTAAATTACAATCT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
113	i53SL28	AAACATCATTAAATTACAATCT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
113	i53SL28	AAACATCATTAAATTACAATCT	12	i52SL12	CCATGTGACAGGCTAGACATAC
113	i53SL28	AAACATCATTAAATTACAATCT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
113	i53SL28	AAACATCATTAAATTACAATCT	14	i52SL14	GCCTGTATATAATGACTAATTG
113	i53SL28	AAACATCATTAAATTACAATCT	15	i52SL15	ATATAATGACTAATTGTAGGAA
113	i53SL28	AAACATCATTAAATTACAATCT	16	i52SL16	TATAATGACTAATTGTAGGAAT
113	i53SL28	AAACATCATTAAATTACAATCT	17	i52SL17	GTTACACTAGCTCCCTTGATGC

113	i53SL28	AAACATCATTAAATTACAATCT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
113	i53SL28	AAACATCATTAAATTACAATCT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
113	i53SL28	AAACATCATTAAATTACAATCT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
113	i53SL28	AAACATCATTAAATTACAATCT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
113	i53SL28	AAACATCATTAAATTACAATCT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
113	i53SL28	AAACATCATTAAATTACAATCT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
113	i53SL28	AAACATCATTAAATTACAATCT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
113	i53SL28	AAACATCATTAAATTACAATCT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
113	i53SL28	AAACATCATTAAATTACAATCT	26	i52SL26	CTTGATAATGCACCACTCTTTA
113	i53SL28	AAACATCATTAAATTACAATCT	27	i52SL27	CAACATAAATGTGAGATAACGT
113	i53SL28	AAACATCATTAAATTACAATCT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
113	i53SL28	AAACATCATTAAATTACAATCT	29	i52SL29	CAGATGATTCATATTTGGTTCT
113	i53SL28	AAACATCATTAAATTACAATCT	30	i52SL30	ACAGATGATTCATATTTGGTTC
113	i53SL28	AAACATCATTAAATTACAATCT	31	i52SL31	TTTTCTAACAGATGATTCATAT
113	i53SL28	AAACATCATTAAATTACAATCT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
113	i53SL28	AAACATCATTAAATTACAATCT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
113	i53SL28	AAACATCATTAAATTACAATCT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
113	i53SL28	AAACATCATTAAATTACAATCT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
113	i53SL28	AAACATCATTAAATTACAATCT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
113	i53SL28	AAACATCATTAAATTACAATCT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
113	i53SL28	AAACATCATTAAATTACAATCT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
113	i53SL28	AAACATCATTAAATTACAATCT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
113	i53SL28	AAACATCATTAAATTACAATCT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
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113	i53SL28	AAACATCATTAAATTACAATCT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
113	i53SL28	AAACATCATTAAATTACAATCT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
113	i53SL28	AAACATCATTAAATTACAATCT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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113	i53SL28	AAACATCATTAAATTACAATCT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
113	i53SL28	AAACATCATTAAATTACAATCT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
113	i53SL28	AAACATCATTAAATTACAATCT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
113	i53SL28	AAACATCATTAAATTACAATCT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
113	i53SL28	AAACATCATTAAATTACAATCT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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113	i53SL28	AAACATCATTAAATTACAATCT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
113	i53SL28	AAACATCATTAAATTACAATCT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
113	i53SL28	AAACATCATTAAATTACAATCT	54	i52SL54	GTCATTATATACAGGCTGCCTC
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113	i53SL28	AAACATCATTAAATTACAATCT	56	i52SL56	TCCTACAATTAGTCATTATATA
113	i53SL28	AAACATCATTAAATTACAATCT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
113	i53SL28	AAACATCATTAAATTACAATCT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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113	i53SL28	AAACATCATTAAATTACAATCT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
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113	i53SL28	AAACATCATTAAATTACAATCT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
113	i53SL28	AAACATCATTAAATTACAATCT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	5	i52SL5	AAATTATTCATTGTGTTATGGC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	6	i52SL6	TTATGGCTAGGATGATGAACAA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	12	i52SL12	CCATGTGACAGGCTAGACATAC

114	i53SL29	GTAACCAGTATTTTATTTTAAA	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	14	i52SL14	GCCTGTATATAATGACTAATTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	15	i52SL15	ATATAATGACTAATTGTAGGAA
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	18	i52SL18	TTACACTAGCTCCCTTGATGCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	20	i52SL20	TGATGCTAGGGGAAATAACTCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	26	i52SL26	CTTGATAATGCACCACTCTTTA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	27	i52SL27	CAACATAAATGTGAGATAACGT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	29	i52SL29	CAGATGATTCATATTTGGTTCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	30	i52SL30	ACAGATGATTCATATTTGGTTC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	31	i52SL31	TTTTCTAACAGATGATTCATAT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	54	i52SL54	GTCATTATATACAGGCTGCCTC
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	56	i52SL56	TCCTACAATTAGTCATTATATA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
115	i53SL30	AAAGGTATCTTTGATACTAACC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
115	i53SL30	AAAGGTATCTTTGATACTAACC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
115	i53SL30	AAAGGTATCTTTGATACTAACC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
115	i53SL30	AAAGGTATCTTTGATACTAACC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
115	i53SL30	AAAGGTATCTTTGATACTAACC	5	i52SL5	AAATTATTCATTGTGTTATGGC
115	i53SL30	AAAGGTATCTTTGATACTAACC	6	i52SL6	TTATGGCTAGGATGATGAACAA
115	i53SL30	AAAGGTATCTTTGATACTAACC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG

115	i53SL30	AAAGGTATCTTTGATACTAACC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
115	i53SL30	AAAGGTATCTTTGATACTAACC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
115	i53SL30	AAAGGTATCTTTGATACTAACC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
115	i53SL30	AAAGGTATCTTTGATACTAACC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
115	i53SL30	AAAGGTATCTTTGATACTAACC	12	i52SL12	CCATGTGACAGGCTAGACATAC
115	i53SL30	AAAGGTATCTTTGATACTAACC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
115	i53SL30	AAAGGTATCTTTGATACTAACC	14	i52SL14	GCCTGTATATAATGACTAATTG
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115	i53SL30	AAAGGTATCTTTGATACTAACC	16	i52SL16	TATAATGACTAATTGTAGGAAT
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115	i53SL30	AAAGGTATCTTTGATACTAACC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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115	i53SL30	AAAGGTATCTTTGATACTAACC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
115	i53SL30	AAAGGTATCTTTGATACTAACC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
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115	i53SL30	AAAGGTATCTTTGATACTAACC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
115	i53SL30	AAAGGTATCTTTGATACTAACC	26	i52SL26	CTTGATAATGCACCACTCTTTA
115	i53SL30	AAAGGTATCTTTGATACTAACC	27	i52SL27	CAACATAAATGTGAGATAACGT
115	i53SL30	AAAGGTATCTTTGATACTAACC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
115	i53SL30	AAAGGTATCTTTGATACTAACC	29	i52SL29	CAGATGATTCATATTTGGTTCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	30	i52SL30	ACAGATGATTCATATTTGGTTC
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115	i53SL30	AAAGGTATCTTTGATACTAACC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
115	i53SL30	AAAGGTATCTTTGATACTAACC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
115	i53SL30	AAAGGTATCTTTGATACTAACC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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115	i53SL30	AAAGGTATCTTTGATACTAACC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
115	i53SL30	AAAGGTATCTTTGATACTAACC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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115	i53SL30	AAAGGTATCTTTGATACTAACC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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115	i53SL30	AAAGGTATCTTTGATACTAACC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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115	i53SL30	AAAGGTATCTTTGATACTAACC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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115	i53SL30	AAAGGTATCTTTGATACTAACC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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115	i53SL30	AAAGGTATCTTTGATACTAACC	56	i52SL56	TCCTACAATTAGTCATTATATA
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115	i53SL30	AAAGGTATCTTTGATACTAACC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
115	i53SL30	AAAGGTATCTTTGATACTAACC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	2	i52SL2	ATATATAGTAGTAAATGCTAGT

116	i53SL37	TTTCATATCTTATTTGGAGGCC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	5	i52SL5	AAATTATTCATTGTGTTATGGC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	6	i52SL6	TTATGGCTAGGATGATGAACAA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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116	i53SL37	TTTCATATCTTATTTGGAGGCC	14	i52SL14	GCCTGTATATAATGACTAATTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	15	i52SL15	ATATAATGACTAATTGTAGGAA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	16	i52SL16	TATAATGACTAATTGTAGGAAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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116	i53SL37	TTTCATATCTTATTTGGAGGCC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	26	i52SL26	CTTGATAATGCACCACTCTTTA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	27	i52SL27	CAACATAAATGTGAGATAACGT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	29	i52SL29	CAGATGATTCATATTTGGTTCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	30	i52SL30	ACAGATGATTCATATTTGGTTC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	31	i52SL31	TTTTCTAACAGATGATTCATAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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116	i53SL37	TTTCATATCTTATTTGGAGGCC	56	i52SL56	TCCTACAATTAGTCATTATATA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC

116	i53SL37	TTTCATATCTTATTTGGAGGCC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
117	i53SL38	CTACTCTTTCATATCTTATTTG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
117	i53SL38	CTACTCTTTCATATCTTATTTG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
117	i53SL38	CTACTCTTTCATATCTTATTTG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
117	i53SL38	CTACTCTTTCATATCTTATTTG	5	i52SL5	AAATTATTCATTGTGTTATGGC
117	i53SL38	CTACTCTTTCATATCTTATTTG	6	i52SL6	TTATGGCTAGGATGATGAACAA
117	i53SL38	CTACTCTTTCATATCTTATTTG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
117	i53SL38	CTACTCTTTCATATCTTATTTG	12	i52SL12	CCATGTGACAGGCTAGACATAC
117	i53SL38	CTACTCTTTCATATCTTATTTG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	14	i52SL14	GCCTGTATATAATGACTAATTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	15	i52SL15	ATATAATGACTAATTGTAGGAA
117	i53SL38	CTACTCTTTCATATCTTATTTG	16	i52SL16	TATAATGACTAATTGTAGGAAT
117	i53SL38	CTACTCTTTCATATCTTATTTG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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117	i53SL38	CTACTCTTTCATATCTTATTTG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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117	i53SL38	CTACTCTTTCATATCTTATTTG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
117	i53SL38	CTACTCTTTCATATCTTATTTG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
117	i53SL38	CTACTCTTTCATATCTTATTTG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
117	i53SL38	CTACTCTTTCATATCTTATTTG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
117	i53SL38	CTACTCTTTCATATCTTATTTG	26	i52SL26	CTTGATAATGCACCACTCTTTA
117	i53SL38	CTACTCTTTCATATCTTATTTG	27	i52SL27	CAACATAAATGTGAGATAACGT
117	i53SL38	CTACTCTTTCATATCTTATTTG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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117	i53SL38	CTACTCTTTCATATCTTATTTG	30	i52SL30	ACAGATGATTCATATTTGGTTC
117	i53SL38	CTACTCTTTCATATCTTATTTG	31	i52SL31	TTTTCTAACAGATGATTCATAT
117	i53SL38	CTACTCTTTCATATCTTATTTG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
117	i53SL38	CTACTCTTTCATATCTTATTTG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
117	i53SL38	CTACTCTTTCATATCTTATTTG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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117	i53SL38	CTACTCTTTCATATCTTATTTG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
117	i53SL38	CTACTCTTTCATATCTTATTTG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
117	i53SL38	CTACTCTTTCATATCTTATTTG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
117	i53SL38	CTACTCTTTCATATCTTATTTG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
117	i53SL38	CTACTCTTTCATATCTTATTTG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
117	i53SL38	CTACTCTTTCATATCTTATTTG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
117	i53SL38	CTACTCTTTCATATCTTATTTG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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117	i53SL38	CTACTCTTTCATATCTTATTTG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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117	i53SL38	CTACTCTTTCATATCTTATTTG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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117	i53SL38	CTACTCTTTCATATCTTATTTG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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117	i53SL38	CTACTCTTTCATATCTTATTTG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
117	i53SL38	CTACTCTTTCATATCTTATTTG	54	i52SL54	GTCATTATATACAGGCTGCCTC
117	i53SL38	CTACTCTTTCATATCTTATTTG	55	i52SL55	AGTCATTATATACAGGCTGCCT
117	i53SL38	CTACTCTTTCATATCTTATTTG	56	i52SL56	TCCTACAATTAGTCATTATATA

117	i53SL38	CTACTCTTTCATATCTTATTTG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
117	i53SL38	CTACTCTTTCATATCTTATTTG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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117	i53SL38	CTACTCTTTCATATCTTATTTG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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117	i53SL38	CTACTCTTTCATATCTTATTTG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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118	i53SL39	GGTCTACTCTTTCATATCTTAT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
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118	i53SL39	GGTCTACTCTTTCATATCTTAT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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118	i53SL39	GGTCTACTCTTTCATATCTTAT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	26	i52SL26	CTTGATAATGCACCACTCTTTA
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119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
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119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
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119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	5	i52SL5	AAATTATTCATTGTGTTATGGC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	6	i52SL6	TTATGGCTAGGATGATGAACAA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	12	i52SL12	CCATGTGACAGGCTAGACATAC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	14	i52SL14	GCCTGTATATAATGACTAATTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	15	i52SL15	ATATAATGACTAATTGTAGGAA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	16	i52SL16	TATAATGACTAATTGTAGGAAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	26	i52SL26	CTTGATAATGCACCACTCTTTA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	27	i52SL27	CAACATAAATGTGAGATAACGT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	29	i52SL29	CAGATGATTCATATTTGGTTCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	30	i52SL30	ACAGATGATTCATATTTGGTTC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	31	i52SL31	TTTTCTAACAGATGATTCATAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC

120	i53SL41	TAGTTGCATGAAGTCAACCATT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	54	i52SL54	GTCATTATATACAGGCTGCCTC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	55	i52SL55	AGTCATTATATACAGGCTGCCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	56	i52SL56	TCCTACAATTAGTCATTATATA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	6	i52SL6	TTATGGCTAGGATGATGAACAA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	12	i52SL12	CCATGTGACAGGCTAGACATAC
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	15	i52SL15	ATATAATGACTAATTGTAGGAA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	16	i52SL16	TATAATGACTAATTGTAGGAAT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	26	i52SL26	CTTGATAATGCACCACTCTTTA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	27	i52SL27	CAACATAAATGTGAGATAACGT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	31	i52SL31	TTTTCTAACAGATGATTCATAT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC

121	i53SL42	GTAGTTGCATGAAGTCAACCAT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	56	i52SL56	TCCTACAATTAGTCATTATATA
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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121	i53SL42	GTAGTTGCATGAAGTCAACCAT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	6	i52SL6	TTATGGCTAGGATGATGAACAA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	16	i52SL16	TATAATGACTAATTGTAGGAAT
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	22	i52SL22	ACTCTGAGGCATGTATTTTACA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	26	i52SL26	CTTGATAATGCACCACTCTTTA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	30	i52SL30	ACAGATGATTCATATTTGGTTC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	31	i52SL31	TTTTCTAACAGATGATTCATAT

122	i53SL43	CATCTTTAAGATCACTTCAAAA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	54	i52SL54	GTCATTATATACAGGCTGCCTC
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	56	i52SL56	TCCTACAATTAGTCATTATATA
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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122	i53SL43	CATCTTTAAGATCACTTCAAAA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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123	i53SL44	TTAGTAATCTGGATATAGTTGG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	5	i52SL5	AAATTATTCATTGTGTTATGGC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	6	i52SL6	TTATGGCTAGGATGATGAACAA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	12	i52SL12	CCATGTGACAGGCTAGACATAC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	14	i52SL14	GCCTGTATATAATGACTAATTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	15	i52SL15	ATATAATGACTAATTGTAGGAA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	16	i52SL16	TATAATGACTAATTGTAGGAAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	18	i52SL18	TTACACTAGCTCCCTTGATGCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	26	i52SL26	CTTGATAATGCACCACTCTTTA

123	i53SL44	TTAGTAATCTGGATATAGTTGG	27	i52SL27	CAACATAAATGTGAGATAACGT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	29	i52SL29	CAGATGATTCATATTTGGTTCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	30	i52SL30	ACAGATGATTCATATTTGGTTC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	31	i52SL31	TTTTCTAACAGATGATTCATAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	54	i52SL54	GTCATTATATACAGGCTGCCTC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	55	i52SL55	AGTCATTATATACAGGCTGCCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	56	i52SL56	TCCTACAATTAGTCATTATATA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	5	i52SL5	AAATTATTCATTGTGTTATGGC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	6	i52SL6	TTATGGCTAGGATGATGAACAA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	12	i52SL12	CCATGTGACAGGCTAGACATAC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	14	i52SL14	GCCTGTATATAATGACTAATTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	15	i52SL15	ATATAATGACTAATTGTAGGAA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	16	i52SL16	TATAATGACTAATTGTAGGAAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	17	i52SL17	GTTACACTAGCTCCCTTGATGC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	18	i52SL18	TTACACTAGCTCCCTTGATGCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	21	i52SL21	AACTCTGAGGCATGTATTTTAC

124	i53SL45	TTGTTTAGTAATCTGGATATAG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	26	i52SL26	CTTGATAATGCACCACTCTTTA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	27	i52SL27	CAACATAAATGTGAGATAACGT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	29	i52SL29	CAGATGATTCATATTTGGTTCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	30	i52SL30	ACAGATGATTCATATTTGGTTC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	31	i52SL31	TTTTCTAACAGATGATTCATAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	54	i52SL54	GTCATTATATACAGGCTGCCTC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	55	i52SL55	AGTCATTATATACAGGCTGCCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	56	i52SL56	TCCTACAATTAGTCATTATATA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	5	i52SL5	AAATTATTCATTGTGTTATGGC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	6	i52SL6	TTATGGCTAGGATGATGAACAA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	12	i52SL12	CCATGTGACAGGCTAGACATAC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	14	i52SL14	GCCTGTATATAATGACTAATTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	15	i52SL15	ATATAATGACTAATTGTAGGAA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	16	i52SL16	TATAATGACTAATTGTAGGAAT

125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	26	i52SL26	CTTGATAATGCACCACTCTTTA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	27	i52SL27	CAACATAAATGTGAGATAACGT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	29	i52SL29	CAGATGATTCATATTTGGTTCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	30	i52SL30	ACAGATGATTCATATTTGGTTC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	31	i52SL31	TTTTCTAACAGATGATTCATAT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	54	i52SL54	GTCATTATATACAGGCTGCCTC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	55	i52SL55	AGTCATTATATACAGGCTGCCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	56	i52SL56	TCCTACAATTAGTCATTATATA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	5	i52SL5	AAATTATTCATTGTGTTATGGC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	6	i52SL6	TTATGGCTAGGATGATGAACAA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	11	i52SL11	GTTTGCTTTGCCATCCATGTGA

126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	12	i52SL12	CCATGTGACAGGCTAGACATAC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	14	i52SL14	GCCTGTATATAATGACTAATTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	15	i52SL15	ATATAATGACTAATTGTAGGAA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	16	i52SL16	TATAATGACTAATTGTAGGAAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	17	i52SL17	GTTACACTAGCTCCCTTGATGC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	18	i52SL18	TTACACTAGCTCCCTTGATGCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	20	i52SL20	TGATGCTAGGGGAAATAACTCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	22	i52SL22	ACTCTGAGGCATGTATTTTACA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	26	i52SL26	CTTGATAATGCACCACTCTTTA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	27	i52SL27	CAACATAAATGTGAGATAACGT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	29	i52SL29	CAGATGATTCATATTTGGTTCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	30	i52SL30	ACAGATGATTCATATTTGGTTC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	31	i52SL31	TTTTCTAACAGATGATTCATAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	54	i52SL54	GTCATTATATACAGGCTGCCTC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	55	i52SL55	AGTCATTATATACAGGCTGCCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	56	i52SL56	TCCTACAATTAGTCATTATATA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	5	i52SL5	AAATTATTCATTGTGTTATGGC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	6	i52SL6	TTATGGCTAGGATGATGAACAA

127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	12	i52SL12	CCATGTGACAGGCTAGACATAC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	14	i52SL14	GCCTGTATATAATGACTAATTG
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	16	i52SL16	TATAATGACTAATTGTAGGAAT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	26	i52SL26	CTTGATAATGCACCACTCTTTA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	27	i52SL27	CAACATAAATGTGAGATAACGT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	29	i52SL29	CAGATGATTCATATTTGGTTCT
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	31	i52SL31	TTTTCTAACAGATGATTCATAT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	54	i52SL54	GTCATTATATACAGGCTGCCTC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	55	i52SL55	AGTCATTATATACAGGCTGCCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	56	i52SL56	TCCTACAATTAGTCATTATATA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	1	i52SL1	TGAATTCTTTCAACTAGAATAA

128	i53SL49	GCCTCCCAAAGCACTAGGATTA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	12	i52SL12	CCATGTGACAGGCTAGACATAC
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	14	i52SL14	GCCTGTATATAATGACTAATTG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	26	i52SL26	CTTGATAATGCACCACTCTTTA
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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128	i53SL49	GCCTCCCAAAGCACTAGGATTA	54	i52SL54	GTCATTATATACAGGCTGCCTC
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129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	6	i52SL6	TTATGGCTAGGATGATGAACAA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	12	i52SL12	CCATGTGACAGGCTAGACATAC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	14	i52SL14	GCCTGTATATAATGACTAATTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	15	i52SL15	ATATAATGACTAATTGTAGGAA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	16	i52SL16	TATAATGACTAATTGTAGGAAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	18	i52SL18	TTACACTAGCTCCCTTGATGCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	22	i52SL22	ACTCTGAGGCATGTATTTTACA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	26	i52SL26	CTTGATAATGCACCACTCTTTA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	27	i52SL27	CAACATAAATGTGAGATAACGT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	29	i52SL29	CAGATGATTCATATTTGGTTCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	30	i52SL30	ACAGATGATTCATATTTGGTTC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	31	i52SL31	TTTTCTAACAGATGATTCATAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA

130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	56	i52SL56	TCCTACAATTAGTCATTATATA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	5	i52SL5	AAATTATTCATTGTGTTATGGC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	6	i52SL6	TTATGGCTAGGATGATGAACAA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	12	i52SL12	CCATGTGACAGGCTAGACATAC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	14	i52SL14	GCCTGTATATAATGACTAATTG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	16	i52SL16	TATAATGACTAATTGTAGGAAT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	20	i52SL20	TGATGCTAGGGGAAATAACTCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	26	i52SL26	CTTGATAATGCACCACTCTTTA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	27	i52SL27	CAACATAAATGTGAGATAACGT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	29	i52SL29	CAGATGATTCATATTTGGTTCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	30	i52SL30	ACAGATGATTCATATTTGGTTC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	31	i52SL31	TTTTCTAACAGATGATTCATAT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	56	i52SL56	TCCTACAATTAGTCATTATATA
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	5	i52SL5	AAATTATTCATTGTGTTATGGC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	12	i52SL12	CCATGTGACAGGCTAGACATAC
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	14	i52SL14	GCCTGTATATAATGACTAATTG
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	16	i52SL16	TATAATGACTAATTGTAGGAAT
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	26	i52SL26	CTTGATAATGCACCACTCTTTA
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	30	i52SL30	ACAGATGATTCATATTTGGTTC
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	31	i52SL31	TTTTCTAACAGATGATTCATAT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	40	i52SL40	TGAAATGCTGGCACTGGGAAAT

132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	56	i52SL56	TCCTACAATTAGTCATTATATA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	12	i52SL12	CCATGTGACAGGCTAGACATAC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	16	i52SL16	TATAATGACTAATTGTAGGAAT
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	26	i52SL26	CTTGATAATGCACCACTCTTTA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	29	i52SL29	CAGATGATTCATATTTGGTTCT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	30	i52SL30	ACAGATGATTCATATTTGGTTC
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	31	i52SL31	TTTTCTAACAGATGATTCATAT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	54	i52SL54	GTCATTATATACAGGCTGCCTC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	56	i52SL56	TCCTACAATTAGTCATTATATA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	5	i52SL5	AAATTATTCATTGTGTTATGGC
134	i53SL55	AGCCAGGCGTGTACCACCACGC	6	i52SL6	TTATGGCTAGGATGATGAACAA
134	i53SL55	AGCCAGGCGTGTACCACCACGC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	14	i52SL14	GCCTGTATATAATGACTAATTG
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	26	i52SL26	CTTGATAATGCACCACTCTTTA
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	29	i52SL29	CAGATGATTCATATTTGGTTCT
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	54	i52SL54	GTCATTATATACAGGCTGCCTC
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136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	1	i52SL1	TGAATTCTTTCAACTAGAATAA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	2	i52SL2	ATATATAGTAGTAAATGCTAGT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	4	i52SL4	TTAAAAAATTATTCATTGTGTT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	5	i52SL5	AAATTATTCATTGTGTTATGGC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	6	i52SL6	TTATGGCTAGGATGATGAACAA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	14	i52SL14	GCCTGTATATAATGACTAATTG
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	16	i52SL16	TATAATGACTAATTGTAGGAAT
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	18	i52SL18	TTACACTAGCTCCCTTGATGCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	19	i52SL19	TACACTAGCTCCCTTGATGCTA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	20	i52SL20	TGATGCTAGGGGAAATAACTCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	21	i52SL21	AACTCTGAGGCATGTATTTTAC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	22	i52SL22	ACTCTGAGGCATGTATTTTACA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	25	i52SL25	CTCCAGTGACCCACAACAGCAG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	26	i52SL26	CTTGATAATGCACCACTCTTTA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	27	i52SL27	CAACATAAATGTGAGATAACGT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	28	i52SL28	TGTTGATGTTCTATGTCACCTT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	29	i52SL29	CAGATGATTCATATTTGGTTCT
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	31	i52SL31	TTTTCTAACAGATGATTCATAT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	54	i52SL54	GTCATTATATACAGGCTGCCTC
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137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	56	i52SL56	TCCTACAATTAGTCATTATATA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	1	i52SL1	TGAATTCTTTCAACTAGAATAA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	4	i52SL4	TTAAAAAATTATTCATTGTGTT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	5	i52SL5	AAATTATTCATTGTGTTATGGC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	6	i52SL6	TTATGGCTAGGATGATGAACAA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	12	i52SL12	CCATGTGACAGGCTAGACATAC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	14	i52SL14	GCCTGTATATAATGACTAATTG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	15	i52SL15	ATATAATGACTAATTGTAGGAA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	16	i52SL16	TATAATGACTAATTGTAGGAAT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	18	i52SL18	TTACACTAGCTCCCTTGATGCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	20	i52SL20	TGATGCTAGGGGAAATAACTCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	26	i52SL26	CTTGATAATGCACCACTCTTTA
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
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138	i53SL59	AGCTCACTGAGCCTTGAACTCT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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139	i53SL60	TAGCTCACTGAGCCTTGAACTC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
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139	i53SL60	TAGCTCACTGAGCCTTGAACTC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
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139	i53SL60	TAGCTCACTGAGCCTTGAACTC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	5	i52SL5	AAATTATTCATTGTGTTATGGC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	6	i52SL6	TTATGGCTAGGATGATGAACAA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	12	i52SL12	CCATGTGACAGGCTAGACATAC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	16	i52SL16	TATAATGACTAATTGTAGGAAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	21	i52SL21	AACTCTGAGGCATGTATTTTAC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	22	i52SL22	ACTCTGAGGCATGTATTTTACA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	25	i52SL25	CTCCAGTGACCCACAACAGCAG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	26	i52SL26	CTTGATAATGCACCACTCTTTA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	27	i52SL27	CAACATAAATGTGAGATAACGT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	28	i52SL28	TGTTGATGTTCTATGTCACCTT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	29	i52SL29	CAGATGATTCATATTTGGTTCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	30	i52SL30	ACAGATGATTCATATTTGGTTC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	31	i52SL31	TTTTCTAACAGATGATTCATAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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140	i53SL61	ATAGCTCACTGAGCCTTGAACT	46	i52SL46	GTATGTCTAGCCTGTCACATGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	54	i52SL54	GTCATTATATACAGGCTGCCTC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	55	i52SL55	AGTCATTATATACAGGCTGCCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	56	i52SL56	TCCTACAATTAGTCATTATATA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	59	i52SL59	GAGCTTTATCCCTTGGGAAACT

140	i53SL61	ATAGCTCACTGAGCCTTGAACT	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	64	i52SL64	CATTATCAAGCCAGCTGCTGTT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	1	i52SL1	TGAATTCTTTCAACTAGAATAA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	5	i52SL5	AAATTATTCATTGTGTTATGGC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	6	i52SL6	TTATGGCTAGGATGATGAACAA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	8	i52SL8	TTTCTGTTAAATTATTTTCCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	11	i52SL11	GTTTGCTTTGCCATCCATGTGA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	12	i52SL12	CCATGTGACAGGCTAGACATAC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	13	i52SL13	GATGCCTCCCCTCCAGCTCCCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	14	i52SL14	GCCTGTATATAATGACTAATTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	15	i52SL15	ATATAATGACTAATTGTAGGAA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	16	i52SL16	TATAATGACTAATTGTAGGAAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	17	i52SL17	GTTACACTAGCTCCCTTGATGC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	18	i52SL18	TTACACTAGCTCCCTTGATGCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	20	i52SL20	TGATGCTAGGGGAAATAACTCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	22	i52SL22	ACTCTGAGGCATGTATTTTACA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	26	i52SL26	CTTGATAATGCACCACTCTTTA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	27	i52SL27	CAACATAAATGTGAGATAACGT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	29	i52SL29	CAGATGATTCATATTTGGTTCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	30	i52SL30	ACAGATGATTCATATTTGGTTC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	31	i52SL31	TTTTCTAACAGATGATTCATAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	54	i52SL54	GTCATTATATACAGGCTGCCTC

141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	55	i52SL55	AGTCATTATATACAGGCTGCCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	56	i52SL56	TCCTACAATTAGTCATTATATA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
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141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	1	i52SL1	TGAATTCTTTCAACTAGAATAA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	2	i52SL2	ATATATAGTAGTAAATGCTAGT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	3	i52SL3	TATAGTAGTAAATGCTAGTCTG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	12	i52SL12	CCATGTGACAGGCTAGACATAC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	14	i52SL14	GCCTGTATATAATGACTAATTG
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	16	i52SL16	TATAATGACTAATTGTAGGAAT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	25	i52SL25	CTCCAGTGACCCACAACAGCAG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	26	i52SL26	CTTGATAATGCACCACTCTTTA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	27	i52SL27	CAACATAAATGTGAGATAACGT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	28	i52SL28	TGTTGATGTTCTATGTCACCTT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	29	i52SL29	CAGATGATTCATATTTGGTTCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	30	i52SL30	ACAGATGATTCATATTTGGTTC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	44	i52SL44	TCCTGTGGCAACAGAAAGCCTT
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	46	i52SL46	GTATGTCTAGCCTGTCACATGG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
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142	i53SL63	GAGACAGAGTCTCACTGTCACC	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	2	i52SL2	ATATATAGTAGTAAATGCTAGT
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143	i53SL64	GATACCTTTTTAAAATAAAATA	4	i52SL4	TTAAAAAATTATTCATTGTGTT
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143	i53SL64	GATACCTTTTTAAAATAAAATA	7	i52SL7	AACAGGATTCTTTGCTTTTTTG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	9	i52SL9	AGTGCCAGCATTTCATTGCCTG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	12	i52SL12	CCATGTGACAGGCTAGACATAC
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143	i53SL64	GATACCTTTTTAAAATAAAATA	14	i52SL14	GCCTGTATATAATGACTAATTG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	16	i52SL16	TATAATGACTAATTGTAGGAAT
143	i53SL64	GATACCTTTTTAAAATAAAATA	17	i52SL17	GTTACACTAGCTCCCTTGATGC
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143	i53SL64	GATACCTTTTTAAAATAAAATA	19	i52SL19	TACACTAGCTCCCTTGATGCTA
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143	i53SL64	GATACCTTTTTAAAATAAAATA	21	i52SL21	AACTCTGAGGCATGTATTTTAC
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143	i53SL64	GATACCTTTTTAAAATAAAATA	23	i52SL23	TACAAGGGTTCCAGAGTTTCCC
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143	i53SL64	GATACCTTTTTAAAATAAAATA	25	i52SL25	CTCCAGTGACCCACAACAGCAG
143	i53SL64	GATACCTTTTTAAAATAAAATA	26	i52SL26	CTTGATAATGCACCACTCTTTA
143	i53SL64	GATACCTTTTTAAAATAAAATA	27	i52SL27	CAACATAAATGTGAGATAACGT
143	i53SL64	GATACCTTTTTAAAATAAAATA	28	i52SL28	TGTTGATGTTCTATGTCACCTT
143	i53SL64	GATACCTTTTTAAAATAAAATA	29	i52SL29	CAGATGATTCATATTTGGTTCT
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143	i53SL64	GATACCTTTTTAAAATAAAATA	32	i52SL32	GAAGTGGCAAGGATGAGGGGAT
143	i53SL64	GATACCTTTTTAAAATAAAATA	33	i52SL33	GGTGCTGAAGTGGCAAGGATGA
143	i53SL64	GATACCTTTTTAAAATAAAATA	34	i52SL34	GGGTGCTGAAGTGGCAAGGATG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	36	i52SL36	GGCTGATGGGTGCTGAAGTGGC
143	i53SL64	GATACCTTTTTAAAATAAAATA	37	i52SL37	AATCAGGCTGATGGGTGCTGAA
143	i53SL64	GATACCTTTTTAAAATAAAATA	38	i52SL38	TGGCACTGGGAAATCAGGCTGA
143	i53SL64	GATACCTTTTTAAAATAAAATA	39	i52SL39	CTGGCACTGGGAAATCAGGCTG
143	i53SL64	GATACCTTTTTAAAATAAAATA	40	i52SL40	TGAAATGCTGGCACTGGGAAAT
143	i53SL64	GATACCTTTTTAAAATAAAATA	41	i52SL41	TCAGGCAATGAAATGCTGGCAC
143	i53SL64	GATACCTTTTTAAAATAAAATA	42	i52SL42	TTCAGGCAATGAAATGCTGGCA
143	i53SL64	GATACCTTTTTAAAATAAAATA	43	i52SL43	AAAGCCTTCAGGCAATGAAATG
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143	i53SL64	GATACCTTTTTAAAATAAAATA	45	i52SL45	ATGGATGGCAAAGCAAACTCCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	46	i52SL46	GTATGTCTAGCCTGTCACATGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	47	i52SL47	CCTGGTATGTCTAGCCTGTCAC
143	i53SL64	GATACCTTTTTAAAATAAAATA	48	i52SL48	CTGGAGGGGAGGCATCAGTTGC
143	i53SL64	GATACCTTTTTAAAATAAAATA	49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA
143	i53SL64	GATACCTTTTTAAAATAAAATA	51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	52	i52SL52	TACAGGCTGCCTCTGGGAGCTG
143	i53SL64	GATACCTTTTTAAAATAAAATA	53	i52SL53	ATATACAGGCTGCCTCTGGGAG
143	i53SL64	GATACCTTTTTAAAATAAAATA	54	i52SL54	GTCATTATATACAGGCTGCCTC
143	i53SL64	GATACCTTTTTAAAATAAAATA	55	i52SL55	AGTCATTATATACAGGCTGCCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	56	i52SL56	TCCTACAATTAGTCATTATATA
143	i53SL64	GATACCTTTTTAAAATAAAATA	57	i52SL57	AGAGTTATTTCCCCTAGCATCA
143	i53SL64	GATACCTTTTTAAAATAAAATA	58	i52SL58	CAGAGTTATTTCCCCTAGCATC
143	i53SL64	GATACCTTTTTAAAATAAAATA	59	i52SL59	GAGCTTTATCCCTTGGGAAACT
143	i53SL64	GATACCTTTTTAAAATAAAATA	60	i52SL60	GGGTCACTGGAGCTTTATCCCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	61	i52SL61	TGGGTCACTGGAGCTTTATCCC
143	i53SL64	GATACCTTTTTAAAATAAAATA	62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA
143	i53SL64	GATACCTTTTTAAAATAAAATA	63	i52SL63	ATTATCAAGCCAGCTGCTGTTG
143	i53SL64	GATACCTTTTTAAAATAAAATA	64	i52SL64	CATTATCAAGCCAGCTGCTGTT

E. Table 1E. Intron 52-Exon 53 SluCas9 guide pairs:

Guide 1 SEQ ID NO	Guide 1 name	Guide 1 sequence	Guide 2 SEQ ID NO	Guide 2 name	Guide 2 sequence
1	i52SL1	TGAATTCTTTCAACTAGAATAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
1	i52SL1	TGAATTCTTTCAACTAGAATAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
1	i52SL1	TGAATTCTTTCAACTAGAATAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
1	i52SL1	TGAATTCTTTCAACTAGAATAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
1	i52SL1	TGAATTCTTTCAACTAGAATAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
1	i52SL1	TGAATTCTTTCAACTAGAATAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
1	i52SL1	TGAATTCTTTCAACTAGAATAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
1	i52SL1	TGAATTCTTTCAACTAGAATAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
1	i52SL1	TGAATTCTTTCAACTAGAATAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
1	i52SL1	TGAATTCTTTCAACTAGAATAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
1	i52SL1	TGAATTCTTTCAACTAGAATAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
2	i52SL2	ATATATAGTAGTAAATGCTAGT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
2	i52SL2	ATATATAGTAGTAAATGCTAGT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG

2	i52SL2	ATATATAGTAGTAAATGCTAGT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
2	i52SL2	ATATATAGTAGTAAATGCTAGT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
2	i52SL2	ATATATAGTAGTAAATGCTAGT	81	E53SL99	GTTAAAGGATTCAACACAATGG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	82	E53SL100	AAATGTTAAAGGATTCAACACA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	84	E53SL102	TACAAGAACACCTTCAGAACCG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
2	i52SL2	ATATATAGTAGTAAATGCTAGT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
2	i52SL2	ATATATAGTAGTAAATGCTAGT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
3	i52SL3	TATAGTAGTAAATGCTAGTCTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
4	i52SL4	TTAAAAAATTATTCATTGTGTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
4	i52SL4	TTAAAAAATTATTCATTGTGTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
4	i52SL4	TTAAAAAATTATTCATTGTGTT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
4	i52SL4	TTAAAAAATTATTCATTGTGTT	81	E53SL99	GTTAAAGGATTCAACACAATGG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	82	E53SL100	AAATGTTAAAGGATTCAACACA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	84	E53SL102	TACAAGAACACCTTCAGAACCG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
4	i52SL4	TTAAAAAATTATTCATTGTGTT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
4	i52SL4	TTAAAAAATTATTCATTGTGTT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

5	i52SL5	AAATTATTCATTGTGTTATGGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
5	i52SL5	AAATTATTCATTGTGTTATGGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
5	i52SL5	AAATTATTCATTGTGTTATGGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
5	i52SL5	AAATTATTCATTGTGTTATGGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
5	i52SL5	AAATTATTCATTGTGTTATGGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
5	i52SL5	AAATTATTCATTGTGTTATGGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
5	i52SL5	AAATTATTCATTGTGTTATGGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
5	i52SL5	AAATTATTCATTGTGTTATGGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
5	i52SL5	AAATTATTCATTGTGTTATGGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
5	i52SL5	AAATTATTCATTGTGTTATGGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
5	i52SL5	AAATTATTCATTGTGTTATGGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
5	i52SL5	AAATTATTCATTGTGTTATGGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
5	i52SL5	AAATTATTCATTGTGTTATGGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
5	i52SL5	AAATTATTCATTGTGTTATGGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
5	i52SL5	AAATTATTCATTGTGTTATGGC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
5	i52SL5	AAATTATTCATTGTGTTATGGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
5	i52SL5	AAATTATTCATTGTGTTATGGC	81	E53SL99	GTTAAAGGATTCAACACAATGG
5	i52SL5	AAATTATTCATTGTGTTATGGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
5	i52SL5	AAATTATTCATTGTGTTATGGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
5	i52SL5	AAATTATTCATTGTGTTATGGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
5	i52SL5	AAATTATTCATTGTGTTATGGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
5	i52SL5	AAATTATTCATTGTGTTATGGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
5	i52SL5	AAATTATTCATTGTGTTATGGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
6	i52SL6	TTATGGCTAGGATGATGAACAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
6	i52SL6	TTATGGCTAGGATGATGAACAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
6	i52SL6	TTATGGCTAGGATGATGAACAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
6	i52SL6	TTATGGCTAGGATGATGAACAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
6	i52SL6	TTATGGCTAGGATGATGAACAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
6	i52SL6	TTATGGCTAGGATGATGAACAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
6	i52SL6	TTATGGCTAGGATGATGAACAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
6	i52SL6	TTATGGCTAGGATGATGAACAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
6	i52SL6	TTATGGCTAGGATGATGAACAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
6	i52SL6	TTATGGCTAGGATGATGAACAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
6	i52SL6	TTATGGCTAGGATGATGAACAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
6	i52SL6	TTATGGCTAGGATGATGAACAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
6	i52SL6	TTATGGCTAGGATGATGAACAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
6	i52SL6	TTATGGCTAGGATGATGAACAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
6	i52SL6	TTATGGCTAGGATGATGAACAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
6	i52SL6	TTATGGCTAGGATGATGAACAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
6	i52SL6	TTATGGCTAGGATGATGAACAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
6	i52SL6	TTATGGCTAGGATGATGAACAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
6	i52SL6	TTATGGCTAGGATGATGAACAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
6	i52SL6	TTATGGCTAGGATGATGAACAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
6	i52SL6	TTATGGCTAGGATGATGAACAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
6	i52SL6	TTATGGCTAGGATGATGAACAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
6	i52SL6	TTATGGCTAGGATGATGAACAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA

7	i52SL7	AACAGGATTCTTTGCTTTTTTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
7	i52SL7	AACAGGATTCTTTGCTTTTTTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
8	i52SL8	TTTCTGTTAAATTATTTTCCTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
9	i52SL9	AGTGCCAGCATTTCATTGCCTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT

10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
10	i52SL10	GCCTGAAGGCTTTCTGTTGCCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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11	i52SL11	GTTTGCTTTGCCATCCATGTGA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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11	i52SL11	GTTTGCTTTGCCATCCATGTGA	82	E53SL100	AAATGTTAAAGGATTCAACACA
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
11	i52SL11	GTTTGCTTTGCCATCCATGTGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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12	i52SL12	CCATGTGACAGGCTAGACATAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
12	i52SL12	CCATGTGACAGGCTAGACATAC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
12	i52SL12	CCATGTGACAGGCTAGACATAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
12	i52SL12	CCATGTGACAGGCTAGACATAC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
12	i52SL12	CCATGTGACAGGCTAGACATAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
12	i52SL12	CCATGTGACAGGCTAGACATAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
12	i52SL12	CCATGTGACAGGCTAGACATAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
12	i52SL12	CCATGTGACAGGCTAGACATAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
12	i52SL12	CCATGTGACAGGCTAGACATAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
12	i52SL12	CCATGTGACAGGCTAGACATAC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
12	i52SL12	CCATGTGACAGGCTAGACATAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
12	i52SL12	CCATGTGACAGGCTAGACATAC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
12	i52SL12	CCATGTGACAGGCTAGACATAC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
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12	i52SL12	CCATGTGACAGGCTAGACATAC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
12	i52SL12	CCATGTGACAGGCTAGACATAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT

12	i52SL12	CCATGTGACAGGCTAGACATAC	81	E53SL99	GTTAAAGGATTCAACACAATGG
12	i52SL12	CCATGTGACAGGCTAGACATAC	82	E53SL100	AAATGTTAAAGGATTCAACACA
12	i52SL12	CCATGTGACAGGCTAGACATAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
12	i52SL12	CCATGTGACAGGCTAGACATAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
12	i52SL12	CCATGTGACAGGCTAGACATAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
12	i52SL12	CCATGTGACAGGCTAGACATAC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
12	i52SL12	CCATGTGACAGGCTAGACATAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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13	i52SL13	GATGCCTCCCCTCCAGCTCCCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
14	i52SL14	GCCTGTATATAATGACTAATTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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14	i52SL14	GCCTGTATATAATGACTAATTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
14	i52SL14	GCCTGTATATAATGACTAATTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
14	i52SL14	GCCTGTATATAATGACTAATTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
14	i52SL14	GCCTGTATATAATGACTAATTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
14	i52SL14	GCCTGTATATAATGACTAATTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
14	i52SL14	GCCTGTATATAATGACTAATTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
14	i52SL14	GCCTGTATATAATGACTAATTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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14	i52SL14	GCCTGTATATAATGACTAATTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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14	i52SL14	GCCTGTATATAATGACTAATTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
14	i52SL14	GCCTGTATATAATGACTAATTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
14	i52SL14	GCCTGTATATAATGACTAATTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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14	i52SL14	GCCTGTATATAATGACTAATTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
14	i52SL14	GCCTGTATATAATGACTAATTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
14	i52SL14	GCCTGTATATAATGACTAATTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
14	i52SL14	GCCTGTATATAATGACTAATTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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14	i52SL14	GCCTGTATATAATGACTAATTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
15	i52SL15	ATATAATGACTAATTGTAGGAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
15	i52SL15	ATATAATGACTAATTGTAGGAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
15	i52SL15	ATATAATGACTAATTGTAGGAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
15	i52SL15	ATATAATGACTAATTGTAGGAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
15	i52SL15	ATATAATGACTAATTGTAGGAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
15	i52SL15	ATATAATGACTAATTGTAGGAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT

15	i52SL15	ATATAATGACTAATTGTAGGAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
15	i52SL15	ATATAATGACTAATTGTAGGAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
15	i52SL15	ATATAATGACTAATTGTAGGAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
15	i52SL15	ATATAATGACTAATTGTAGGAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
15	i52SL15	ATATAATGACTAATTGTAGGAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
15	i52SL15	ATATAATGACTAATTGTAGGAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
15	i52SL15	ATATAATGACTAATTGTAGGAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
15	i52SL15	ATATAATGACTAATTGTAGGAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
15	i52SL15	ATATAATGACTAATTGTAGGAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
15	i52SL15	ATATAATGACTAATTGTAGGAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
15	i52SL15	ATATAATGACTAATTGTAGGAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
15	i52SL15	ATATAATGACTAATTGTAGGAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
15	i52SL15	ATATAATGACTAATTGTAGGAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
15	i52SL15	ATATAATGACTAATTGTAGGAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
15	i52SL15	ATATAATGACTAATTGTAGGAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
15	i52SL15	ATATAATGACTAATTGTAGGAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
15	i52SL15	ATATAATGACTAATTGTAGGAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
16	i52SL16	TATAATGACTAATTGTAGGAAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
16	i52SL16	TATAATGACTAATTGTAGGAAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
16	i52SL16	TATAATGACTAATTGTAGGAAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
16	i52SL16	TATAATGACTAATTGTAGGAAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
16	i52SL16	TATAATGACTAATTGTAGGAAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
16	i52SL16	TATAATGACTAATTGTAGGAAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
16	i52SL16	TATAATGACTAATTGTAGGAAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
16	i52SL16	TATAATGACTAATTGTAGGAAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
16	i52SL16	TATAATGACTAATTGTAGGAAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
16	i52SL16	TATAATGACTAATTGTAGGAAT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
16	i52SL16	TATAATGACTAATTGTAGGAAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
16	i52SL16	TATAATGACTAATTGTAGGAAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
16	i52SL16	TATAATGACTAATTGTAGGAAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
16	i52SL16	TATAATGACTAATTGTAGGAAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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16	i52SL16	TATAATGACTAATTGTAGGAAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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16	i52SL16	TATAATGACTAATTGTAGGAAT	82	E53SL100	AAATGTTAAAGGATTCAACACA
16	i52SL16	TATAATGACTAATTGTAGGAAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
16	i52SL16	TATAATGACTAATTGTAGGAAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
16	i52SL16	TATAATGACTAATTGTAGGAAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
16	i52SL16	TATAATGACTAATTGTAGGAAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
16	i52SL16	TATAATGACTAATTGTAGGAAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
17	i52SL17	GTTACACTAGCTCCCTTGATGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
17	i52SL17	GTTACACTAGCTCCCTTGATGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
17	i52SL17	GTTACACTAGCTCCCTTGATGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
17	i52SL17	GTTACACTAGCTCCCTTGATGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
17	i52SL17	GTTACACTAGCTCCCTTGATGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
17	i52SL17	GTTACACTAGCTCCCTTGATGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
17	i52SL17	GTTACACTAGCTCCCTTGATGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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17	i52SL17	GTTACACTAGCTCCCTTGATGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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17	i52SL17	GTTACACTAGCTCCCTTGATGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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17	i52SL17	GTTACACTAGCTCCCTTGATGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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17	i52SL17	GTTACACTAGCTCCCTTGATGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
17	i52SL17	GTTACACTAGCTCCCTTGATGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA

17	i52SL17	GTTACACTAGCTCCCTTGATGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
17	i52SL17	GTTACACTAGCTCCCTTGATGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
17	i52SL17	GTTACACTAGCTCCCTTGATGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
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18	i52SL18	TTACACTAGCTCCCTTGATGCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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18	i52SL18	TTACACTAGCTCCCTTGATGCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
18	i52SL18	TTACACTAGCTCCCTTGATGCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
18	i52SL18	TTACACTAGCTCCCTTGATGCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
18	i52SL18	TTACACTAGCTCCCTTGATGCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
18	i52SL18	TTACACTAGCTCCCTTGATGCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
18	i52SL18	TTACACTAGCTCCCTTGATGCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
18	i52SL18	TTACACTAGCTCCCTTGATGCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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18	i52SL18	TTACACTAGCTCCCTTGATGCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
18	i52SL18	TTACACTAGCTCCCTTGATGCT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
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18	i52SL18	TTACACTAGCTCCCTTGATGCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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18	i52SL18	TTACACTAGCTCCCTTGATGCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
18	i52SL18	TTACACTAGCTCCCTTGATGCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
18	i52SL18	TTACACTAGCTCCCTTGATGCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
18	i52SL18	TTACACTAGCTCCCTTGATGCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
18	i52SL18	TTACACTAGCTCCCTTGATGCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
18	i52SL18	TTACACTAGCTCCCTTGATGCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
18	i52SL18	TTACACTAGCTCCCTTGATGCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
18	i52SL18	TTACACTAGCTCCCTTGATGCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
19	i52SL19	TACACTAGCTCCCTTGATGCTA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
19	i52SL19	TACACTAGCTCCCTTGATGCTA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
19	i52SL19	TACACTAGCTCCCTTGATGCTA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
19	i52SL19	TACACTAGCTCCCTTGATGCTA	81	E53SL99	GTTAAAGGATTCAACACAATGG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	82	E53SL100	AAATGTTAAAGGATTCAACACA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	84	E53SL102	TACAAGAACACCTTCAGAACCG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
19	i52SL19	TACACTAGCTCCCTTGATGCTA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
19	i52SL19	TACACTAGCTCCCTTGATGCTA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
20	i52SL20	TGATGCTAGGGGAAATAACTCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
20	i52SL20	TGATGCTAGGGGAAATAACTCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG

20	i52SL20	TGATGCTAGGGGAAATAACTCT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
20	i52SL20	TGATGCTAGGGGAAATAACTCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
20	i52SL20	TGATGCTAGGGGAAATAACTCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
20	i52SL20	TGATGCTAGGGGAAATAACTCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
20	i52SL20	TGATGCTAGGGGAAATAACTCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
21	i52SL21	AACTCTGAGGCATGTATTTTAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
21	i52SL21	AACTCTGAGGCATGTATTTTAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
21	i52SL21	AACTCTGAGGCATGTATTTTAC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
21	i52SL21	AACTCTGAGGCATGTATTTTAC	81	E53SL99	GTTAAAGGATTCAACACAATGG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	82	E53SL100	AAATGTTAAAGGATTCAACACA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
21	i52SL21	AACTCTGAGGCATGTATTTTAC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
21	i52SL21	AACTCTGAGGCATGTATTTTAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
22	i52SL22	ACTCTGAGGCATGTATTTTACA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
22	i52SL22	ACTCTGAGGCATGTATTTTACA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
22	i52SL22	ACTCTGAGGCATGTATTTTACA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
22	i52SL22	ACTCTGAGGCATGTATTTTACA	81	E53SL99	GTTAAAGGATTCAACACAATGG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	82	E53SL100	AAATGTTAAAGGATTCAACACA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	84	E53SL102	TACAAGAACACCTTCAGAACCG
22	i52SL22	ACTCTGAGGCATGTATTTTACA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
22	i52SL22	ACTCTGAGGCATGTATTTTACA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG

22	i52SL22	ACTCTGAGGCATGTATTTTACA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	81	E53SL99	GTTAAAGGATTCAACACAATGG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	82	E53SL100	AAATGTTAAAGGATTCAACACA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
23	i52SL23	TACAAGGGTTCCAGAGTTTCCC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
24	i52SL24	ACAAGGGTTCCAGAGTTTCCCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
25	i52SL25	CTCCAGTGACCCACAACAGCAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
25	i52SL25	CTCCAGTGACCCACAACAGCAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC

25	i52SL25	CTCCAGTGACCCACAACAGCAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
25	i52SL25	CTCCAGTGACCCACAACAGCAG	81	E53SL99	GTTAAAGGATTCAACACAATGG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
25	i52SL25	CTCCAGTGACCCACAACAGCAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
25	i52SL25	CTCCAGTGACCCACAACAGCAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
26	i52SL26	CTTGATAATGCACCACTCTTTA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
26	i52SL26	CTTGATAATGCACCACTCTTTA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
26	i52SL26	CTTGATAATGCACCACTCTTTA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
26	i52SL26	CTTGATAATGCACCACTCTTTA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
26	i52SL26	CTTGATAATGCACCACTCTTTA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
26	i52SL26	CTTGATAATGCACCACTCTTTA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
26	i52SL26	CTTGATAATGCACCACTCTTTA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
26	i52SL26	CTTGATAATGCACCACTCTTTA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
26	i52SL26	CTTGATAATGCACCACTCTTTA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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26	i52SL26	CTTGATAATGCACCACTCTTTA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
26	i52SL26	CTTGATAATGCACCACTCTTTA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
26	i52SL26	CTTGATAATGCACCACTCTTTA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
26	i52SL26	CTTGATAATGCACCACTCTTTA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
26	i52SL26	CTTGATAATGCACCACTCTTTA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
26	i52SL26	CTTGATAATGCACCACTCTTTA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
26	i52SL26	CTTGATAATGCACCACTCTTTA	81	E53SL99	GTTAAAGGATTCAACACAATGG
26	i52SL26	CTTGATAATGCACCACTCTTTA	82	E53SL100	AAATGTTAAAGGATTCAACACA
26	i52SL26	CTTGATAATGCACCACTCTTTA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
26	i52SL26	CTTGATAATGCACCACTCTTTA	84	E53SL102	TACAAGAACACCTTCAGAACCG
26	i52SL26	CTTGATAATGCACCACTCTTTA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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26	i52SL26	CTTGATAATGCACCACTCTTTA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
27	i52SL27	CAACATAAATGTGAGATAACGT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
27	i52SL27	CAACATAAATGTGAGATAACGT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
27	i52SL27	CAACATAAATGTGAGATAACGT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
27	i52SL27	CAACATAAATGTGAGATAACGT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
27	i52SL27	CAACATAAATGTGAGATAACGT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
27	i52SL27	CAACATAAATGTGAGATAACGT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
27	i52SL27	CAACATAAATGTGAGATAACGT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
27	i52SL27	CAACATAAATGTGAGATAACGT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
27	i52SL27	CAACATAAATGTGAGATAACGT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
27	i52SL27	CAACATAAATGTGAGATAACGT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
27	i52SL27	CAACATAAATGTGAGATAACGT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
27	i52SL27	CAACATAAATGTGAGATAACGT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
27	i52SL27	CAACATAAATGTGAGATAACGT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
27	i52SL27	CAACATAAATGTGAGATAACGT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
27	i52SL27	CAACATAAATGTGAGATAACGT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
27	i52SL27	CAACATAAATGTGAGATAACGT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
27	i52SL27	CAACATAAATGTGAGATAACGT	81	E53SL99	GTTAAAGGATTCAACACAATGG
27	i52SL27	CAACATAAATGTGAGATAACGT	82	E53SL100	AAATGTTAAAGGATTCAACACA
27	i52SL27	CAACATAAATGTGAGATAACGT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
27	i52SL27	CAACATAAATGTGAGATAACGT	84	E53SL102	TACAAGAACACCTTCAGAACCG
27	i52SL27	CAACATAAATGTGAGATAACGT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
27	i52SL27	CAACATAAATGTGAGATAACGT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
27	i52SL27	CAACATAAATGTGAGATAACGT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
28	i52SL28	TGTTGATGTTCTATGTCACCTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	66	E53SL30	CTTTTGGATTGCATCTACTGTA

28	i52SL28	TGTTGATGTTCTATGTCACCTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
28	i52SL28	TGTTGATGTTCTATGTCACCTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
28	i52SL28	TGTTGATGTTCTATGTCACCTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
28	i52SL28	TGTTGATGTTCTATGTCACCTT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
28	i52SL28	TGTTGATGTTCTATGTCACCTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
28	i52SL28	TGTTGATGTTCTATGTCACCTT	81	E53SL99	GTTAAAGGATTCAACACAATGG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	82	E53SL100	AAATGTTAAAGGATTCAACACA
28	i52SL28	TGTTGATGTTCTATGTCACCTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
28	i52SL28	TGTTGATGTTCTATGTCACCTT	84	E53SL102	TACAAGAACACCTTCAGAACCG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
28	i52SL28	TGTTGATGTTCTATGTCACCTT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
28	i52SL28	TGTTGATGTTCTATGTCACCTT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
29	i52SL29	CAGATGATTCATATTTGGTTCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
29	i52SL29	CAGATGATTCATATTTGGTTCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
29	i52SL29	CAGATGATTCATATTTGGTTCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
29	i52SL29	CAGATGATTCATATTTGGTTCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
29	i52SL29	CAGATGATTCATATTTGGTTCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
29	i52SL29	CAGATGATTCATATTTGGTTCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
29	i52SL29	CAGATGATTCATATTTGGTTCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
29	i52SL29	CAGATGATTCATATTTGGTTCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
29	i52SL29	CAGATGATTCATATTTGGTTCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
29	i52SL29	CAGATGATTCATATTTGGTTCT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
29	i52SL29	CAGATGATTCATATTTGGTTCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
29	i52SL29	CAGATGATTCATATTTGGTTCT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
29	i52SL29	CAGATGATTCATATTTGGTTCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
29	i52SL29	CAGATGATTCATATTTGGTTCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
29	i52SL29	CAGATGATTCATATTTGGTTCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
29	i52SL29	CAGATGATTCATATTTGGTTCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
29	i52SL29	CAGATGATTCATATTTGGTTCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
29	i52SL29	CAGATGATTCATATTTGGTTCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
29	i52SL29	CAGATGATTCATATTTGGTTCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
29	i52SL29	CAGATGATTCATATTTGGTTCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
29	i52SL29	CAGATGATTCATATTTGGTTCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
29	i52SL29	CAGATGATTCATATTTGGTTCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
29	i52SL29	CAGATGATTCATATTTGGTTCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
30	i52SL30	ACAGATGATTCATATTTGGTTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
30	i52SL30	ACAGATGATTCATATTTGGTTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
30	i52SL30	ACAGATGATTCATATTTGGTTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
30	i52SL30	ACAGATGATTCATATTTGGTTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
30	i52SL30	ACAGATGATTCATATTTGGTTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
30	i52SL30	ACAGATGATTCATATTTGGTTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
30	i52SL30	ACAGATGATTCATATTTGGTTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
30	i52SL30	ACAGATGATTCATATTTGGTTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
30	i52SL30	ACAGATGATTCATATTTGGTTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
30	i52SL30	ACAGATGATTCATATTTGGTTC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
30	i52SL30	ACAGATGATTCATATTTGGTTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
30	i52SL30	ACAGATGATTCATATTTGGTTC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
30	i52SL30	ACAGATGATTCATATTTGGTTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
30	i52SL30	ACAGATGATTCATATTTGGTTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
30	i52SL30	ACAGATGATTCATATTTGGTTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG

30	i52SL30	ACAGATGATTCATATTTGGTTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
30	i52SL30	ACAGATGATTCATATTTGGTTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
30	i52SL30	ACAGATGATTCATATTTGGTTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
30	i52SL30	ACAGATGATTCATATTTGGTTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
30	i52SL30	ACAGATGATTCATATTTGGTTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
30	i52SL30	ACAGATGATTCATATTTGGTTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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30	i52SL30	ACAGATGATTCATATTTGGTTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
31	i52SL31	TTTTCTAACAGATGATTCATAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
31	i52SL31	TTTTCTAACAGATGATTCATAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
31	i52SL31	TTTTCTAACAGATGATTCATAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
31	i52SL31	TTTTCTAACAGATGATTCATAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
31	i52SL31	TTTTCTAACAGATGATTCATAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
31	i52SL31	TTTTCTAACAGATGATTCATAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
31	i52SL31	TTTTCTAACAGATGATTCATAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
31	i52SL31	TTTTCTAACAGATGATTCATAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
31	i52SL31	TTTTCTAACAGATGATTCATAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
31	i52SL31	TTTTCTAACAGATGATTCATAT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
31	i52SL31	TTTTCTAACAGATGATTCATAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
31	i52SL31	TTTTCTAACAGATGATTCATAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
31	i52SL31	TTTTCTAACAGATGATTCATAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
31	i52SL31	TTTTCTAACAGATGATTCATAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
31	i52SL31	TTTTCTAACAGATGATTCATAT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
31	i52SL31	TTTTCTAACAGATGATTCATAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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31	i52SL31	TTTTCTAACAGATGATTCATAT	82	E53SL100	AAATGTTAAAGGATTCAACACA
31	i52SL31	TTTTCTAACAGATGATTCATAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
31	i52SL31	TTTTCTAACAGATGATTCATAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
31	i52SL31	TTTTCTAACAGATGATTCATAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
31	i52SL31	TTTTCTAACAGATGATTCATAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
31	i52SL31	TTTTCTAACAGATGATTCATAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
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32	i52SL32	GAAGTGGCAAGGATGAGGGGAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT

33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
33	i52SL33	GGTGCTGAAGTGGCAAGGATGA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	81	E53SL99	GTTAAAGGATTCAACACAATGG
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	82	E53SL100	AAATGTTAAAGGATTCAACACA
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	84	E53SL102	TACAAGAACACCTTCAGAACCG
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
34	i52SL34	GGGTGCTGAAGTGGCAAGGATG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
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35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	81	E53SL99	GTTAAAGGATTCAACACAATGG
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	82	E53SL100	AAATGTTAAAGGATTCAACACA

35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
35	i52SL35	TGGGTGCTGAAGTGGCAAGGAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
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36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
36	i52SL36	GGCTGATGGGTGCTGAAGTGGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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37	i52SL37	AATCAGGCTGATGGGTGCTGAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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37	i52SL37	AATCAGGCTGATGGGTGCTGAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
37	i52SL37	AATCAGGCTGATGGGTGCTGAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC

38	i52SL38	TGGCACTGGGAAATCAGGCTGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	81	E53SL99	GTTAAAGGATTCAACACAATGG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	82	E53SL100	AAATGTTAAAGGATTCAACACA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
38	i52SL38	TGGCACTGGGAAATCAGGCTGA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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39	i52SL39	CTGGCACTGGGAAATCAGGCTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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39	i52SL39	CTGGCACTGGGAAATCAGGCTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
39	i52SL39	CTGGCACTGGGAAATCAGGCTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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40	i52SL40	TGAAATGCTGGCACTGGGAAAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA

40	i52SL40	TGAAATGCTGGCACTGGGAAAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
40	i52SL40	TGAAATGCTGGCACTGGGAAAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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41	i52SL41	TCAGGCAATGAAATGCTGGCAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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41	i52SL41	TCAGGCAATGAAATGCTGGCAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
41	i52SL41	TCAGGCAATGAAATGCTGGCAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
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42	i52SL42	TTCAGGCAATGAAATGCTGGCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
42	i52SL42	TTCAGGCAATGAAATGCTGGCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG

43	i52SL43	AAAGCCTTCAGGCAATGAAATG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
43	i52SL43	AAAGCCTTCAGGCAATGAAATG	81	E53SL99	GTTAAAGGATTCAACACAATGG
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
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43	i52SL43	AAAGCCTTCAGGCAATGAAATG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
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44	i52SL44	TCCTGTGGCAACAGAAAGCCTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
45	i52SL45	ATGGATGGCAAAGCAAACTCCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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45	i52SL45	ATGGATGGCAAAGCAAACTCCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT

46	i52SL46	GTATGTCTAGCCTGTCACATGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
46	i52SL46	GTATGTCTAGCCTGTCACATGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
46	i52SL46	GTATGTCTAGCCTGTCACATGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
46	i52SL46	GTATGTCTAGCCTGTCACATGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
46	i52SL46	GTATGTCTAGCCTGTCACATGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
46	i52SL46	GTATGTCTAGCCTGTCACATGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
46	i52SL46	GTATGTCTAGCCTGTCACATGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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46	i52SL46	GTATGTCTAGCCTGTCACATGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
46	i52SL46	GTATGTCTAGCCTGTCACATGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
46	i52SL46	GTATGTCTAGCCTGTCACATGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
46	i52SL46	GTATGTCTAGCCTGTCACATGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	81	E53SL99	GTTAAAGGATTCAACACAATGG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	82	E53SL100	AAATGTTAAAGGATTCAACACA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
47	i52SL47	CCTGGTATGTCTAGCCTGTCAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
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48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	81	E53SL99	GTTAAAGGATTCAACACAATGG
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48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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48	i52SL48	CTGGAGGGGAGGCATCAGTTGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
49	i52SL49	GCTGCCTCTGGGAGCTGGAGGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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50	i52SL50	CAGGCTGCCTCTGGGAGCTGGA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC

51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
51	i52SL51	ACAGGCTGCCTCTGGGAGCTGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
52	i52SL52	TACAGGCTGCCTCTGGGAGCTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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53	i52SL53	ATATACAGGCTGCCTCTGGGAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	81	E53SL99	GTTAAAGGATTCAACACAATGG

53	i52SL53	ATATACAGGCTGCCTCTGGGAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
53	i52SL53	ATATACAGGCTGCCTCTGGGAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
54	i52SL54	GTCATTATATACAGGCTGCCTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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54	i52SL54	GTCATTATATACAGGCTGCCTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
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54	i52SL54	GTCATTATATACAGGCTGCCTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
54	i52SL54	GTCATTATATACAGGCTGCCTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
54	i52SL54	GTCATTATATACAGGCTGCCTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
54	i52SL54	GTCATTATATACAGGCTGCCTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
54	i52SL54	GTCATTATATACAGGCTGCCTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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54	i52SL54	GTCATTATATACAGGCTGCCTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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54	i52SL54	GTCATTATATACAGGCTGCCTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
54	i52SL54	GTCATTATATACAGGCTGCCTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
54	i52SL54	GTCATTATATACAGGCTGCCTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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54	i52SL54	GTCATTATATACAGGCTGCCTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
54	i52SL54	GTCATTATATACAGGCTGCCTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
54	i52SL54	GTCATTATATACAGGCTGCCTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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55	i52SL55	AGTCATTATATACAGGCTGCCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
55	i52SL55	AGTCATTATATACAGGCTGCCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
55	i52SL55	AGTCATTATATACAGGCTGCCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
55	i52SL55	AGTCATTATATACAGGCTGCCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
55	i52SL55	AGTCATTATATACAGGCTGCCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
55	i52SL55	AGTCATTATATACAGGCTGCCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
55	i52SL55	AGTCATTATATACAGGCTGCCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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55	i52SL55	AGTCATTATATACAGGCTGCCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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55	i52SL55	AGTCATTATATACAGGCTGCCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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55	i52SL55	AGTCATTATATACAGGCTGCCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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55	i52SL55	AGTCATTATATACAGGCTGCCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
55	i52SL55	AGTCATTATATACAGGCTGCCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
55	i52SL55	AGTCATTATATACAGGCTGCCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
55	i52SL55	AGTCATTATATACAGGCTGCCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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56	i52SL56	TCCTACAATTAGTCATTATATA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
56	i52SL56	TCCTACAATTAGTCATTATATA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
56	i52SL56	TCCTACAATTAGTCATTATATA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
56	i52SL56	TCCTACAATTAGTCATTATATA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
56	i52SL56	TCCTACAATTAGTCATTATATA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
56	i52SL56	TCCTACAATTAGTCATTATATA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
56	i52SL56	TCCTACAATTAGTCATTATATA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG

56	i52SL56	TCCTACAATTAGTCATTATATA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
56	i52SL56	TCCTACAATTAGTCATTATATA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
56	i52SL56	TCCTACAATTAGTCATTATATA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
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56	i52SL56	TCCTACAATTAGTCATTATATA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
56	i52SL56	TCCTACAATTAGTCATTATATA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
56	i52SL56	TCCTACAATTAGTCATTATATA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
56	i52SL56	TCCTACAATTAGTCATTATATA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
56	i52SL56	TCCTACAATTAGTCATTATATA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
56	i52SL56	TCCTACAATTAGTCATTATATA	81	E53SL99	GTTAAAGGATTCAACACAATGG
56	i52SL56	TCCTACAATTAGTCATTATATA	82	E53SL100	AAATGTTAAAGGATTCAACACA
56	i52SL56	TCCTACAATTAGTCATTATATA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
56	i52SL56	TCCTACAATTAGTCATTATATA	84	E53SL102	TACAAGAACACCTTCAGAACCG
56	i52SL56	TCCTACAATTAGTCATTATATA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
56	i52SL56	TCCTACAATTAGTCATTATATA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
56	i52SL56	TCCTACAATTAGTCATTATATA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
57	i52SL57	AGAGTTATTTCCCCTAGCATCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	81	E53SL99	GTTAAAGGATTCAACACAATGG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	82	E53SL100	AAATGTTAAAGGATTCAACACA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	84	E53SL102	TACAAGAACACCTTCAGAACCG

58	i52SL58	CAGAGTTATTTCCCCTAGCATC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
58	i52SL58	CAGAGTTATTTCCCCTAGCATC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	81	E53SL99	GTTAAAGGATTCAACACAATGG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	82	E53SL100	AAATGTTAAAGGATTCAACACA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	84	E53SL102	TACAAGAACACCTTCAGAACCG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
59	i52SL59	GAGCTTTATCCCTTGGGAAACT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
60	i52SL60	GGGTCACTGGAGCTTTATCCCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG

61	i52SL61	TGGGTCACTGGAGCTTTATCCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	81	E53SL99	GTTAAAGGATTCAACACAATGG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	82	E53SL100	AAATGTTAAAGGATTCAACACA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
61	i52SL61	TGGGTCACTGGAGCTTTATCCC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
62	i52SL62	AGCCAGCTGCTGTTGTGGGTCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
63	i52SL63	ATTATCAAGCCAGCTGCTGTTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

64	i52SL64	CATTATCAAGCCAGCTGCTGTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	81	E53SL99	GTTAAAGGATTCAACACAATGG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	82	E53SL100	AAATGTTAAAGGATTCAACACA
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	84	E53SL102	TACAAGAACACCTTCAGAACCG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
64	i52SL64	CATTATCAAGCCAGCTGCTGTT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

F. Table 1F. Exon 53-Intron 53 SluCas9 guide pairs:

Guide 1 SEQ ID NO	Guide 1 name	Guide 1 sequence	Guide 2 SEQ ID NO	Guide 2 name	Guide 2 sequence
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
88	i53SL3	AGAGTAGACCTGTTACTTTTTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

89	i53SL4	TAGACCTGTTACTTTTTCTAGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
89	i53SL4	TAGACCTGTTACTTTTTCTAGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	81	E53SL99	GTTAAAGGATTCAACACAATGG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	82	E53SL100	AAATGTTAAAGGATTCAACACA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG

90	i53SL5	TCTAGGAAGGAATTAAGCCCGA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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91	i53SL6	CAATTTTGAAGTGATCTTAAAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
91	i53SL6	CAATTTTGAAGTGATCTTAAAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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92	i53SL7	TCTACCTTGACTCAAAAGTCTA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	81	E53SL99	GTTAAAGGATTCAACACAATGG
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	82	E53SL100	AAATGTTAAAGGATTCAACACA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	84	E53SL102	TACAAGAACACCTTCAGAACCG
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	85	E53SL103	AAGTACAAGAACACCTTCAGAA

92	i53SL7	TCTACCTTGACTCAAAAGTCTA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
92	i53SL7	TCTACCTTGACTCAAAAGTCTA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	81	E53SL99	GTTAAAGGATTCAACACAATGG
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
93	i53SL8	CTTGACTCAAAAGTCTACTGGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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93	i53SL8	CTTGACTCAAAAGTCTACTGGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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94	i53SL9	TCATGCCTGTAATCCTAGTGCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	84	E53SL102	TACAAGAACACCTTCAGAACCG

94	i53SL9	TCATGCCTGTAATCCTAGTGCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
94	i53SL9	TCATGCCTGTAATCCTAGTGCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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95	i53SL10	CATGCCTGTAATCCTAGTGCTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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95	i53SL10	CATGCCTGTAATCCTAGTGCTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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95	i53SL10	CATGCCTGTAATCCTAGTGCTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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95	i53SL10	CATGCCTGTAATCCTAGTGCTT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	81	E53SL99	GTTAAAGGATTCAACACAATGG
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	82	E53SL100	AAATGTTAAAGGATTCAACACA
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	84	E53SL102	TACAAGAACACCTTCAGAACCG
95	i53SL10	CATGCCTGTAATCCTAGTGCTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA

96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
96	i53SL11	GCCTGTAATCCTAGTGCTTTGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	81	E53SL99	GTTAAAGGATTCAACACAATGG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	82	E53SL100	AAATGTTAAAGGATTCAACACA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
97	i53SL12	AATCCTAGTGCTTTGGGAGGCC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	82	E53SL100	AAATGTTAAAGGATTCAACACA

98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
98	i53SL13	CTAGTGCTTTGGGAGGCCAAGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	81	E53SL99	GTTAAAGGATTCAACACAATGG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	82	E53SL100	AAATGTTAAAGGATTCAACACA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	84	E53SL102	TACAAGAACACCTTCAGAACCG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
99	i53SL14	GGCCAAGGAAGGAGAATTGCTT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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100	i53SL15	CAAAAATTTTTAAAAAATTAGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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100	i53SL15	CAAAAATTTTTAAAAAATTAGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
100	i53SL15	CAAAAATTTTTAAAAAATTAGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
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101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	81	E53SL99	GTTAAAGGATTCAACACAATGG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
101	i53SL16	ATTTTTAAAAAATTAGCCAGGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
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102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT

102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
102	i53SL17	TTTAAAAAATTAGCCAGGCGTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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103	i53SL18	AGCCAGGCGTGGTGGTACACGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	82	E53SL100	AAATGTTAAAGGATTCAACACA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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104	i53SL19	CCTGGCTAGTAGTCCCAGCTAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
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105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	84	E53SL102	TACAAGAACACCTTCAGAACCG
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
105	i53SL20	CTGGCTAGTAGTCCCAGCTACT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT

106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
106	i53SL21	GCTAGTAGTCCCAGCTACTAGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
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107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
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107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
107	i53SL22	AGTCCCAGCTACTAGGGAGGCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA

108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
108	i53SL23	CCAGCTACTAGGGAGGCTGAGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	81	E53SL99	GTTAAAGGATTCAACACAATGG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
109	i53SL24	GCTACTAGGGAGGCTGAGGCAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC

110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
110	i53SL25	GACTGCTTGAGCCCCAGAGTTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
111	i53SL26	GATTGTGCCACTGCACTTTAGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
111	i53SL26	GATTGTGCCACTGCACTTTAGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
111	i53SL26	GATTGTGCCACTGCACTTTAGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
111	i53SL26	GATTGTGCCACTGCACTTTAGC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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111	i53SL26	GATTGTGCCACTGCACTTTAGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
111	i53SL26	GATTGTGCCACTGCACTTTAGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
111	i53SL26	GATTGTGCCACTGCACTTTAGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG

112	i53SL27	ATTGTGCCACTGCACTTTAGCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
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112	i53SL27	ATTGTGCCACTGCACTTTAGCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
112	i53SL27	ATTGTGCCACTGCACTTTAGCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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113	i53SL28	AAACATCATTAAATTACAATCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
113	i53SL28	AAACATCATTAAATTACAATCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
113	i53SL28	AAACATCATTAAATTACAATCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
113	i53SL28	AAACATCATTAAATTACAATCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
113	i53SL28	AAACATCATTAAATTACAATCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
113	i53SL28	AAACATCATTAAATTACAATCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
113	i53SL28	AAACATCATTAAATTACAATCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
113	i53SL28	AAACATCATTAAATTACAATCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
113	i53SL28	AAACATCATTAAATTACAATCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
113	i53SL28	AAACATCATTAAATTACAATCT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
113	i53SL28	AAACATCATTAAATTACAATCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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113	i53SL28	AAACATCATTAAATTACAATCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
113	i53SL28	AAACATCATTAAATTACAATCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
113	i53SL28	AAACATCATTAAATTACAATCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
113	i53SL28	AAACATCATTAAATTACAATCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
113	i53SL28	AAACATCATTAAATTACAATCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
113	i53SL28	AAACATCATTAAATTACAATCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
113	i53SL28	AAACATCATTAAATTACAATCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
113	i53SL28	AAACATCATTAAATTACAATCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
113	i53SL28	AAACATCATTAAATTACAATCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
113	i53SL28	AAACATCATTAAATTACAATCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG

114	i53SL29	GTAACCAGTATTTTATTTTAAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
114	i53SL29	GTAACCAGTATTTTATTTTAAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
114	i53SL29	GTAACCAGTATTTTATTTTAAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
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114	i53SL29	GTAACCAGTATTTTATTTTAAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
114	i53SL29	GTAACCAGTATTTTATTTTAAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
114	i53SL29	GTAACCAGTATTTTATTTTAAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
115	i53SL30	AAAGGTATCTTTGATACTAACC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
115	i53SL30	AAAGGTATCTTTGATACTAACC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
115	i53SL30	AAAGGTATCTTTGATACTAACC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
115	i53SL30	AAAGGTATCTTTGATACTAACC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
115	i53SL30	AAAGGTATCTTTGATACTAACC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
115	i53SL30	AAAGGTATCTTTGATACTAACC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
115	i53SL30	AAAGGTATCTTTGATACTAACC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
115	i53SL30	AAAGGTATCTTTGATACTAACC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
115	i53SL30	AAAGGTATCTTTGATACTAACC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
115	i53SL30	AAAGGTATCTTTGATACTAACC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
115	i53SL30	AAAGGTATCTTTGATACTAACC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
115	i53SL30	AAAGGTATCTTTGATACTAACC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
115	i53SL30	AAAGGTATCTTTGATACTAACC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
115	i53SL30	AAAGGTATCTTTGATACTAACC	81	E53SL99	GTTAAAGGATTCAACACAATGG
115	i53SL30	AAAGGTATCTTTGATACTAACC	82	E53SL100	AAATGTTAAAGGATTCAACACA
115	i53SL30	AAAGGTATCTTTGATACTAACC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
115	i53SL30	AAAGGTATCTTTGATACTAACC	84	E53SL102	TACAAGAACACCTTCAGAACCG
115	i53SL30	AAAGGTATCTTTGATACTAACC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
115	i53SL30	AAAGGTATCTTTGATACTAACC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
115	i53SL30	AAAGGTATCTTTGATACTAACC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG

116	i53SL37	TTTCATATCTTATTTGGAGGCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
116	i53SL37	TTTCATATCTTATTTGGAGGCC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
116	i53SL37	TTTCATATCTTATTTGGAGGCC	81	E53SL99	GTTAAAGGATTCAACACAATGG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	82	E53SL100	AAATGTTAAAGGATTCAACACA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
116	i53SL37	TTTCATATCTTATTTGGAGGCC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
116	i53SL37	TTTCATATCTTATTTGGAGGCC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
117	i53SL38	CTACTCTTTCATATCTTATTTG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
117	i53SL38	CTACTCTTTCATATCTTATTTG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
117	i53SL38	CTACTCTTTCATATCTTATTTG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
117	i53SL38	CTACTCTTTCATATCTTATTTG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
117	i53SL38	CTACTCTTTCATATCTTATTTG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
117	i53SL38	CTACTCTTTCATATCTTATTTG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
117	i53SL38	CTACTCTTTCATATCTTATTTG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
117	i53SL38	CTACTCTTTCATATCTTATTTG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
117	i53SL38	CTACTCTTTCATATCTTATTTG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
117	i53SL38	CTACTCTTTCATATCTTATTTG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
117	i53SL38	CTACTCTTTCATATCTTATTTG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
117	i53SL38	CTACTCTTTCATATCTTATTTG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
117	i53SL38	CTACTCTTTCATATCTTATTTG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
117	i53SL38	CTACTCTTTCATATCTTATTTG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
117	i53SL38	CTACTCTTTCATATCTTATTTG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
117	i53SL38	CTACTCTTTCATATCTTATTTG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
117	i53SL38	CTACTCTTTCATATCTTATTTG	81	E53SL99	GTTAAAGGATTCAACACAATGG
117	i53SL38	CTACTCTTTCATATCTTATTTG	82	E53SL100	AAATGTTAAAGGATTCAACACA
117	i53SL38	CTACTCTTTCATATCTTATTTG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
117	i53SL38	CTACTCTTTCATATCTTATTTG	84	E53SL102	TACAAGAACACCTTCAGAACCG
117	i53SL38	CTACTCTTTCATATCTTATTTG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
117	i53SL38	CTACTCTTTCATATCTTATTTG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
117	i53SL38	CTACTCTTTCATATCTTATTTG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
118	i53SL39	GGTCTACTCTTTCATATCTTAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC

118	i53SL39	GGTCTACTCTTTCATATCTTAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
118	i53SL39	GGTCTACTCTTTCATATCTTAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
118	i53SL39	GGTCTACTCTTTCATATCTTAT	81	E53SL99	GTTAAAGGATTCAACACAATGG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	82	E53SL100	AAATGTTAAAGGATTCAACACA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
118	i53SL39	GGTCTACTCTTTCATATCTTAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
118	i53SL39	GGTCTACTCTTTCATATCTTAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
119	i53SL40	AATTCCTTCCTAGAAAAAGTAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG

120	i53SL41	TAGTTGCATGAAGTCAACCATT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
120	i53SL41	TAGTTGCATGAAGTCAACCATT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
120	i53SL41	TAGTTGCATGAAGTCAACCATT	81	E53SL99	GTTAAAGGATTCAACACAATGG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	82	E53SL100	AAATGTTAAAGGATTCAACACA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	84	E53SL102	TACAAGAACACCTTCAGAACCG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
120	i53SL41	TAGTTGCATGAAGTCAACCATT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
120	i53SL41	TAGTTGCATGAAGTCAACCATT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	81	E53SL99	GTTAAAGGATTCAACACAATGG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	82	E53SL100	AAATGTTAAAGGATTCAACACA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
121	i53SL42	GTAGTTGCATGAAGTCAACCAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	70	E53SL34	ACATTTCATTCAACTGTTGCCT

122	i53SL43	CATCTTTAAGATCACTTCAAAA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
122	i53SL43	CATCTTTAAGATCACTTCAAAA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
122	i53SL43	CATCTTTAAGATCACTTCAAAA	81	E53SL99	GTTAAAGGATTCAACACAATGG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	82	E53SL100	AAATGTTAAAGGATTCAACACA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	84	E53SL102	TACAAGAACACCTTCAGAACCG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
122	i53SL43	CATCTTTAAGATCACTTCAAAA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
122	i53SL43	CATCTTTAAGATCACTTCAAAA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
123	i53SL44	TTAGTAATCTGGATATAGTTGG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
123	i53SL44	TTAGTAATCTGGATATAGTTGG	81	E53SL99	GTTAAAGGATTCAACACAATGG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	82	E53SL100	AAATGTTAAAGGATTCAACACA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	84	E53SL102	TACAAGAACACCTTCAGAACCG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
123	i53SL44	TTAGTAATCTGGATATAGTTGG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
123	i53SL44	TTAGTAATCTGGATATAGTTGG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT

124	i53SL45	TTGTTTAGTAATCTGGATATAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
124	i53SL45	TTGTTTAGTAATCTGGATATAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
124	i53SL45	TTGTTTAGTAATCTGGATATAG	81	E53SL99	GTTAAAGGATTCAACACAATGG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
124	i53SL45	TTGTTTAGTAATCTGGATATAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
124	i53SL45	TTGTTTAGTAATCTGGATATAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	81	E53SL99	GTTAAAGGATTCAACACAATGG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	82	E53SL100	AAATGTTAAAGGATTCAACACA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	84	E53SL102	TACAAGAACACCTTCAGAACCG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
125	i53SL46	AAAGTTAATTTTGTTTAGTAAT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC

126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	81	E53SL99	GTTAAAGGATTCAACACAATGG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	82	E53SL100	AAATGTTAAAGGATTCAACACA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	84	E53SL102	TACAAGAACACCTTCAGAACCG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
126	i53SL47	TTTTGAGTCAAGGTAGAGAATA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
127	i53SL48	CTAGCCAGTAGACTTTTGAGTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	67	E53SL31	TTTTGGATTGCATCTACTGTAT

128	i53SL49	GCCTCCCAAAGCACTAGGATTA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	81	E53SL99	GTTAAAGGATTCAACACAATGG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	82	E53SL100	AAATGTTAAAGGATTCAACACA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	84	E53SL102	TACAAGAACACCTTCAGAACCG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
128	i53SL49	GCCTCCCAAAGCACTAGGATTA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	81	E53SL99	GTTAAAGGATTCAACACAATGG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	82	E53SL100	AAATGTTAAAGGATTCAACACA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	84	E53SL102	TACAAGAACACCTTCAGAACCG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
129	i53SL50	CTTCCTTGGCCTCCCAAAGCAC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	66	E53SL30	CTTTTGGATTGCATCTACTGTA

130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
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130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	82	E53SL100	AAATGTTAAAGGATTCAACACA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	84	E53SL102	TACAAGAACACCTTCAGAACCG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
130	i53SL51	GGCCTCAAGCAATTCTCCTTCC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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131	i53SL52	GTAGAGATGGGTTCTTGAACTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	84	E53SL102	TACAAGAACACCTTCAGAACCG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
131	i53SL52	GTAGAGATGGGTTCTTGAACTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT

132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	81	E53SL99	GTTAAAGGATTCAACACAATGG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	82	E53SL100	AAATGTTAAAGGATTCAACACA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	84	E53SL102	TACAAGAACACCTTCAGAACCG
132	i53SL53	AAATTTTTGTTTTCTGTAGAGA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	81	E53SL99	GTTAAAGGATTCAACACAATGG
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133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
133	i53SL54	AAAATTTTTGTTTTCTGTAGAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

134	i53SL55	AGCCAGGCGTGTACCACCACGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
134	i53SL55	AGCCAGGCGTGTACCACCACGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
134	i53SL55	AGCCAGGCGTGTACCACCACGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
134	i53SL55	AGCCAGGCGTGTACCACCACGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
134	i53SL55	AGCCAGGCGTGTACCACCACGC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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134	i53SL55	AGCCAGGCGTGTACCACCACGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
134	i53SL55	AGCCAGGCGTGTACCACCACGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
134	i53SL55	AGCCAGGCGTGTACCACCACGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
134	i53SL55	AGCCAGGCGTGTACCACCACGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
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135	i53SL56	CCTAGTAGCTGGGACTACTAGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
135	i53SL56	CCTAGTAGCTGGGACTACTAGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG

135	i53SL56	CCTAGTAGCTGGGACTACTAGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	81	E53SL99	GTTAAAGGATTCAACACAATGG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	82	E53SL100	AAATGTTAAAGGATTCAACACA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	84	E53SL102	TACAAGAACACCTTCAGAACCG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
136	i53SL57	CTGCCTCAGCCTCCCTAGTAGC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	66	E53SL30	CTTTTGGATTGCATCTACTGTA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	67	E53SL31	TTTTGGATTGCATCTACTGTAT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	70	E53SL34	ACATTTCATTCAACTGTTGCCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	72	E53SL90	CCAAAAGAAAATCACAGAAACC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	80	E53SL98	TTCAACACAATGGCTGGAAGCT
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	81	E53SL99	GTTAAAGGATTCAACACAATGG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	82	E53SL100	AAATGTTAAAGGATTCAACACA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	83	E53SL101	GCAACAGTTGAATGAAATGTTA
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	84	E53SL102	TACAAGAACACCTTCAGAACCG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	85	E53SL103	AAGTACAAGAACACCTTCAGAA

137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
137	i53SL58	CCTGCCTCAGCCTCCCTAGTAG	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	81	E53SL99	GTTAAAGGATTCAACACAATGG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	82	E53SL100	AAATGTTAAAGGATTCAACACA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	84	E53SL102	TACAAGAACACCTTCAGAACCG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
138	i53SL59	AGCTCACTGAGCCTTGAACTCT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	81	E53SL99	GTTAAAGGATTCAACACAATGG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	82	E53SL100	AAATGTTAAAGGATTCAACACA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	84	E53SL102	TACAAGAACACCTTCAGAACCG

139	i53SL60	TAGCTCACTGAGCCTTGAACTC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
139	i53SL60	TAGCTCACTGAGCCTTGAACTC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	66	E53SL30	CTTTTGGATTGCATCTACTGTA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	67	E53SL31	TTTTGGATTGCATCTACTGTAT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	70	E53SL34	ACATTTCATTCAACTGTTGCCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	72	E53SL90	CCAAAAGAAAATCACAGAAACC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	80	E53SL98	TTCAACACAATGGCTGGAAGCT
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	81	E53SL99	GTTAAAGGATTCAACACAATGG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	82	E53SL100	AAATGTTAAAGGATTCAACACA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	83	E53SL101	GCAACAGTTGAATGAAATGTTA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	84	E53SL102	TACAAGAACACCTTCAGAACCG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	85	E53SL103	AAGTACAAGAACACCTTCAGAA
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
140	i53SL61	ATAGCTCACTGAGCCTTGAACT	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	81	E53SL99	GTTAAAGGATTCAACACAATGG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	82	E53SL100	AAATGTTAAAGGATTCAACACA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	83	E53SL101	GCAACAGTTGAATGAAATGTTA

141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	84	E53SL102	TACAAGAACACCTTCAGAACCG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
141	i53SL62	CTGTCACCCAGGCTAAAGTGCA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	66	E53SL30	CTTTTGGATTGCATCTACTGTA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	67	E53SL31	TTTTGGATTGCATCTACTGTAT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	70	E53SL34	ACATTTCATTCAACTGTTGCCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	72	E53SL90	CCAAAAGAAAATCACAGAAACC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
142	i53SL63	GAGACAGAGTCTCACTGTCACC	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	80	E53SL98	TTCAACACAATGGCTGGAAGCT
142	i53SL63	GAGACAGAGTCTCACTGTCACC	81	E53SL99	GTTAAAGGATTCAACACAATGG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	82	E53SL100	AAATGTTAAAGGATTCAACACA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	83	E53SL101	GCAACAGTTGAATGAAATGTTA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	84	E53SL102	TACAAGAACACCTTCAGAACCG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	85	E53SL103	AAGTACAAGAACACCTTCAGAA
142	i53SL63	GAGACAGAGTCTCACTGTCACC	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
142	i53SL63	GAGACAGAGTCTCACTGTCACC	87	E53SL105	TAGTTGAAAGAATTCAGAATCA
143	i53SL64	GATACCTTTTTAAAATAAAATA	65	E53SL29	CCTTGGTTTCTGTGATTTTCTT
143	i53SL64	GATACCTTTTTAAAATAAAATA	66	E53SL30	CTTTTGGATTGCATCTACTGTA
143	i53SL64	GATACCTTTTTAAAATAAAATA	67	E53SL31	TTTTGGATTGCATCTACTGTAT
143	i53SL64	GATACCTTTTTAAAATAAAATA	68	E53SL32	ACCCTCCTTCCATGACTCAAGC
143	i53SL64	GATACCTTTTTAAAATAAAATA	69	E53SL33	CTTCCATGACTCAAGCTTGGCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	70	E53SL34	ACATTTCATTCAACTGTTGCCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	71	E53SL35	TCAACTGTTGCCTCCGGTTCTG
143	i53SL64	GATACCTTTTTAAAATAAAATA	72	E53SL90	CCAAAAGAAAATCACAGAAACC
143	i53SL64	GATACCTTTTTAAAATAAAATA	73	E53SL91	GCCAAGCTTGAGTCATGGAAGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	74	E53SL92	AGCCAAGCTTGAGTCATGGAAG
143	i53SL64	GATACCTTTTTAAAATAAAATA	75	E53SL93	CAGAGCCAAGCTTGAGTCATGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	76	E53SL94	AGGCCAGAGCCAAGCTTGAGTC
143	i53SL64	GATACCTTTTTAAAATAAAATA	77	E53SL95	AGAAGCTGAGCAGGTCTTAGGA
143	i53SL64	GATACCTTTTTAAAATAAAATA	78	E53SL96	AAGGAAGAAGCTGAGCAGGTCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	79	E53SL97	GGAAGCTAAGGAAGAAGCTGAG
143	i53SL64	GATACCTTTTTAAAATAAAATA	80	E53SL98	TTCAACACAATGGCTGGAAGCT
143	i53SL64	GATACCTTTTTAAAATAAAATA	81	E53SL99	GTTAAAGGATTCAACACAATGG
143	i53SL64	GATACCTTTTTAAAATAAAATA	82	E53SL100	AAATGTTAAAGGATTCAACACA

143	i53SL64	GATACCTTTTTAAAATAAAATA	83	E53SL101	GCAACAGTTGAATGAAATGTTA
143	i53SL64	GATACCTTTTTAAAATAAAATA	84	E53SL102	TACAAGAACACCTTCAGAACCG
143	i53SL64	GATACCTTTTTAAAATAAAATA	85	E53SL103	AAGTACAAGAACACCTTCAGAA
143	i53SL64	GATACCTTTTTAAAATAAAATA	86	E53SL104	AGTTGAAAGAATTCAGAATCAG
143	i53SL64	GATACCTTTTTAAAATAAAATA	87	E53SL105	TAGTTGAAAGAATTCAGAATCA

Compositions

[0097] In some embodiments, a composition is provided comprising one or more guide RNAs, or one or more nucleic acids encoding one or more guide RNAs, comprising or consisting of one or more guide sequence of **Tables 1A-1C**.

[0098] In some embodiments, a composition is provided comprising one or more guide RNAs, or one or more nucleic acids encoding one or more guide RNAs, wherein the guide RNA comprises at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is 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%, at least 99%, or 100% identical to a guide sequence of **Tables 1A-1C**, or to a guide sequence comprising at least 16, 17, 18, 19, or 20 nucleotides of a guide sequence of **Tables 1A-1C**. In particular embodiments, a composition is provided comprising one or more guide RNAs, or one or more nucleic acids encoding one or more guide RNAs, wherein the guide RNA comprises at least 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is at least 70%, at least 75%, at least 80%, at least 85%, or 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% identical to a guide sequence comprising at least 20 nucleotides of a guide sequence of **Tables 1A-1C**. In other particular embodiments, a composition is provided comprising one or more guide RNAs, or one or more nucleic acids encoding one or more guide RNAs, wherein the guide RNA comprises no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is at least 70%, at least 75%, at least 80%, at least 85%, or at least 90% identical to guide sequence comprising no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C**.

[0099] In some embodiments, a composition is provided comprising two or more guide RNAs, or a nucleic acid encoding two or more guide RNAs, wherein each guide RNA comprises a guide sequence of **Tables 1A-1C**, or at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, or is 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%, at least 99%, or 100% identical to a guide sequence of Tables 1A-1C or to a guide sequence comprising at least 16, 17, 18, 19, or 20 nucleotides of a guide sequence of **Tables 1A-1C**. In

particular embodiments, a composition is provided comprising two or more guide RNAs, or a nucleic acid encoding two or more guide RNAs, wherein each guide RNA comprises at least 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is 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%, at least 99%, or 100% identical to a guide sequence comprising at least 20 nucleotides of a guide sequence selected from **Tables 1A-1C**. In other particular embodiments, a composition is provided comprising two or more guide RNAs, or nucleic acid encoding two or more guide RNAs, wherein at least one of the two or more guide RNAs, optionally each guide RNA, comprises no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is 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%, at least 99%, or 100% identical to a guide sequence comprising no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 nucleotides of a guide sequence selected from **Tables 1A-1C**.

[00100] In some embodiments, a composition is provided comprising a pair of guide RNAs, or nucleic acid encoding a pair of guide RNAs, wherein the pair of guide RNAs comprises sequences 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%, at least 99%, or 100% identical to a guide sequence to any of the pairs disclosed in **Tables 1D-1F**. In some embodiments, a composition is provided comprising a pair of guide RNAs, or nucleic acid encoding a pair of guide RNAs, wherein the pair of guide RNAs comprises sequences from any of the pairs disclosed in **Tables 1D-1F**. In some embodiments, a composition is provided comprising any of the pairs of guide RNA sequences disclosed in **Tables 1D-1F**.

[00101] In some embodiments, a composition is provided comprising one or more nucleic acid molecules, wherein at least one of the molecules comprises a nucleic acid encoding: a) a SluCas9; and b) a first and a second guide RNA comprising a first and a second guide sequence, wherein the first and second guide sequence are selected from any one of the guide sequence pairs of **Tables 1D-1F**.

[00102] In some embodiments, a composition is provided comprising two nucleic acid molecules, wherein at least one of the molecules comprises a nucleic acid encoding a first and a second guide RNA comprising a first and a second guide sequence, wherein the first and second guide sequence are selected from any one of the guide sequence pairs of **Tables 1D-1F**, optionally wherein the nucleic acid does not comprise a nucleic acid encoding an endonuclease.

[00103] In some embodiments, the composition further comprises an endonuclease or a nucleic acid encoding an endonuclease. An exemplary endonuclease for use with each of the guide RNAs or pairs of guide RNAs is provided herein, for example, the guide sequences provided in **Tables 1A-1F** are for use with a SluCas9 endonuclease.

[00104] In some embodiments, a composition is provided comprising a single nucleic acid molecule comprising a nucleic acid encoding any of the guide RNAs disclosed herein, or any of the pairs of guide RNAs disclosed herein, and optionally a nucleic acid encoding an endonuclease.

[00105] In some embodiments, a composition is provided comprising at least two nucleic acid molecules comprising a nucleic acid encoding any of the guide RNAs disclosed herein, or any of the pairs of guide RNAs disclosed herein, and optionally a nucleic acid encoding an endonuclease, wherein at least one nucleic acid molecule does not comprise a nucleic acid encoding an endonuclease.

[00106] The disclosure herein may reference a "first and a second spacer" or a "first and a second guide RNA, gRNA, or sgRNA" followed by one or more pairs of specific sequences. It should be noted that the order of the sequences in the pair is not intended to be restricted to the order in which they are presented/described. For example, the phrase "the first sgRNA and the second sgRNA comprise the sequences of SEQ ID NOs: 10 and 15" could mean that the first sgRNA comprises the sequence of SEQ ID NO: 10 and the second sgRNA sequence comprises the sequence of SEQ ID NO: 15, or this phrase could mean that the first sgRNA comprises the sequence of SEQ ID NO: 15 and the second sgRNA sequence comprises the sequence of SEQ ID NO: 10.

[00107] In some embodiments, the first and/or the second nucleic acid, if present, comprises at least two guide RNAs. In some embodiments, the first and/or the second nucleic acid, if present, comprises at least three guide RNAs. In some embodiments, the first and/or the second nucleic acid, if present, comprises at least four guide RNAs. In some embodiments, the first and/or the second nucleic acid, if present, comprises at least five guide RNAs. In some embodiments, the first and/or the second nucleic acid, if present, comprises at least six guide RNAs. In some embodiments, the first nucleic acid encodes an endonuclease and at least one, at least two, or at least three guide RNAs. In some embodiments, the first nucleic acid comprises an endonuclease and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid. In some embodiments, the first nucleic acid encodes an endonuclease and from one to three guide RNAs. In some embodiments, the first nucleic acid comprises 1, 2, 3, 4, 5, or 6 guide RNAs, but does not encode an endonuclease.

[00108] In some embodiments, the second nucleic acid, if present, encodes at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs. In some embodiments, the second nucleic acid, if present, encodes from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid In some embodiments, the second nucleic acid, if present, encodes from one to six guide RNAs. In some embodiments, the second nucleic acid, if present, encodes 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, or 2-3 guide RNAs. In some embodiments, the second nucleic acid, if present, encodes 2, 3, 4, 5, or 6 guide RNAs. In some embodiments, the second nucleic acid comprises 1, 2, 3, 4, 5, or 6 guide RNAs, but does not encode an endonuclease.

[00109] In some embodiments, a single nucleic acid molecule comprises a nucleic acid encoding a Cas9 and a nucleic acid encoding two guide RNAs, wherein the nucleic acid molecule encodes no more than two guide RNAs.

[00110] In some embodiments, the single nucleic acid molecule is a single vector or comprised in a single vector. In some embodiments, the single vector expresses the two guide RNAs and Cas9. In some embodiments, a pair of guide RNAs and a Cas9 are provided on a single vector. In some embodiments, the single vector comprises a nucleic acid encoding a pair of guide RNAs and a nucleic acid encoding a SaCas9 or SluCas9. In some embodiments, two guide RNAs and a Cas9 are encoded on a single vector. In some embodiments, the single vector comprises a nucleic acid encoding a first guide RNA, a nucleic acid encoding a second guide RNA, and a nucleic acid encoding a SaCas9 or SluCas9.

[00111] In some embodiments, the first nucleic acid molecule encodes for a Cas9 molecule and also encodes for one or more copies of a first guide RNA and one or more copies of a second guide RNA. In some embodiments, the first nucleic acid molecule encodes for a Cas9 molecule, but does not encode for any guide RNAs. In some embodiments, the second nucleic acid molecule encodes for one or more copies of a first guide RNA and one or more copies of a second guide RNA, wherein the second nucleic acid molecule does not encode for a Cas9 molecule.

[00112] In some embodiments, any of the guides disclosed herein may be used as a research tool, e.g., to study trafficking, expression, and processing by cells.

A. Guide pairs targeting intron 52 and intron 53 of the DMD gene

[00113] In some embodiments, a composition is provided comprising a pair of guide RNAs, wherein the pair of guide RNAs comprises or consists of any one of the pairs of guide sequences of **Table 1D**. In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 1-64; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 88-143. In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and the second guide RNA is selected from any one of SEQ ID NOs: 88-143. In some embodiments, the pair of guide RNAs is capable of excising at least a portion (such as all) of exon 53 of the DMD gene (*see, e.g.,* **Figure 1** or **Figure 4**, top).

[00114] In some embodiments, a composition is provided comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least

90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first and a second guide sequence selected from any one of the following pairs of first and second guide sequences:

a. SEQ ID NOs: 88 and 1; 88 and 2; 88 and 3; 88 and 4; 88 and 5; 88 and 6; 88 and 7; 88 and 8; 88 and 9; 88 and 10; 88 and 11; 88 and 12; 88 and 13; 88 and 14; 88 and 15; 88 and 16; 88 and 17; 88 and 18; 88 and 19; 88 and 20; 88 and 21; 88 and 22; 88 and 23; 88 and 24; 88 and 25; 88 and 26; 88 and 27; 88 and 28; 88 and 29; 88 and 30; 88 and 31; 88 and 32; 88 and 33; 88 and 34; 88 and 35; 88 and 36; 88 and 37; 88 and 38; 88 and 39; 88 and 40; 88 and 41; 88 and 42; 88 and 43; 88 and 44; 88 and 45; 88 and 46; 88 and 47; 88 and 48; 88 and 49; 88 and 50; 88 and 51; 88 and 52; 88 and 53; 88 and 54; 88 and 55; 88 and 56; 88 and 57; 88 and 58; 88 and 59; 88 and 60; 88 and 61; 88 and 62; 88 and 63; 88 and 64; 89 and 1; 89 and 2; 89 and 3; 89 and 4; 89 and 5; 89 and 6; 89 and 7; 89 and 8; 89 and 9; 89 and 10; 89 and 11; 89 and 12; 89 and 13; 89 and 14; 89 and 15; 89 and 16; 89 and 17; 89 and 18; 89 and 19; 89 and 20; 89 and 21; 89 and 22; 89 and 23; 89 and 24; 89 and 25; 89 and 26; 89 and 27; 89 and 28; 89 and 29; 89 and 30; 89 and 31; 89 and 32; 89 and 33; 89 and 34; 89 and 35; 89 and 36; 89 and 37; 89 and 38; 89 and 39; 89 and 40; 89 and 41; 89 and 42; 89 and 43; 89 and 44; 89 and 45; 89 and 46; 89 and 47; 89 and 48; 89 and 49; 89 and 50; 89 and 51; 89 and 52; 89 and 53; 89 and 54; 89 and 55; 89 and 56; 89 and 57; 89 and 58; 89 and 59; 89 and 60; 89 and 61; 89 and 62; 89 and 63; 89 and 64; 90 and 1; 90 and 2; 90 and 3; 90 and 4; 90 and 5; 90 and 6; 90 and 7; 90 and 8; 90 and 9; 90 and 10; 90 and 11; 90 and 12; 90 and 13; 90 and 14; 90 and 15; 90 and 16; 90 and 17; 90 and 18; 90 and 19; 90 and 20; 90 and 21; 90 and 22; 90 and 23; 90 and 24; 90 and 25; 90 and 26; 90 and 27; 90 and 28; 90 and 29; 90 and 30; 90 and 31; 90 and 32; 90 and 33; 90 and 34; 90 and 35; 90 and 36; 90 and 37; 90 and 38; 90 and 39; 90 and 40; 90 and 41; 90 and 42; 90 and 43; 90 and 44; 90 and 45; 90 and 46; 90 and 47; 90 and 48; 90 and 49; 90 and 50; 90 and 51; 90 and 52; 90 and 53; 90 and 54; 90 and 55; 90 and 56; 90 and 57; 90 and 58; 90 and 59; 90 and 60; 90 and 61; 90 and 62; 90 and 63; 90 and 64; 91 and 1; 91 and 2; 91 and 3; 91 and 4; 91 and 5; 91 and 6; 91 and 7; 91 and 8; 91 and 9; 91 and 10; 91 and 11; 91 and 12; 91 and 13; 91 and 14; 91 and 15; 91 and 16; 91 and 17; 91 and 18; 91 and 19; 91 and 20; 91 and 21; 91 and 22; 91 and 23; 91 and 24; 91 and 25; 91 and 26; 91 and 27; 91 and 28; 91 and 29; 91 and 30; 91 and 31; 91 and 32; 91 and 33; 91 and 34; 91 and 35; 91 and 36; 91 and 37; 91 and 38; 91 and 39; 91 and 40; 91 and 41; 91 and 42; 91 and 43; 91 and 44; 91 and 45; 91 and 46; 91 and 47; 91 and 48; 91 and 49; 91 and 50; 91 and 51; 91 and 52; 91 and 53; 91 and 54; 91 and 55; 91 and 56; 91 and 57; 91 and 58; 91 and 59; 91 and 60; 91 and 61; 91 and 62; 91 and 63; 91 and 64; 92 and 1; 92 and 2; 92 and 3; 92 and 4; 92 and 5; 92 and 6; 92 and 7; 92 and 8; 92 and 9; 92 and 10; 92 and 11; 92 and 12; 92 and 13; 92 and 14; 92 and 15; 92 and 16; 92 and 17; 92 and 18; 92 and 19; 92 and 20; 92 and 21; 92 and 22; 92 and 23; 92 and 24; 92 and 25; 92 and 26; 92 and 27; 92 and 28; 92 and 29; 92 and 30; 92 and 31; 92 and 32; 92 and 33; 92 and 34; 92 and 35; 92 and 36; 92 and 37; 92

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b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

[00115] In some embodiments, a composition is provided comprising: one or more nucleic acid molecules encoding a SluCas9 and at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first guide sequence and a second guide sequence selected from any of the pairs of guide sequences shown in **Table 1D**.

[00116] In some embodiments, the disclosure provides for one or more nucleic acid molecules encoding a pair of guide RNAs comprising a first guide RNA and a second guide RNA, wherein the first guide RNA and the second guide RNA target intron 52 and intron 53 of the DMD gene. In some

embodiments, the guide RNAs are for use with a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules also encode for a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules are in a composition further comprising a SluCas9 endonuclease. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 28. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 35. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 36. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 37. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 38. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 39. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 40. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 41. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 42. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 9. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 44. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 10. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 45. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 46. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 11. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 47. In some embodiments, the

first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 12. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 48. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 13. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 53. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 54. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 55. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 56. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 14. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 15. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 16. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 17. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 57. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 18. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 58. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 19. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 20. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 59. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 23. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 24. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 60. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 62. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 63. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 64. In some embodiments, the first guide RNA

comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 25. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 113 and the second guide RNA comprises the sequence of SEQ ID NO: 26. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 28. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 35. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 36. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 37. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 38. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 39. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 40. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 41. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 42. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 9. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 44. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 10. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 45. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 46. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 11. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 47. In some embodiments, the first guide RNA comprises the sequence

of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 12. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 48. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 13. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 53. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 54. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 55. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 56. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 14. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 15. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 16. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 17. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 57. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 18. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 58. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 19. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 20. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 59. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 23. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 24. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 60. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 62. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 63. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 64. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO:

115 and the second guide RNA comprises the sequence of SEQ ID NO: 25. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 26. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide

RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 122 and the second guide RNA comprises the sequence of SEQ ID NO: 28. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 28. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 35. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 36. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 37. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 38. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 39. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 40. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 41. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 92 and the second guide RNA comprises the sequence of SEQ ID NO: 42. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 1. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 2. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the

sequence of SEQ ID NO: 3. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 5. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 6. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 28. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 35. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 36. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 37. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 38. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 39. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 40. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 41. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 93 and the second guide RNA comprises the sequence of SEQ ID NO: 42. In some embodiments the guide RNAs each comprise a scaffold sequence comprising the sequence of SEQ ID NO: 901.

[00117] In some embodiments, a composition is provided comprising or consisting of a single nucleic acid molecule comprising: (i) a nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; or (ii) a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or (iii) a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs. In such embodiments, each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Table 1D**, and further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

[00118] In some embodiments, a composition is provided comprising or consisting of two nucleic acid molecules comprising:

i. a first nucleic acid encoding SluCas9; and
a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

ii. a first nucleic acid encoding SluCas9 and
1. at least one, at least two, or at least three guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:
1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

iii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and
a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

iv. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and
a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from the pairs of guide sequences shown in **Table 1D**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

B. Guide pairs targeting intron 52 and exon 53, or exon 53 and intron 53 of the DMD gene

[00119] In some embodiments, a composition is provided comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of exon 53 of the DMD gene, and wherein the fragment comprises a splice acceptor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice

acceptor site, and a second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice acceptor site (**Figure 4**, middle). In particular embodiments, the first guide RNA targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice acceptor site, and the second guide RNA targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice acceptor site. In some embodiments, the fragment of the DMD gene comprises a splice acceptor site and further comprises a portion of exon 53 and an adjoining portion of intron 52 of the DMD gene. In particular embodiments, the first guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 1-200 of SEQ ID NO: 144, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 201-400 of SEQ ID NO: 144. In SEQ ID NO: 144 shown below, the splice acceptor site (nucleotides 175-202 of SEQ ID NO: 144) is underlined.

[00120] SEQ ID NO: 144:

TCAGGAAAATAATTTAACAGAAACTAATATTTGCCATCAAAAAAGCAAAGAATCCTGTT
GTTCATCATCCTAGCCATAACACAATGAATAATTTTTTAAATAAGCAACATAAATGTGAG
ATAACGTTTGGAAGTTACATTTAAAATGTCTCCTCCAGACTAGCATTTACTACTATATATT
TATTTTTCCTTTTATTCTAGTTGAAAGAATTCAGAATCAGTGGGATGAAGTACAAGAACA
CCTTCAGAACCGGAGGCAACAGTTGAATGAAATGTTAAAGGATTCAACACAATGGCTGG
AAGCTAAGGAAGAAGCTGAGCAGGTCTTAGGACAGGCCAGAGCCAAGCTTGAGTCATGG
AAGGAGGGTCCCTATACAGTAGATGCAATCCAAAAGAAAATC.

[00121] In some embodiments, a composition is provided comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of exon 53 of the DMD gene, and wherein the fragment comprises a splice donor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice donor site, and a second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice donor site (**Figure 4**, bottom). In particular embodiments, the first guide RNA targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice donor site, and the second guide RNA targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice donor site. In some embodiments, the fragment of the DMD gene comprises a splice donor site and further comprises a portion of intron 53 and an adjoining portion of exon 53 of the DMD gene. In particular embodiments, the first guide RNA targets a sequence within nucleotides 1-200 of SEQ ID NO: 145, and the second guide RNA targets a sequence within nucleobases 201-400 of SEQ ID NO: 145. In SEQ ID NO: 145 shown below, the splice donor site (nucleobases 198-207 of SEQ ID NO: 145) is underlined.

[00122] SEQ ID NO: 145:

AGAATCAGTGGGATGAAGTACAAGAACACCTTCAGAACCGGAGGCAACAGTTGAATGA

AATGTTAAAGGATTCAACACAATGGCTGGAAGCTAAGGAAGAAGCTGAGCAGGTCTTAG
GACAGGCCAGAGCCAAGCTTGAGTCATGGAAGGAGGGTCCCTATACAGTAGATGCAATC
CAAAAGAAAATCACAGAAACCAAGGTTAGTATCAAAGATACCTTTTTAAAATAAAATAC
TGGTTACATTTGATAAAATTATACCATAGATTGTAATTTAATGATGTTTAATGTAAAGTTA
TTAACAGAAAATCACGTTAAAGCTGAAATGAACAGTAGACTTTGTATATTTATTTTCTTA
GAGACAGAGTCTCACTGTCACCCAGGCTAAAGTGCAGTGGCACA.

[00123] Any of the above embodiments may further comprise an endonuclease or a nucleic acid encoding an endonuclease, optionally a SluCas9 or a nucleic acid encoding a SluCas9.

[00124] In some embodiments, a composition is provided comprising a pair of guide RNAs, wherein the pair of guide RNAs comprises or consists of any one of the pairs of guide sequences of any one of **Table 1E**. In some embodiments, a composition is provided comprising a pair of guide RNAs, wherein the pair of guide RNAs comprises or consists of any one of the pairs of guide sequences of any one of **Table 1F**.

[00125] In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 1-64; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 65-87. In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of SEQ ID NOs: 65-87; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 88-143. In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and the second guide RNA is selected from any one of SEQ ID NOs: 65-87. In some embodiments, a composition is provided comprising a pair of guide RNAs or a nucleic acid encoding a pair of guide RNAs, wherein the first guide RNA is selected from any one of SEQ ID NOs: 65-87; and the second guide RNA is selected from any one of SEQ ID NOs: 88-143. In some embodiments, the first guide RNA targets a sequence in intron 53 of a DMD gene and the second guide RNA targets a sequence in exon 53 of the DMD gene. In some embodiments, the first guide RNA targets a sequence in exon 53 of a DMD gene and the second guide RNA targets a sequence in intron 52 of the DMD gene. In some embodiments, the at least one pair of guide RNAs is capable of excising a fragment of the DMD gene, wherein the fragment comprises a splice donor site or a splice acceptor site, and optionally wherein the fragment is between 5 and 400

nucleotides in length. In particular embodiments, the excised fragment of the DMD gene does not comprise an entire exon of the DMD gene. In some embodiments, the pair of guide RNAs is capable of inducing skipping of at least a portion (such as all) of exon 53 of the DMD gene.

[00126] In some embodiments, a composition is provided comprising at least one pair of guide RNAs disclosed herein, once expressed in vitro or in vivo in combination with a SluCas9 endonuclease, the at least one pair of guide RNAs (i) excises exon 53 of a DMD gene, (ii) excises a fragment of the DMD gene comprising a portion of intron 53 and an adjoining portion of exon 53, wherein the excised fragment of the DMD gene comprises a splice donor site, or (iii) excises a fragment of the DMD gene comprising a portion of exon 53 and an adjoining portion of intron 52, wherein the excised fragment of the DMD gene comprises a splice acceptor site. In some such embodiments, the size of the excised fragment of the DMD gene is between 5 and 400 nucleotides in length, such as between 5 and 375, 5 and 350, 5 and 325, 5 and 300, 5 and 275, 5 and 250, 5 and 225, 5 and 200, 5 and 175, 5 and 150, 5 and 125, 5 and 100, 20 and 400, 20 and 375, 20 and 350, 20 and 325, 20 and 300, 20 and 275, 20 and 250, 20 and 225, 20 and 200, 20 and 175, 20 and 150, 20 and 125, 20 and 100, 50 and 400, 50 and 375, 50 and 350, 50 and 325, 50 and 300, 50 and 275, 50 and 250, 50 and 225, 50 and 200, 50 and 175, 50 and 150, 50 and 125, or 50 and 100 nucleotides in length.

[00127] In some embodiments, a composition is provided comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first and a second guide sequence selected from any one of the following pairs of first and second guide sequences:

a. SEQ ID NOs: 1 and 65; 1 and 66; 1 and 67; 1 and 68; 1 and 69; 1 and 70; 1 and 71; 1 and 72; 1 and 73; 1 and 74; 1 and 75; 1 and 76; 1 and 77; 1 and 78; 1 and 79; 1 and 80; 1 and 81; 1 and 82; 1 and 83; 1 and 84; 1 and 85; 1 and 86; 1 and 87; 2 and 65; 2 and 66; 2 and 67; 2 and 68; 2 and 69; 2 and 70; 2 and 71; 2 and 72; 2 and 73; 2 and 74; 2 and 75; 2 and 76; 2 and 77; 2 and 78; 2 and 79; 2 and 80; 2 and 81; 2 and 82; 2 and 83; 2 and 84; 2 and 85; 2 and 86; 2 and 87; 3 and 65; 3 and 66; 3 and 67; 3 and 68; 3 and 69; 3 and 70; 3 and 71; 3 and 72; 3 and 73; 3 and 74; 3 and 75; 3 and 76; 3 and 77; 3 and 78; 3 and 79; 3 and 80; 3 and 81; 3 and 82; 3 and 83; 3 and 84; 3 and 85; 3 and 86; 3 and 87; 4 and 65; 4 and 66; 4 and 67; 4 and 68; 4 and 69; 4 and 70; 4 and 71; 4 and 72; 4 and 73; 4 and 74; 4 and 75; 4 and 76; 4 and 77; 4 and 78; 4 and 79; 4 and 80; 4 and 81; 4 and 82; 4 and 83; 4 and 84; 4 and 85; 4 and 86; 4 and 87; 5 and 65; 5 and 66; 5 and 67; 5 and 68; 5 and 69; 5 and 70; 5 and 71; 5 and 72; 5 and 73; 5 and 74; 5 and 75; 5 and 76; 5 and 77; 5 and 78; 5 and 79; 5 and 80; 5 and 81; 5 and 82; 5 and 83; 5 and 84; 5 and 85; 5 and 86; 5 and 87; 6 and 65; 6 and 66; 6 and 67; 6 and 68; 6 and 69; 6 and 70; 6 and 71; 6 and 72; 6 and 73; 6 and 74; 6 and 75; 6 and 76; 6 and 77; 6 and 78; 6 and 79; 6 and 80; 6 and

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b. SEQ ID NOs: 88 and 65; 88 and 66; 88 and 67; 88 and 68; 88 and 69; 88 and 70; 88 and 71; 88 and 72; 88 and 73; 88 and 74; 88 and 75; 88 and 76; 88 and 77; 88 and 78; 88 and 79; 88 and 80; 88 and 81; 88 and 82; 88 and 83; 88 and 84; 88 and 85; 88 and 86; 88 and 87; 89 and 65; 89 and 66; 89 and 67; 89 and 68; 89 and 69; 89 and 70; 89 and 71; 89 and 72; 89 and 73; 89 and 74; 89 and 75; 89 and 76; 89 and 77; 89 and 78; 89 and 79; 89 and 80; 89 and 81; 89 and 82; 89 and 83; 89 and 84; 89 and 85; 89 and 86; 89 and 87; 90 and 65; 90 and 66; 90 and 67; 90 and 68; 90 and 69; 90 and 70; 90 and 71; 90 and 72; 90 and 73; 90 and 74; 90 and 75; 90 and 76; 90 and 77; 90 and 78; 90 and 79; 90 and 80; 90 and 81; 90 and 82; 90 and 83; 90 and 84; 90 and 85; 90 and 86; 90 and 87; 91 and 65; 91 and 66; 91 and 67; 91 and 68; 91 and 69; 91 and 70; 91 and 71; 91 and 72; 91 and 73; 91 and 74; 91 and 75; 91 and 76; 91 and 77; 91 and 78; 91 and 79; 91 and 80; 91 and 81; 91 and 82; 91 and 83; 91 and 84; 91 and 85; 91 and 86; 91 and 87; 92 and 65; 92 and 66; 92 and 67; 92 and 68; 92 and 69; 92 and 70; 92 and 71; 92 and 72; 92 and 73; 92 and 74; 92 and 75; 92 and 76; 92 and 77; 92 and 78; 92 and 79; 92 and 80; 92 and 81; 92 and 82; 92 and 83; 92 and 84; 92 and 85; 92 and 86; 92 and 87; 93 and 65; 93 and 66; 93 and 67; 93 and 68; 93 and 69; 93 and 70; 93 and 71; 93 and 72; 93 and 73; 93 and 74; 93 and 75; 93 and 76; 93 and 77; 93 and 78; 93 and 79; 93 and 80; 93 and 81; 93 and 82; 93 and 83; 93 and 84; 93 and 85; 93 and 86; 93 and 87; 94 and 65; 94 and 66; 94 and 67; 94 and 68; 94 and 69; 94 and 70; 94 and 71; 94 and 72; 94 and 73; 94 and 74; 94 and 75; 94 and 76; 94 and 77; 94 and 78; 94 and 79; 94 and 80; 94 and 81; 94 and 82; 94 and 83; 94 and 84; 94 and 85; 94 and 86; 94 and 87; 95 and 65; 95 and 66; 95 and 67; 95 and 68; 95 and 69; 95 and 70; 95 and 71; 95 and 72; 95 and 73; 95 and 74; 95 and 75; 95 and 76; 95 and 77; 95 and 78; 95 and 79; 95 and 80; 95 and 81; 95 and 82; 95 and 83; 95 and 84; 95 and 85; 95 and 86; 95 and 87; 96 and 65; 96 and 66; 96 and 67; 96 and 68; 96 and 69; 96 and 70; 96 and 71; 96 and 72; 96 and 73; 96 and 74; 96 and 75; 96 and 76; 96 and 77; 96 and 78; 96 and 79; 96 and 80; 96 and 81; 96 and 82; 96 and 83; 96 and 84; 96 and 85; 96 and 86; 96 and 87; 97

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[00128] In some embodiments, the disclosure provides for one or more nucleic acid molecules encoding a pair of guide RNAs comprising a first guide RNA and a second guide RNA, wherein the first guide RNA and the second guide RNA target intron 52 and exon 53 of the DMD gene. In some embodiments, the guide RNAs are for use with a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules also encode for a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules are in a composition further comprising a SluCas9 endonuclease. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide

RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 2 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the

sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of

SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 35 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 36 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some

embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 37 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 38 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 39 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the

first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA

comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 57 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 58 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 19 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 20 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments the guide RNAs each comprise a scaffold sequence comprising the sequence of SEQ ID NO: 901.

[00129] In some embodiments, the disclosure provides for one or more nucleic acid molecules encoding a pair of guide RNAs comprising a first guide RNA and a second guide RNA, wherein the

first guide RNA and the second guide RNA target exon 53 and intron 53 of the DMD gene. In some embodiments, the guide RNAs are for use with a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules also encode for a SluCas9 endonuclease. In some embodiments, the one or more nucleic acid molecules are in a composition further comprising a SluCas9 endonuclease. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 82. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 83. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO:

119 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 84. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 85. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 68. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide

RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 69. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 70. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 71. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises

the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 73. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 74. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 75. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of

SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 76. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 80. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 116 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 117 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 118 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 119 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 120 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 121 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments, the first guide RNA comprises the sequence of SEQ ID NO: 90 and the second guide RNA comprises the sequence of SEQ ID NO: 81. In some embodiments the guide RNAs each comprise a scaffold sequence comprising the sequence of SEQ ID NO: 901.

[00130] In some embodiments, a composition is provided comprising or consisting of a single nucleic acid molecule comprising: (i) a nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; or (ii) a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or (iii) a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs. In such embodiments, each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Table 1E or 1F**, and further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

[00131] In some embodiments, a composition is provided comprising or consisting of two nucleic acid molecules comprising:

v. a first nucleic acid encoding SluCas9; and

a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

vi. a first nucleic acid encoding SluCas9 and

1. at least one, at least two, or at least three guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:

4. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
5. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
6. from one to six guide RNAs;

vii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and

a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

viii. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and

a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from the pairs of guide sequences shown in **Table 1E or 1F**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs.

C. Guide pairs targeting a splice acceptor site or a splice donor site of the DMD gene

[00132] In some embodiments, a composition is provided comprising (a) a pair of guide RNA molecules or a nucleic acid encoding a pair of RNA molecules, wherein the first guide RNA targets a region upstream of a splice acceptor site or a splice donor site in a DMD gene and wherein the second guide RNA targets a region downstream of a splice acceptor site or a splice donor site in the DMD gene, and (b) an endonuclease or a nucleic acid encoding an endonuclease. In some embodiments, the endonuclease is a *Staphylococcus lugdunensis* Cas9 (SluCas9). In one particular embodiment, the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an exon of the DMD gene. In another particular embodiment, the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an intron of the DMD gene. In another particular embodiment, the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an exon of the DMD gene. In another particular embodiment, the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an intron of the DMD gene.

[00133] In some embodiments, the splice acceptor site or splice donor site is in intron 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, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, or 78 of the DMD gene. In particular embodiments, the splice acceptor site or splice donor site is in intron 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 or 57 of the DMD gene.

[00134] In some embodiments of the disclosed compositions, the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides upstream of the splice acceptor or splice donor site. In some embodiments, the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides downstream of the splice acceptor or splice donor site.

Scaffold Sequences

[00135] Each of the guide sequences shown in **Tables 1A-1F** may further comprise additional nucleotides to form or encode a crRNA, e.g., using any known sequence appropriate for the Cas9 being used. In some embodiments, the crRNA comprises (5' to 3') at least a spacer sequence and a first complementarity domain. The first complementary domain is sufficiently complementary to a second complementarity domain, which may be part of the same molecule in the case of an sgRNA or in a tracrRNA in the case of a dual or modular gRNA, to form a duplex. See, e.g., US 2017/0007679 for detailed discussion of crRNA and gRNA domains, including first and second complementarity domains.

[00136] A single-molecule guide RNA (sgRNA) can comprise, in the 5' to 3' direction, an optional spacer extension sequence, a spacer sequence, a minimum CRISPR repeat sequence, a single-molecule guide linker, a minimum tracrRNA sequence, a 3' tracrRNA sequence and/or an optional tracrRNA extension sequence. The optional tracrRNA extension can comprise elements that contribute additional functionality (*e.g.*, stability) to the guide RNA. The single-molecule guide linker can link the minimum CRISPR repeat and the minimum tracrRNA sequence to form a hairpin structure. The optional tracrRNA extension can comprise one or more hairpins. In particular embodiments, the disclosure provides for an sgRNA comprising a spacer sequence and a tracrRNA sequence.

[00137] The guide RNA can be considered to comprise a scaffold sequence necessary for endonuclease binding and a spacer sequence required to bind to the genomic target sequence. In some embodiments, the guide RNA comprises any of the scaffold sequences disclosed herein and any of the spacer sequences disclosed herein. In some embodiments, the guide RNA comprises any of the scaffold sequences disclosed herein and any of the spacer sequences disclosed herein, without any nucleotides between the scaffold sequence and the spacer sequence.

An exemplary scaffold sequence suitable for use with SaCas9 to follow the guide sequence at its 3' end is:

GTTTAAGTACTCTGTGCTGGAAACAGCACAGAATCTACTTAAACAAGGCAAAATGCCGT GTTTATCTCGTCAACTTGTTGGCGAGA (SEQ ID NO: 500) in 5' to 3' orientation. In some embodiments, an exemplary scaffold sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 500, or a sequence that differs from SEQ ID NO: 500 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00138] In some embodiments, a variant of an SaCas9 scaffold sequence may be used. In some embodiments, the SaCas9 scaffold to follow the guide sequence at its 3' end is referred to as "SaScaffoldV1" and is:

GTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGT

CAACTTGTTGGCGAGAT (SEQ ID NO: 501) in 5' to 3' orientation. In some embodiments, an exemplary scaffold sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 501, or a sequence that differs from SEQ ID NO: 501 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00139] In some embodiments, a variant of an SaCas9 scaffold sequence may be used. In some embodiments, the SaCas9 scaffold to follow the guide sequence at its 3' end is referred to as "SaScaffoldV2" and is:
GTTTAAGTACTCTGTGCTGGAAACAGCACAGAATCTACTTAAACAAGGCAAAATGCCGT
GTTTATCTCGTCAACTTGTTGGCGAGAT (SEQ ID NO: 502) in 5' to 3' orientation. In some embodiments, an exemplary scaffold sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 502, or a sequence that differs from SEQ ID NO: 502 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00140] In some embodiments, a variant of an SaCas9 scaffold sequence may be used. In some embodiments, the SaCas9 scaffold to follow the guide sequence at its 3' end is referred to as "SaScaffoldV3" and is:
GTTTAAGTACTCTGGAAACAGAATCTACTTAAACAAGGCAAAATGCCGTGTTTATCTCGT
CAACTTGTTGGCGAGAT (SEQ ID NO: 503) in 5' to 3' orientation. In some embodiments, an exemplary scaffold sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 503, or a sequence that differs from SEQ ID NO: 503 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00141] In some embodiments, a variant of an SaCas9 scaffold sequence may be used. In some embodiments, the SaCas9 scaffold to follow the guide sequence at its 3' end is referred to as "SaScaffoldV5" and is:
GTTTCAGTACTCTGGAAACAGAATCTACTGAAACAAGGCAAAATGCCGTGTTTATCTCGT
CAACTTGTTGGCGAGAT (SEQ ID NO: 504) in 5' to 3' orientation. In some embodiments, an exemplary scaffold sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 504, or a sequence that differs from SEQ ID NO: 504 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00142] Two exemplary scaffold sequences suitable for use with SluCas9 to follow the guide sequence at its 3' end are:
GTTTTAGTACTCTGGAAACAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCAT
CAATTTATTGGTGGGA (SEQ ID NO: 600), or
GTTTAAGTACTCTGTGCTGGAAACAGCACAGAATCTACTGAAACAAGACAATATGTCGT

GTTTATCCCATCAATTTATTGGTGGGA (SEQ ID NO: 601) in 5' to 3' orientation. In some embodiments, an exemplary sequence for use with SluCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 600 or SEQ ID NO: 601, or a sequence that differs from SEQ ID NO: 600 or SEQ ID NO: 601 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00143] Another exemplary scaffold sequences suitable for use with SluCas9 to follow the guide sequence at its 3' end is:
GTTTCAGTACTCTGGAAACAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCAT CAATTTATTGGTGGGAT (SEQ ID NO: 901) in 5' to 3' orientation. In some embodiments, an exemplary sequence for use with SluCas9 to follow the 3' end of the guide sequence is a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID NO: 901, or a sequence that differs from SEQ ID NO: 901 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00144] Exemplary scaffold sequences suitable for use with SluCas9 to follow the guide sequence at its 3' end are also shown below in the 5' to 3' orientation.

[00145] **Table 7**:

Scaffold ID	**SEQ ID NO**	**Scaffold Sequence (5' to 3')**	**Homology to Slu v5**	**Streak of Homology to Slu v5 (# nucleotides)**
Wildtype	900	GTTTTAGTACTCTGGAAACAGAATCTACTGAA ACAAGACAATATGTCGTGTTTATCCCATCAAT TTATTGGTGGGAT	N/A	N/A
Slu-VCGT-4.5	601	GTTTAAGTACTCTGTGCTGGAAACAGCACAG AATCTACTGAAACAAGACAATATGTCGTGTTT ATCCCATCAATTTATTGGTGGGA	N/A	N/A
Slu_v5	901	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGACAATATGTCGTGTTTATCCCATCAAT TTATTGGTGGGAT	100.00%	77
Slu_v5-1	902	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGACAATATGTCGTGTTTATCCCATCAATTTA TTGGTGGGAT	87.50%	47
Slu_v5-2	903	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGgCAAaATGcCGTGTTTATCCCATCAATT TATTGGTGGGAT	96.10%	37
Slu_v5-3	904	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGACAATATGTCGcgcccaTCCCATCAATTT ATTGGTGGGAT	94.81%	48
Slu_v5-4	905	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGACAATATGTCGTGTTTATgggTTgAATT TATTcGacccAT	91.55%	55
Slu_v5-5	906	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGgCAAaATGcCGTGTTTATCCCATCAATTTAT TGGTGGGAT	83.75%	31
Slu_v5-6	907	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGACAATATGTCGcgcccaTCCCATCAATTTATT GGTGGGAT	82.50%	23

Slu_v5-7	908	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGACAATATGTCGTGTTTATgggTTgAATTTAT TcGacccAT	78.38%	25
Slu_v5-8	909	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGgCAAaATGcCGcgcccaTCCCATCAATTTA TTGGTGGGAT	90.91%	37
Slu_v5-9	910	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGgCAAaATGcCGTGTTTATgggTTgAATTT ATTcGacccAT	87.32%	37
Slu_v5-10	911	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGACAATATGTCGcgcccaTgggTTgAATTTA TTcGacccAT	82.89%	48
Slu_v5-11	912	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGgCAAaATGcCGcgcccaTCCCATCAATTTATTG GTGGGAT	78.75%	23
Slu_v5-12	913	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGgCAAaATGcCGTGTTTATgggTTgAATTTATTc GacccAT	74.32%	9
Slu_v5-13	914	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGACAATATGTCGcgcccaTgggTTgAATTTATTc GacccAT	70.89%	18
Slu_v5-14	915	GTTTCAGTACTCTGGAAACAGAATCTACTGAA ACAAGgCAAaATGcCGcgcccaTgggTTgAATTTAT TcGacccAT	78.95%	37
Slu_v5-15	916	GTTTggTaACcTaGGAAACTagATCTTaccAAACA AGgCAAaATGcCGcgcccaTgggTTgAATTTATTcGa cccAT	67.09%	8
Slu v4	917	GTTTCAGTACTCTGTGCTGGAAACAGCACAGA ATCTACTGAAACAAGACAATATGTCGTGTTTA TCCCATCAATTTATTGGTGGGAT	N/A	N/A

[00146] In some embodiments, the scaffold sequence suitable for use with SaCas9 to follow the guide sequence at its 3' end is selected from any one of SEQ ID NOs: 500-504 in 5' to 3 orientation. In some embodiments, an exemplary sequence for use with SaCas9 to follow the 3' end of the guide sequence is a sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to any one off SEQ ID NOs: 500-504, or a sequence that differs from any one of SEQ ID NOs: 500-504 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00147] In some embodiments, the scaffold sequence suitable for use with SluCas9 to follow the guide sequence at its 3' end is selected from any one of SEQ ID NOs: 900 or 601, or 901-917 in 5' to 3 orientation. In some embodiments, an exemplary sequence for use with SluCas9 to follow the 3' end of the guide sequence is a sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to any one off SEQ ID NOs: 900 or 601, or 901-917, or a sequence that differs from any one of SEQ ID NOs: 900 or 601, or 901-917 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides. In particular embodiments, an exemplary sequence for use with SluCas9 to follow the 3' end of the guide sequence is a sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to SEQ ID

NO: 901, or a sequence that differs from any one of SEQ ID NO: 901 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00148] In some embodiments, any scaffold sequence (e.g., any of the scaffold sequences disclosed herein) is suitable for use with any sRGN disclosed herein, such as any one of sRGN1, sRGN2, sRGN3, sRGN3.1, sRGN3.2, sRGN3.3, sRGN4, or a nucleic acid molecule encoding the same. In some embodiments, a scaffold sequence suitable for use with a sRGN, such as at the 3' end of a guide RNA sequence within an expression vector comprising the sRGN (e.g., an expression vector as shown in FIGS. 5A-5B) is selected from any one of SEQ ID NOs: 500-504, 601, or 900-917. In some embodiments, a scaffold sequence suitable for use with a sRGN, such as at the 3' end of a guide RNA sequence within an expression vector comprising the sRGN (e.g., an expression vector as shown in FIGS. 5A-5B) is a sequence that is at least 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to any one of SEQ ID NOs: 500-504, 601, or 900-917, or a sequence that differs from any one of SEQ ID NOs: 500-504, 601, or 900-917 by no more than 1, 2, 3, 4, 5, 10, 15, 20, or 25 nucleotides.

[00149] In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 500. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 501. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 502. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 503. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 504. In some embodiments, comprising a pair of gRNAs, one of the gRNAs comprises a sequence selected from any one of SEQ ID NOs: 500-504. In some embodiments, comprising a pair of gRNAs, both of the gRNAs comprise a sequence selected from any one of SEQ ID NOs: 500-504. In some embodiments, comprising a pair of gRNAs, the nucleotides 3' of the guide sequence of the gRNAs are the same sequence. In some embodiments, comprising a pair of gRNAs, the nucleotides 3' of the guide sequence of the gRNAs are different sequences.

[00150] In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 901. In some embodiments, comprising a pair of gRNAs, one of the gRNAs comprises a sequence comprising SEQ ID NO: 901. In some embodiments, comprising a pair of gRNAs, both of the gRNAs comprise a sequence comprising SEQ ID NO: 901.

[00151] In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 900. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 601. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 900. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 901. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 902. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 903. In some

embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 904. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 905. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 906. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 907. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 908. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 909. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 910. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 911. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 912. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 913. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 914. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 915. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 916. In some embodiments, the nucleic acid encoding the gRNA comprises a sequence comprising SEQ ID NO: 917. In some embodiments, comprising a pair of gRNAs, one of the gRNAs comprises a sequence selected from any one of SEQ ID NOs: 900 or 601, or 901-917. In some embodiments, comprising a pair of gRNAs, both of the gRNAs comprise a sequence selected from any one of SEQ ID NOs: 900 or 601, or 901-917. In some embodiments, comprising a pair of gRNAs, the nucleotides 3' of the guide sequence of the gRNAs are the same sequence. In some embodiments, comprising a pair of gRNAs, the nucleotides 3' of the guide sequence of the gRNAs are different sequences.

[00152] In some embodiments, the scaffold sequence comprises one or more alterations in the stem loop 1 as compared to the stem loop 1 of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). In some embodiments, the scaffold sequence comprises one or more alterations in the stem loop 2 as compared to the stem loop 2 of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). In some embodiments, the scaffold sequence comprises one or more alterations in the tetraloop as compared to the tetraloop of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). In some embodiments, the scaffold sequence comprises one or more alterations in the repeat region as compared to the repeat region of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). In some embodiments, the scaffold sequence comprises one or more alterations in the anti-repeat region as

compared to the anti-repeat region of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). In some embodiments, the scaffold sequence comprises one or more alterations in the linker region as compared to the linker region of a wildtype SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 900) or a reference SluCas9 scaffold sequence (e.g., a scaffold comprising the sequence of SEQ ID NO: 901). See, e.g., Nishimasu et al., 2015, Cell, 162:1113-1126 for description of regions of a scaffold.

[00153] Where a tracrRNA is used, in some embodiments, it comprises (5' to 3') a second complementary domain and a proximal domain. In the case of a sgRNA, guide sequences together with additional nucleotides (e.g., SEQ ID Nos: 500-504 (for SaCas9), and 900 or 601, or 901-917 (for SluCas9)) form or encode a sgRNA. In some embodiments, an sgRNA comprises (5' to 3') at least a spacer sequence, a first complementary domain, a linking domain, a second complementary domain, and a proximal domain. A sgRNA or tracrRNA may further comprise a tail domain. The linking domain may be hairpin-forming. See, e.g., US 2017/0007679 for detailed discussion and examples of crRNA and gRNA domains, including second complementarity domains, linking domains, proximal domains, and tail domains.

[00154] In some embodiments, the disclosure provides for specific nucleic acid sequences encoding one or more guide RNA components (e.g., any of the spacer and or scaffold sequences disclosed herein). The disclosure contemplates RNA equivalents of any of the DNA sequences provided herein (i.e., in which "T"s are replaced with "U"s), or DNA equivalents of any of the RNA sequences provided herein (i.e., in which "U"s are replaced with "T"s), as well as complements (including reverse complements) of any of the sequences disclosed herein.

[00155] In some embodiments, a composition is provided comprising a guide RNA, or nucleic acid encoding a guide RNA, wherein the guide RNA further comprises a trRNA. In each composition and method embodiment described herein, the crRNA (comprising the spacer sequence) and trRNA may be associated as a single RNA (sgRNA) or may be on separate RNAs (dgRNA). In the context of sgRNAs, the crRNA and trRNA components may be covalently linked, e.g., via a phosphodiester bond or other covalent bond.

Vectors

[00156] In any embodiment comprising a nucleic acid molecule encoding a guide RNA and/or a Cas9 (such as a SluCas9), the nucleic acid molecule may be a vector. In some embodiments, a composition is provided comprising a single nucleic acid molecule encoding at least one guide RNA and Cas9 (such as a SluCas9), wherein the nucleic acid molecule is a vector. In some embodiments, a composition is provided comprising more than one nucleic acid molecule encoding a guide RNA and Cas9 (such as a SluCas9), wherein the nucleic acid molecule is a vector. In some embodiments, a composition is provided comprising more than one nucleic acid molecule wherein one molecule

encodes one or more guide RNA, and the other molecule encodes a Cas9 (such as a SluCas9) plus or minus at least one guide RNA, wherein the nucleic acid molecule is a vector.

[00157] Any type of vector, such as any of those described herein, may be used. In some embodiments, the vector is a lipid nanoparticle. In some embodiments, the vector is a viral vector. In some embodiments, the viral vector is a non-integrating viral vector (i.e., that does not insert sequence from the vector into a host chromosome). In some embodiments, the viral vector is an adeno-associated virus vector (AAV), a lentiviral vector, an integrase-deficient lentiviral vector, an adenoviral vector, a vaccinia viral vector, an alphaviral vector, or a herpes simplex viral vector. In some embodiments, the vector comprises a muscle-specific promoter. Exemplary muscle-specific promoters include a muscle creatine kinase promoter, a desmin promoter, an MHCK7 promoter, or an SPc5-12 promoter. *See* US 2004/0175727 A1; Wang et al., *Expert Opin Drug Deliv*. (2014) 11, 345–364; Wang et al., *Gene Therapy* (2008) 15, 1489–1499. In some embodiments, the muscle-specific promoter is a CK8 promoter. In some embodiments, the muscle-specific promoter is a CK8e promoter. In any of the foregoing embodiments, the vector may be an adeno-associated virus vector (AAV).

[00158] In some embodiments, the vector is a lipid nanoparticle comprising an endonuclease (e.g., any of the endonucleases disclosed herein) and one or more of any of the guide RNAs disclosed herein. In some embodiments, the vector is a lipid nanoparticle comprising a nucleic acid encoding an endonuclease (e.g., any of the endonucleases disclosed herein) and one or more of any of the guide RNAs disclosed herein. In some embodiments, the vector is a lipid nanoparticle comprising a nucleic acid encoding an endonuclease (e.g., any of the endonucleases disclosed herein) and a nucleic acid encoding one or more of any of the guide RNAs disclosed herein.

[00159] Where a vector is used, it may be a viral vector, such as a non-integrating viral vector. In some embodiments, the viral vector is an adeno-associated virus vector, a lentiviral vector, an integrase-deficient lentiviral vector, an adenoviral vector, a vaccinia viral vector, an alphaviral vector, or a herpes simplex viral vector. In some embodiments, the viral vector is an adeno-associated virus (AAV) vector. In some embodiments, the AAV vector is an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAVrh10 (*see, e.g.*, SEQ ID NO: 81 of US 9,790,472, which is incorporated by reference herein in its entirety), AAVrh74 (*see, e.g.*, SEQ ID NO: 1 of US 2015/0111955, which is incorporated by reference herein in its entirety), or AAV9 vector, wherein the number following AAV indicates the AAV serotype. In some embodiments, the AAV vector is a single-stranded AAV (ssAAV). In some embodiments, the AAV vector is a double-stranded AAV (dsAAV). Any variant of an AAV vector or serotype thereof, such as a self-complementary AAV (scAAV) vector, is encompassed within the general terms AAV vector, AAV1 vector, etc. See, e.g., McCarty et al., *Gene Ther*. 2001;8:1248–54, Naso et al., *BioDrugs* 2017; 31:317-334, and references cited therein for detailed discussion of various AAV vectors. In some embodiments, the AAV vector size is measured in length of nucleotides from ITR to ITR, inclusive of both ITRs. In some embodiments, the AAV

vector is less than 5 kb in size from ITR to ITR, inclusive of both ITRs. In particular embodiments, the AAV vector is less than 4.9 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV vector is less than 4.85 kb in size from ITR to ITR, inclusive of both ITRs. In further embodiments, the AAV vector is less than 4.8 kb in size from ITR to ITR, inclusive of both ITRs. In further embodiments, the AAV vector is less than 4.75 kb in size from ITR to ITR, inclusive of both ITRs. In further embodiments, the AAV vector is less than 4.7 kb in size from ITR to ITR, inclusive of both ITRs. In some embodiments, the vector is between 3.9-5 kb, 4-5 kb, 4.2-5 kb, 4.4-5 kb, 4.6-5 kb, 4.7-5 kb, 3.9-4.9 kb, 4.2-4.9 kb, 4.4-4.9 kb, 4.7-4.9 kb, 3.9-4.85 kb, 4.2-4.85 kb, 4.4-4.85 kb, 4.6-4.85 kb, 4.7-4.85 kb, 4.7-4.9 kb, 3.9-4.8 kb, 4.2-4.8 kb, 4.4-4.8 kb or 4.6-4.8 kb from ITR to ITR in size, inclusive of both ITRs. In some embodiments, the vector is between 4.4-4.85 kb in size from ITR to ITR, inclusive of both ITRs. In some embodiments, the vector is an AAV9 vector.

[00160] In some embodiments, the vector (e.g., viral vector, such as an adeno-associated viral vector) comprises a tissue-specific (e.g., muscle-specific) promoter, e.g., which is operatively linked to a sequence encoding the guide RNA and/or the Cas protein. In some embodiments, the muscle-specific promoter is a muscle creatine kinase promoter, a desmin promoter, an MHCK7 promoter, or an SPc5-12 promoter. In some embodiments, the muscle-specific promoter is a CK8 promoter. In some embodiments, the muscle-specific promoter is a CK8e promoter. Muscle-specific promoters are described in detail, e.g., in US2004/0175727 A1; Wang et al., *Expert Opin Drug Deliv.* (2014) 11, 345–364; Wang et al., *Gene Therapy* (2008) 15, 1489–1499. In some embodiments, the tissue-specific promoter is a neuron-specific promoter, such as an enolase promoter. See, e.g., Naso et al., *BioDrugs* 2017; 31:317-334; Dashkoff et al., *Mol Ther Methods Clin Dev.* 2016;3:16081, and references cited therein for detailed discussion of tissue-specific promoters including neuron-specific promoters.

[00161] In some embodiments, in addition to guide RNA and Cas9 (such as a SluCas9) sequences, the vectors further comprise nucleic acids that do not encode guide RNAs. Nucleic acids that do not encode guide RNA and Cas9 (such as a SluCas9) include, but are not limited to, promoters, enhancers, and regulatory sequences. In some embodiments, the vector comprises one or more nucleotide sequence(s) encoding a crRNA, a trRNA, or a crRNA and trRNA. In some embodiments, the muscle specific promoter is the CK8 promoter. The CK8 promoter has the following sequence (SEQ ID NO. 700):

```
1     CTAGACTAGC ATGCTGCCCA TGTAAGGAGG CAAGGCCTGG GGACACCCGA GATGCCTGGT
61    TATAATTAAC CCAGACATGT GGCTGCCCCC CCCCCCCCAA CACCTGCTGC CTCTAAAAAT
121   AACCCTGCAT GCCATGTTCC CGGCGAAGGG CCAGCTGTCC CCCGCCAGCT AGACTCAGCA
181   CTTAGTTTAG GAACCAGTGA GCAAGTCAGC CCTTGGGGCA GCCCATACAA GGCCATGGGG
241   CTGGGCAAGC TGCACGCCTG GGTCCGGGGT GGGCACGGTG CCCGGGCAAC GAGCTGAAAG
301   CTCATCTGCT CTCAGGGGCC CCTCCCTGGG GACAGCCCCT CCTGGCTAGT CACACCCTGT
361   AGGCTCCTCT ATATAACCCA GGGGCACAGG GGCTGCCCTC ATTCTACCAC CACCTCCACA
421   GCACAGACAG ACACTCAGGA GCCAGCCAGC
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[00162] In some embodiments, the muscle-cell cell specific promoter is a variant of the CK8 promoter, called CK8e. In some embodiments, the size of the CK8e promoter is 436 bp. The CK8e promoter has the following sequence (SEQ ID NO. 701):

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   1      TGCCCATGTA AGGAGGCAAG GCCTGGGGAC ACCCGAGATG CCTGGTTATA ATTAACCCAG
  61      ACATGTGGCT GCCCCCCCCC CCCCAACACC TGCTGCCTCT AAAAATAACC CTGCATGCCA
 121      TGTTCCCGGC GAAGGGCCAG CTGTCCCCCG CCAGCTAGAC TCAGCACTTA GTTTAGGAAC
 181      CAGTGAGCAA GTCAGCCCTT GGGGCAGCCC ATACAAGGCC ATGGGGCTGG GCAAGCTGCA
 241      CGCCTGGGTC CGGGGTGGGC ACGGTGCCCG GGCAACGAGC TGAAAGCTCA TCTGCTCTCA
 301      GGGGCCCCTC CCTGGGGACA GCCCCTCCTG GCTAGTCACA CCCTGTAGGC TCCTCTATAT
 361      AACCCAGGGG CACAGGGGCT GCCCTCATTC TACCACCACC TCCACAGCAC AGACAGACAC
 421      TCAGGAGCCA GCCAGC
```

[00163] In some embodiments, the Ck8e promoter comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 701.

[00164] In some embodiments, the vector comprises one or more of a U6, H1, or 7SK promoter. In some embodiments, the U6 promoter is the human U6 promoter (*e.g.*, the U6L promoter or U6S promoter). In some embodiments, the promoter is the murine U6 promoter. In some embodiments, the 7SK promoter is a human 7SK promoter. In some embodiments, the 7SK promoter is the 7SK1 promoter. In some embodiments, the 7SK promoter is the 7SK2 promoter. In some embodiments, the H1 promoter is a human H1 promoter (*e.g.*, the H1L promoter or the H1S promoter). In some embodiments, the vector comprises multiple guide sequences, wherein each guide sequence is under the control of a separate promoter. In some embodiments, each of the multiple guide sequences comprises a different sequence. In some embodiments, each of the multiple guide sequences comprise the same sequence (e.g., each of the multiple guide sequences comprise the same spacer sequence). In some embodiments, each of the multiple guide sequences comprises the same spacer sequence and the same scaffold sequence. In some embodiments, each of the multiple guide sequences comprises different spacer sequences and different scaffold sequences. In some embodiments, each of the multiple guide sequences comprises the same spacer sequence, but comprises a different scaffold sequence. In some embodiments, each of the multiple guide sequences comprises different spacer sequences and different scaffold sequences. In some embodiments, each of the separate promoters comprises the same nucleotide sequence (*e.g.,* the U6 promoter sequence). In some embodiments, each of the separate promoters comprises a different nucleotide sequence (*e.g.*, the U6, H1, and/or 7SK promoter sequence).

[00165] In some embodiments, the U6 promoter comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 702:

```
cgagtccaac acccgtggga atcccatggg caccatggcc cctcgctcca aaaatgcttt       60
cgcgtcgcgc agacactgct cggtagtttc ggggatcagc gtttgagtaa gagcccgcgt      120
ctgaaccctc cgcgccgccc cggccccagt ggaaagacgc gcaggcaaaa cgcaccacgt      180
gacggagcgt gaccgcgcgc cgagcgcgcg ccaaggtcgg gcaggaagag ggcctatttc      240
ccatgattcc ttcatatttg catatacgat acaaggctgt tagagagata attagaatta      300
atttgactgt aaacacaaag atattagtac aaaatacgtg acgtagaaag taataatttc      360
ttgggtagtt tgcagtttta aaattatgtt ttaaaatgga ctatcatatg cttaccgtaa      420
cttgaaagta tttcgatttc ttggctttat atatcttgtg gaaaggacga aa              472
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[00166] In some embodiments, the H1 promoter comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 703:

```
gctcggcgcg cccatatttg catgtcgcta tgtgttctgg gaaatcacca taaacgtgaa       60
atgtctttgg atttgggaat cttataagtt ctgtatgaga ccacggta                  108
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[00167] In some embodiments, the 7SK promoter comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 704:

```
tgacggcgcg ccctgcagta tttagcatgc cccacccatc tgcaaggcat tctggatagt       60
gtcaaaacag ccggaaatca agtccgttta tctcaaactt tagcattttg ggaataaatg      120
atatttgcta tgctggttaa attagatttt agttaaattt cctgctgaag ctctagtacg      180
ataagtaact tgacctaagt gtaaagttga gatttccttc aggtttatat agcttgtgcg      240
ccgcctgggt a                                                          251
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[00168] In some embodiments, the U6 promoter is a hU6c promoter and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 705:

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAG
ATAATTGGAATTAATTTGACTGTAAACACAAAGATATTAGTACAAAATACGTGACGTAG
AAAGTAATAATTTCTTGGGTAGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCAT
ATGCTTACCGTAACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGAC
GAAACACC.

[00169] In some embodiments, the U6 promoter is a variant of the hU6c promoter. In some embodiments, the variant of the hU6c promoter comprises alternative nucleotides as compared to the sequence of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter comprises fewer nucleotides as compared to the 249 nucleotides of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter has fewer nucleotides in the nucleosome binding sequence of the hU6c promoter of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter lacks all of or at least a portion of (e.g., at least 5, 10, 15, 20, 25, or 30 nucleotides) the nucleotides corresponding to nucleotides 96-125 of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter lacks all of or at least a portion of (e.g., at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, or 60 nucleotides) the nucleotides corresponding to nucleotides 81-140 of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter lacks all of or at least a portion of (e.g., at least 10, 20, 30, 40, 50, 60, 65, 70, 75, 80, or 85 nucleotides) the nucleotides corresponding to nucleotides 66-150 of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter lacks all of or at least a portion of (e.g., at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, or 120 nucleotides) the nucleotides corresponding to nucleotides 51-170 of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter lacks the nucleotides corresponding to nucleotides 96-125 of SEQ ID NO: 705. In some embodiments, the variant of the hU6c promoter comprises 129-219 nucleotides. In

some embodiments, the variant of the hU6c promoter comprises 219 nucleotides. In some embodiments, the variant of the hU6c promoter comprises 189 nucleotides. In some embodiments, the variant of the hU6c promoter comprises 159 nucleotides. In some embodiments, the variant of the hU6c promoter comprises 129 nucleotides.

[00170] In some embodiments, the U6 promoter is hU6d30 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9001:

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAG
ATAATTGGAATTAATTTGACTGTAAACACAAAGATATAATTTCTTGGGTAGTTTGCAGTT
TTAAAATTATGTTTTAAAATGGACTATCATATGCTTACCGTAACTTGAAAGTATTTCGATT
TCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACC.

[00171] In some embodiments, the U6 promoter is hU6d60 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9002:

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAG
ATAATTGGAATTAATTTGACGTTTGCAGTTTTAAAATTATGTTTTAAAATGGACTATCATA
TGCTTACCGTAACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACG
AAACACC.

[00172] In some embodiments, the U6 promoter is hU6d90 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9003:

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCTGTTAGAGAG
ATAATATTATGTTTTAAAATGGACTATCATATGCTTACCGTAACTTGAAAGTATTTCGATT
TCTTGGCTTTATATATCTTGTGGAAAGGACGAAACACC.

[00173] In some embodiments, the U6 promoter is hU6d120 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9004:

GAGGGCCTATTTCCCATGATTCCTTCATATTTGCATATACGATACAAGGCGGACTATCAT
ATGCTTACCGTAACTTGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGAC
GAAACACC.

[00174] In some embodiments, the 7SK promoter is a 7SK2 promoter and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 706:

CTGCAGTATTTAGCATGCCCCACCCATCTGCAAGGCATTCTGGATAGTGTCAAAACAGCC
GGAAATCAAGTCCGTTTATCTCAAACTTTAGCATTTTGGGAATAAATGATATTTGCTATG
CTGGTTAAATTAGATTTTAGTTAAATTTCCTGCTGAAGCTCTAGTACGATAAGCAACTTG

ACCTAAGTGTAAAGTTGAGACTTCCTTCAGGTTTATATAGCTTGTGCGCCGCTTGGGTAC
CTC.

[00175] In some embodiments, the 7SK promoter is a variant of the 7SK2 promoter. In some embodiments, the variant of the 7SK2 promoter comprises alternative nucleotides as compared to the sequence of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter e.g., comprises fewer nucleotides as compared to the 243 nucleotides of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter has fewer nucleotides in the nucleosome binding sequence of the 7SK2 promoter of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter lacks all of or at least a portion of (e.g., at least 5, 10, 15, 20, 25, or 30 nucleotides) the nucleotides corresponding to nucleotides 95-124 of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter lacks all of or at least a portion of (e.g., at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, or 60 nucleotides) the nucleotides corresponding to nucleotides 81-140 of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter lacks all of or at least a portion of (e.g., at least 10, 20, 30, 40, 50, 60, 65, 70, 75, 80, 85 or 90 nucleotides) the nucleotides corresponding to nucleotides 67-156 of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter lacks all of or at least a portion of (e.g., at least 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, or 120 nucleotides) the nucleotides corresponding to nucleotides 52-171 of SEQ ID NO: 706. In some embodiments, the variant of the 7SK2 promoter comprises 123-213 nucleotides. In some embodiments, the variant of the 7SK2 promoter comprises 213 nucleotides. In some embodiments, the variant of the 7SK2 promoter comprises 183 nucleotides. In some embodiments, the variant of the 7SK2 promoter comprises 153 nucleotides. In some embodiments, the variant of the 7SK2 promoter comprises 123 nucleotides.

[00176] In some embodiments, the 7SK promoter is 7SKd30 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9006:

CTGCAGTATTTAGCATGCCCCACCCATCTGCAAGGCATTCTGGATAGTGTCAAAACAGCC
GGAAATCAAGTCCGTTTATCTCAAACTTTAGCATTTAAATTAGATTTTAGTTAAATTTCCT
GCTGAAGCTCTAGTACGATAAGCAACTTGACCTAAGTGTAAAGTTGAGACTTCCTTCAGG
TTTATATAGCTTGTGCGCCGCTTGGGTACCTC.

[00177] In some embodiments, the 7SK promoter is 7SKd60 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9007:

CTGCAGTATTTAGCATGCCCCACCCATCTGCAAGGCATTCTGGATAGTGTCAAAACAGCC
GGAAATCAAGTCCGTTTATCTTAAATTTCCTGCTGAAGCTCTAGTACGATAAGCAACTTG
ACCTAAGTGTAAAGTTGAGACTTCCTTCAGGTTTATATAGCTTGTGCGCCGCTTGGGTAC
CTC.

[00178] In some embodiments, the 7SK promoter is 7SKd90 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9008:

CTGCAGTATTTAGCATGCCCCACCCATCTGCAAGGCATTCTGGATAGTGTCAAAACAGCC GGAAATAGCTCTAGTACGATAAGCAACTTGACCTAAGTGTAAAGTTGAGACTTCCTTCAG GTTTATATAGCTTGTGCGCCGCTTGGGTACCTC.

[00179] In some embodiments, the 7SK promoter is 7SKd120 and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 9009:

[00180] CTGCAGTATTTAGCATGCCCCACCCATCTGCAAGGCATTCTGGATAGTGTCAG CAACTTGACCTAAGTGTAAAGTTGAGACTTCCTTCAGGTTTATATAGCTTGTGCGCCGCTT GGGTACCTC.In some embodiments, the H1 promoter is a H1m or mH1 promoter and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 707:

AATATTTGCATGTCGCTATGTGTTCTGGGAAATCACCATAAACGTGAAATGTCTTTGGAT TTGGGAATCTTATAAGTTCTGTATGAGACCACTCTTTCCC.

[00181] In some embodiments, the promoter is an M11 promoter and comprises a nucleotide sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 708:

ATATTTAGCATGTCGCTATGTGTTCTGGGAAACTTGACCTAAGTGTAAAGTTGAGATTTC CTTCAGGTTTATATAGTTCTGTATGAGACCACTCTTTCCC.

[00182] In some embodiments, the vector comprises multiple inverted terminal repeats (ITRs). These ITRs may be of an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, or AAV9 serotype. In some embodiments, the ITRs are of an AAV2 serotype. In some embodiments, the 5' ITR comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the sequence of SEQ ID NO: 709:

GGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCCG ACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTGG CCAACTCCATCACTAGGGGTTCCT.

[00183] In some embodiments, the 5' ITR comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the sequence of SEQ ID NO: 939:

CGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGGCCGGGCGACCAAAGGTCGCCC GACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAGCGAGCGCGCAGAGAGGGAGTG GCCAACTCCATCACTAGGGGTTCCT.

[00184] In some embodiments, the 3'ITR comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the sequence of SEQ ID NO: 710:

AGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGG CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAG CGAGCGCGCAGAGAGGGA.

[00185] In some embodiments, the 3' ITR comprises a sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the sequence of SEQ ID NO: 940:

AGGAACCCCTAGTGATGGAGTTGGCCACTCCCTCTCTGCGCGCTCGCTCGCTCACTGAGG CCGGGCGACCAAAGGTCGCCCGACGCCCGGGCTTTGCCCGGGCGGCCTCAGTGAGCGAG CGAGCGCGCAGAGAGGGAA.

[00186] In some embodiments, a vector comprising a single nucleic acid molecule encoding 1) two or more guide RNA comprising any one or more of the spacer sequences of **Table s 1A-1F**; and 2) a SluCas9 is provided. In some embodiments, the vector is an AAV vector. In some embodiments, the AAV vector is administered to a subject to treat DMD. In some embodiments, only one vector is needed due to the use of a particular guide sequence that is useful in the context of SaCas9 or SluCas9.

[00187] In some embodiments, the vector comprises a nucleic acid encoding a Cas9 protein (e.g., an SaCas9 or SluCas9 protein) and further comprises a nucleic acid encoding one or more single guide RNA(s). In some embodiments, the nucleic acid encoding the Cas9 (such as a SluCas9) protein is under the control of a CK8e promoter. In some embodiments, the nucleic acid encoding the guide RNA sequence is under the control of a hU6c promoter. In some embodiments, the vector is AAV9.

[00188] In some embodiments, the vector comprises multiple nucleic acids encoding more than one guide RNA. In some embodiments, the vector comprises two nucleic acids encoding two different guide RNA sequences.

[00189] In some embodiments, the vector comprises a nucleic acid encoding a Cas9 protein (such as a SluCas9), a nucleic acid encoding a first guide RNA, and a nucleic acid encoding a second guide RNA. In some embodiments, the vector does not comprise a nucleic acid encoding more than two guide RNAs. In some embodiments, the vector comprises a single nucleic acid molecule, wherein the single nucleic acid molecule comprises a nucleic acid encoding a Cas9 (such as a SluCas9) protein, a nucleic acid encoding a first guide RNA, and a nucleic acid that is the reverse complement to the coding sequence for the second guide RNA. In some embodiments, the vector comprises a single nucleic acid molecule, wherein the single nucleic acid molecule comprises a nucleic acid encoding a Cas9 (such as a SluCas9) protein, a nucleic acid that is the reverse complement to the coding sequence for the first guide RNA, and a nucleic acid that is the reverse complement to the coding sequence for the second guide RNA. In some embodiments, the nucleic acid encoding a Cas9 protein

(such as a SluCas9) is under the control of the CK8e promoter. In some embodiments, the first guide is under the control of the hU6c promoter and the second guide is under the control of the hU6c promoter. In some embodiments, the first guide is under the control of the 7SK2 promoter, and the second guide is under the control of the H1m promoter. In some embodiments, the first guide is under the control of the H1m promoter, and the second guide is under the control of the 7SK2 promoter. In some embodiments, the first guide is under the control of the hU6c promoter, and the second guide is under the control of the H1m promoter. In some embodiments, the first guide is under the control of the H1m promoter, and the second guide is under the control of the hU6c promoter. In some embodiments, the nucleic acid encoding the Cas9 protein is: a) between the nucleic acids encoding the guide RNAs, b) between the nucleic acids that are the reverse complement to the coding sequences for the guide RNAs, c) between the nucleic acid encoding the first guide RNA and the nucleic acid that is the reverse complement to the coding sequence for the second guide RNA, d) between the nucleic acid encoding the second guide RNA and the nucleic acid that is the reverse complement to the coding sequence for the first guide RNA, e) 5' to the nucleic acids encoding the guide RNAs, f) 5' to the nucleic acids that are the reverse complements to the coding sequences for the guide RNAs, g) 5' to a nucleic acid encoding one of the guide RNAs and 5' to a nucleic acid that is the reverse complement to the coding sequence for the other guide RNA, h) 3' to the nucleic acids encoding the guide RNAs, i) 3' to the nucleic acids that are the reverse complements to the coding sequences for the guide RNAs, or j) 3' to a nucleic acid encoding one of the guide RNAs and 3' to a nucleic acid that is the reverse complement to the coding sequence for the other guide RNA. In some embodiments, any of the vectors disclosed herein is AAV9. In preferred embodiments, the AAV9 vector is less than 5 kb from ITR to ITR in size, inclusive of both ITRs. In particular embodiments, the AAV9 vector is less than 4.9 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.85 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.8 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.75 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.7 kb from ITR to ITR in size, inclusive of both ITRs. In some embodiments, the vector is between 3.9-5 kb, 4-5 kb, 4.2-5 kb, 4.4-5 kb, 4.6-5 kb, 4.7-5 kb, 3.9-4.9 kb, 4.2-4.9 kb, 4.4-4.9 kb, 4.7-4.9 kb, 3.9-4.85 kb, 4.2-4.85 kb, 4.4-4.85 kb, 4.6-4.85 kb, 4.7-4.85 kb, 4.7-4.9 kb, 3.9-4.8 kb, 4.2-4.8 kb, 4.4-4.8 kb or 4.6-4.8 kb from ITR to ITR in size, inclusive of both ITRs. In some embodiments, the vector is between 4.4-4.85 kb from ITR to ITR in size, inclusive of both ITRs. In some embodiments, the vector is an AAV9 vector.

[00190] In some embodiments, any of the vectors disclosed herein comprises a nucleic acid encoding at least a first guide RNA and a second guide RNA. In some embodiments, the nucleic acid comprises a spacer-encoding sequence for the first guide RNA, a scaffold-encoding sequence for the first guide RNA, a spacer-encoding sequence for the second guide RNA, and a scaffold-encoding

sequence of the second guide RNA. In some embodiments, the scaffold-encoding sequence for the first guide RNA is identical to the scaffold-encoding sequence for the second guide RNA. In some embodiments, the scaffold-encoding sequence for the first guide RNA is different from the scaffold-encoding sequence for the nucleic acid encoding the second guide RNA. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises a sequence selected from the group consisting of SEQ ID Nos: 500-504 (for SaCas9) and 601 or 900-917 (for SluCas9), and the scaffold-encoding sequence for the second guide RNA comprises a different sequence selected from the group consisting of SEQ ID Nos: 500-504 (for SaCas9) and 601 or 900-917 (for SluCas9). In particular embodiments, the scaffold-encoding sequence for the first guide RNA comprises a sequence comprising the sequence of SEQ ID NO: 901. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 901. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 500, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 501. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 500, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 502. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 500, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 503. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 500, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 504. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 501, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 502. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 501, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 503. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 501, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 504. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 502, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 503. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 502, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 504. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 503, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 504. In particular embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 504, and the scaffold-encoding sequence for the second

guide RNA comprises the sequence of SEQ ID NO: 504. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 900. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 901. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 902. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 903. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 904. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 905. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 906. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 907. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 908. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 909. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 910. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 911. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 912. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 913. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 914. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ

ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 915. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 916. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 600, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 917. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 902. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 903. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 904. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 905. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 906. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 907. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 908. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 909. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 910. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 911. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 912. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 913. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 914. In some embodiments, the scaffold-encoding sequence for the first guide RNA

comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 915. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 916. In some embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 917. In particular embodiments, the scaffold-encoding sequence for the first guide RNA comprises the sequence of SEQ ID NO: 901, and the scaffold-encoding sequence for the second guide RNA comprises the sequence of SEQ ID NO: 901. In some embodiments, the spacer encoding sequence for the first guide RNA is the same as the spacer-encoding sequence in the second guide RNA, and the scaffold-encoding sequence for the first guide RNA is different from the scaffold-encoding sequence in the nucleic acid encoding the second guide RNA.

[00191] In some embodiments, the AAV vector is in a particular configuration. Some examples of these AAV vector configurations are provided herein, and the order of elements in these exemplary vectors are referenced in a 5' to 3' manner with respect to the plus strand. For these configurations, it should be understood that the recited elements may not be directly contiguous, and that one or more nucleotides or one or more additional elements may be present between the recited elements. However, in some embodiments, it is possible that no nucleotides or no additional elements are present between the recited elements. Also, unless otherwise stated, "a promoter for expression of element X" means that the promoter is oriented in a manner to facilitate expression of the recited element X. In addition, unless otherwise stated, references to an "sgRNA scaffold sequence" or "a guide RNA scaffold sequence" are synonymous with "a nucleotide sequence/nucleic acid encoding an sgRNA scaffold sequence" or "a nucleotide sequence/nucleic acid encoding a guide RNA scaffold sequence." In some embodiments, the disclosure provides for a nucleic acid encoding an SaCas9 (e.g., an SaCas9-KKH) or SluCas9. In some embodiments, the nucleic acid encodes for one or more nuclear localization signals (e.g., the SV40 NLS and/or the c-Myc NLS) on the C-terminus of the encoded SaCas9 or SluCas9. In some embodiments, the nucleic acid encodes for one or more NLSs (e.g., the SV40 NLS and/or the c-Myc NLS) on the C-terminus of the encoded SaCas9 or SluCas9, and the nucleic acid does not encode for an NLS on the N-terminus of the encoded SaCas9 or SluCas9. In some embodiments, the nucleic acid encodes for one or more nuclear localization signals (e.g., the SV40 NLS and/or the c-Myc NLS) on the N-terminus of the encoded SaCas9 or SluCas9. In some embodiments, the nucleic acid encodes for one or more NLSs (e.g., the SV40 NLS and/or the c-Myc NLS) on the N-terminus of the encoded SaCas9 or SluCas9, and the nucleic acid does not encode for an NLS on the C-terminus of the encoded SaCas9 or SluCas9. In some embodiments, the nucleic acid encodes for one or more nuclear localization signals (e.g., the SV40 NLS and/or the c-Myc NLS) on the C-terminus of the encoded SaCas9 or SluCas9 and also encodes for one or more NLSs on the N-terminus of the encoded SaCas9 or SluCas9 (e.g., the SV40 NLS and/or the c-Myc

NLS). In some embodiments, the nucleic acid encodes one NLS. In some embodiments, the nucleic acid encodes two NLSs. In some embodiments, the nucleic acid encodes three NLSs. The one, two, or three NLS may all be C-terminal, N-terminal, or any combination of C- and N-terminal. The NLS may be fused/attached directly to the C- or N-terminus or to another NLS, or may be fused/attached indirectly attached through a linker. In some embodiments, an additional domain may be: a) fused to the N- or C-terminus of the Cas protein (e.g., a Cas9 protein), b) fused to the N-terminus of an NLS fused to the N-terminus of a Cas protein, or c) fused to the C-terminus of an NLS fused to the C-terminus of a Cas protein, with or without a linker. In some embodiments, an NLS is fused to the N- and/or C-terminus of the Cas protein by means of a linker. In some embodiments, an NLS is fused to the N-terminus of an N-terminally-fused NLS on a Cas protein by means of a linker, and/or an NLS is fused to the C-terminus of a C-terminally fused NLS on a Cas protein by means of a linker. In some embodiments, the linker is GSVD (SEQ ID NO: 550) or GSGS (SEQ ID NO: 551). In some embodiments, the Cas protein comprises a c-Myc NLS fused to the N-terminus of the Cas protein (or to an N-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises an SV40 NLS fused to the C-terminus of the Cas protein (or to a C-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises a nucleoplasmin NLS fused to the C-terminus of the Cas protein (or to a C-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises: a) a c-Myc NLS fused to the N-terminus of the Cas protein, optionally by means of a linker, b) an SV40 NLS fused to the C-terminus of the Cas protein, optionally by means of a linker, and c) a nucleoplasmin NLS fused to the C-terminus of the SV40 NLS, optionally by means of a linker. In some embodiments, the Cas protein comprises: a) a c-Myc NLS fused to the N-terminus of the Cas protein, optionally by means of a linker, b) a nucleoplasmin NLS fused to the C-terminus of the Cas protein, optionally by means of a linker, and c) an SV40 NLS fused to the C-terminus of the nucleoplasmin NLS, optionally by means of a linker. In some embodiments, a c-myc NLS is fused to the N-terminus of the Cas and an SV40 NLS and/or nucleoplasmin NLS is fused to the C-terminus of the Cas. In some embodiments, a c-myc NLS is fused to the N-terminus of the Cas (e.g., by means of a linker such as GSVD), an SV40 NLS is fused to the C-terminus of the Cas (e.g., by means of a linker such as GSGS), and a nucleoplasmin NLS is fused to the C-terminus of the SV-40 NLS (e.g., by means of a linker such as GSGS).

[00192] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of a promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding SaCas9 (e.g., CK8e), a nucleic acid encoding SaCas9, a polyadenylation sequence, a promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA

scaffold sequence. In some embodiments, the first sgRNA is associated with weaker expression than the second sgRNA when compared individually in a sgRNA expression assay, e.g., in an assay in which each guide is separately assessed (i.e., not in the same construct) using the same promoter, same concentration of genetic material/vector/RNP in substantially the same conditions (e.g., time, pH, temperature, buffer conditions). In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA is any of the hU6c promoters disclosed herein. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 705. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9001. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9002. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9003. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9004. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA is any of the 7SK2 promoters disclosed herein. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 705. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9006. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9007. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9008. In some embodiments the promoter for expression of the nucleic acid encoding the first sgRNA comprises SEQ ID NO: 9009. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA is any of the hU6c promoters disclosed herein. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 705. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9001. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9002. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9003. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9004. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA is any of the 7SK2 promoters disclosed herein. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 705. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9006. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9007. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9008. In some embodiments

the promoter for expression of the nucleic acid encoding the second sgRNA comprises SEQ ID NO: 9009. In some embodiments the promoter for expression of the nucleic acid encoding the second sgRNA is any of the H1m promoters disclosed herein. In some embodiments, the promoter for SaCas9 is the CK8e promoter. In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to a nucleic acid sequence encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to two nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to three nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the one or more NLSs is an SV40 NLS. In some embodiments, the one or more NLSs is a c-Myc NLS. In some embodiments, the one or more NLSs is a nucleoplasmin NLS. In some embodiments, the NLS is fused to the SaCas9 with a linker.

[00193] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of an hU6c promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding SaCas9 (e.g., CK8e), a nucleic acid encoding SaCas9, a polyadenylation sequence, an hU6c promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence. In some embodiments, the first sgRNA and the second sgRNA are selected from **Tables 1A-1F**. In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to a nucleic acid sequence encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to two nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to three nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the one or more NLSs is an SV40 NLS. In some embodiments, the one or more NLSs is a c-Myc NLS. In some embodiments, the NLS is fused to the SaCas9 with a linker.

[00194] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of an hU6c promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding SaCas9 (e.g., CK8e), a nucleic acid encoding SaCas9, a polyadenylation sequence, an 7SK promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence. In some embodiments, the first sgRNA and the second sgRNA are selected from **Tables 1A-1F**. In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to a nucleic acid sequence encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding SaCas9 is fused to two nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding

SaCas9 is fused to three nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the one or more NLSs is an SV40 NLS. In some embodiments, the one or more NLSs is a c-Myc NLS. In some embodiments, the NLS is fused to the SaCas9 with a linker.

[00195] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of an hU6c promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding Cas9 (e.g., CK8e), a nucleic acid encoding Cas9, a polyadenylation sequence, an H1m promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence. In some embodiments, the first sgRNA and the second sgRNA are selected from **Tables 1A and 1F**. In some embodiments, the nucleic acid sequence encoding Cas9 is fused to a nucleic acid sequence encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding Cas9 is fused to two nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding Cas9 is fused to three nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the one or more NLSs is an SV40 NLS. In some embodiments, the one or more NLSs is a c-Myc NLS. In some embodiments, the NLS is fused to the Cas9 with a linker.

[00196] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of an 7SK promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding Cas9 (e.g., CK8e), a nucleic acid encoding Cas9, a polyadenylation sequence, an H1m promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence. In some embodiments, the first sgRNA and the second sgRNA are selected from **Tables 1A-1F**. In some embodiments, the nucleic acid sequence encoding Cas9 is fused to a nucleic acid sequence encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding Cas9 is fused to two nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the nucleic acid sequence encoding Cas9 is fused to three nucleic acid sequences each encoding a nuclear localization sequence (NLS). In some embodiments, the one or more NLSs is an SV40 NLS. In some embodiments, the one or more NLSs is a c-Myc NLS. In some embodiments, the NLS is fused to the Cas9 with a linker.

[00197] In some embodiments, the disclosure provides for a composition comprising at least two nucleic acids. In some embodiments, the composition comprises at least two nucleic acid molecules, wherein the first nucleic acid molecule comprises a sequence encoding an endonuclease (such as a SluCas9) wherein the second nucleic acid molecule encodes a first guide RNA and a second guide RNA, wherein the first guide RNA and the second guide RNA are not the same sequence, and wherein the second nucleic acid molecule does not encode an endonuclease. In some embodiments,

the first nucleic acid molecule also encodes a copy of the first guide RNA and a copy of the second guide RNA. In some embodiments, the first nucleic acid molecule does not encode any guide RNAs. In some embodiments, the second nucleic acid molecule encodes two copies of the first guide RNA and two copies of the second guide RNA. In some embodiments, the second nucleic molecule encodes two copies of the first guide RNA, and one copy of the second guide RNA. In some embodiments, the second nucleic acid molecule encodes one copy of the first guide RNA, and two copies of the second guide RNA. In some embodiments, the second nucleic acid molecule comprises two copies of the first guide RNA, and three copies of the second guide RNA. In some embodiments, the second nucleic acid molecule comprises three copies of the first guide RNA, and two copies of the second guide RNA. In some embodiments, the second nucleic acid does not encode a Cas protein. In some embodiments, the second nucleic acid molecule encodes three copies of the first guide RNA and three copies of the second guide RNA. In some embodiments, the first nucleic acid molecule comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first guide RNA scaffold sequence, the reverse complement of a nucleotide sequence encoding the first guide RNA sequence, the reverse complement of a promoter for expression of the nucleotide sequence encoding the first guide RNA sequence, a promoter for expression of a nucleotide sequence encoding the endonuclease, a nucleotide sequence encoding an endonuclease, a polyadenylation sequence, a promoter for expression of the second guide RNA in the same direction as the promoter for the endonuclease, the second guide RNA sequence, and a second guide RNA scaffold sequence. In some embodiments, the promoter for expression of the nucleotide sequence encoding the first guide RNA sequence in the first nucleic acid molecule is a U6 promoter and the promoter for expression of the nucleotide sequence encoding the second guide RNA in the first nucleic acid molecule is a U6 promoter.

[00198] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: a promoter for expression of a nucleic acid encoding a first sgRNA, a nucleic acid encoding the first sgRNA guide sequence, the first sgRNA scaffold sequence, a promoter for expression of Cas9 (e.g., CK8e), a nucleic acid encoding Cas9 (such as SluCas9), a polyadenylation sequence, a promoter for expression of a second sgRNA, the second sgRNA guide sequence, and a second sgRNA scaffold sequence.

[00199] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first sgRNA scaffold sequence, the reverse complement of a nucleic acid encoding a first sgRNA guide sequence, the reverse complement of a promoter for expression of the nucleic acid encoding the first sgRNA, a promoter for expression of a nucleic acid encoding Cas9 (e.g., CK8e), a nucleic acid encoding Cas9 (such as SluCas9), a polyadenylation sequence, a promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence.

[00200] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: a promoter for expression of a nucleic acid encoding a first sgRNA, a nucleic acid encoding the first sgRNA guide sequence, a first sgRNA scaffold sequence, a promoter for expression of a second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence, a promoter for Cas9 (e.g., CK8e), a nucleic acid encoding Cas9 (such as SluCas9), and a polyadenylation sequence.

[00201] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: a promoter for expression of a nucleic acid encoding Cas9 (e.g., CK8e), a nucleic acid encoding Cas9 (such as SluCas9), a polyadenylation sequence, a promoter for expression of the nucleic acid encoding a first guide RNA, a nucleic acid encoding the first sgRNA guide sequence, a first sgRNA scaffold sequence, a promoter for expression of the second sgRNA, a second sgRNA guide sequence, and a second sgRNA scaffold sequence.

[00202] In some embodiments, the AAV vector comprises from 5' to 3' with respect to the plus strand: a first sgRNA scaffold sequence (e.g., V5), a nucleic acid encoding a first sgRNA guide sequence (e.g., Slu3 or Slu7), a promoter (e.g., U6) for expression of the nucleic acid encoding the first sgRNA guide sequence, a promoter (e.g., CK8e) for expression (in the opposite direction of expression of the nucleic acid encoding the first sgRNA guide sequence) of a nucleic acid encoding a SluCas9, a nucleic acid encoding a first NLS, a nucleic acid encoding a SluCas9, a nucleic acid encoding a second NLS, a nucleic acid encoding a third NLS, a promoter (e.g., U6) for expression (in the same direction as expression of the nucleic acid encoding the SluCas9) of a second sgRNA guide sequence (e.g., Slu 7 or Slu 3), a nucleic acid encoding the second sgRNA guide sequence, and a second sgRNA scaffold sequence (e.g., V5).

[00203] In a particular embodiment, the AAV vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a first scaffold sequence (such as the scaffold sequence of SEQ ID NO: 901), the reverse complement of a nucleic acid encoding a guide RNA sequence selected from SEQ ID NOs: 1-143, the reverse complement of a U6 promoter for expression of the nucleic acid encoding the guide RNA sequence, a CK8e promoter for expression (in the opposite direction of expression of the nucleic acid encoding the sgRNA guide sequence) of a nucleic acid encoding a SluCas9, a nucleic acid encoding a c-Myc NLS, a nucleic acid encoding a SluCas9, a nucleic acid encoding a SV40 NLS, a nucleic acid encoding a NP NLS, a U6 promoter for expression (in the same direction as expression of the nucleic acid encoding the SluCas9) of a guide RNA sequence of any one of SEQ ID NOs: 1-143, a nucleic acid encoding the guide RNA sequence, and a second V5 scaffold sequence (such as the scaffold sequence of SEQ ID NO: 901).

[00204] In some embodiments, the first nucleic acid molecule is in a first vector (e.g., AAV9), and the second nucleic acid is in a separate second vector. In some embodiments, the first vector is AAV9. In some embodiments, the second vector is AAV9. In preferred embodiments, the AAV9 vector is less than 5 kb from ITR to ITR in size, inclusive of both ITRs. In particular embodiments,

the AAV9 vector is less than 4.9 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.85 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.8 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.75 kb from ITR to ITR in size, inclusive of both ITRs. In further embodiments, the AAV9 vector is less than 4.7 kb from ITR to ITR in size, inclusive of both ITRs. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: a promoter for expression of a first copy of a first guide RNA (e.g., a U6 promoter), a first copy of a nucleotide sequence encoding a first guide RNA, a first copy of a nucleotide sequence encoding a first guide RNA scaffold, a promoter for expression of a second copy of the first guide RNA (e.g., a H1 promoter), a second copy of the nucleotide sequence encoding the first guide RNA, a second copy of the nucleotide sequence encoding the first guide RNA scaffold, a promoter for expression of a second guide RNA (e.g., a 7SK promoter), a nucleotide sequence encoding a second guide RNA, and a nucleotide sequence encoding a second guide RNA scaffold. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: a promoter for expression of a first guide RNA (e.g., a U6 promoter), a nucleotide sequence encoding a first guide RNA, a nucleotide sequence encoding a first guide RNA scaffold, a promoter for expression of a second guide RNA (e.g., a 7SK promoter), a nucleotide sequence encoding a second guide RNA, and a nucleotide sequence encoding a second guide RNA scaffold. In some embodiments, the second vector comprises a stuffer sequence (e.g., a 3'UTR desmin sequence) between the nucleotide sequence encoding the first guide scaffold sequence and the promoter for expression of the second guide sequence. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a nucleotide sequence encoding a scaffold for a first guide RNA, the reverse complement of a nucleotide sequence encoding a first guide RNA, the reverse complement of a promoter for expression of the first guide RNA (e.g., a U6c promoter), a promoter for expression of a second guide RNA (e.g., a U6c promoter), a nucleotide sequence encoding a second guide RNA, and a nucleotide sequence encoding a second guide RNA scaffold. In some embodiments, the second vector comprises a stuffer sequence (e.g., a 3'UTR desmin sequence) between the reverse complement of the promoter for expression of the first guide RNA and the promoter for expression of the second guide RNA. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a nucleotide sequence encoding a first copy of a first guide RNA scaffold, the reverse complement of a nucleotide sequence encoding a first copy of the first guide RNA, the reverse complement of a promoter for expression of the first copy of the first guide RNA (e.g., a 7SK2 promoter), the reverse complement of a second copy of the nucleotide sequence encoding the first guide RNA scaffold, the reverse complement of a second copy of the nucleotide sequence encoding the first guide RNA, the reverse complement of a promoter for expression of the second copy of the nucleotide sequence encoding the first guide RNA (e.g., a hU6c promoter), a promoter for expression of a first copy of a second guide

RNA (e.g., a hU6c promoter), a first copy of a nucleotide sequence encoding a second guide RNA, a first copy of a nucleotide sequence encoding a second guide RNA scaffold, a promoter for expression of a second copy of the second guide RNA (e.g., a 7Sk2 promoter), a second copy of the nucleotide sequence encoding the second guide RNA, and a second copy of the nucleotide sequence encoding the second guide RNA scaffold. In some embodiments, the second vector comprises a stuffer sequence (e.g., a 3'UTR desmin sequence) between the reverse complement of the promoter for expression of the second copy of the first guide RNA and the promoter for expression of the first copy of the second guide RNA. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a nucleotide sequence encoding a first copy of a first guide RNA scaffold, the reverse complement of a first copy of a nucleotide sequence encoding the first guide RNA, the reverse complement of a promoter for expression of the first copy of the first guide RNA (e.g., a 7SK2 promoter), the reverse complement of a first copy of a nucleotide sequence encoding a second guide RNA scaffold, the reverse complement of a nucleotide sequence encoding the first copy of the second guide RNA, the reverse complement of a promoter for expression of the first copy of the second guide RNA (e.g., a hU6c promoter), a promoter for expression of a second copy of the second guide RNA (e.g., a hU6c promoter), a second copy of the nucleotide sequence encoding the second guide RNA, a second copy of the nucleotide sequence encoding the second guide RNA scaffold, a promoter for expression of a second copy of the first guide RNA (e.g., a 7SK2 promoter), a second copy of the nucleotide sequence encoding the first guide RNA, and a second copy of the nucleotide sequence encoding the first guide RNA scaffold. In some embodiments, the second vector comprises a stuffer sequence (e.g., a 3'UTR desmin sequence) between the reverse complement of the promoter for expression of the first copy of the second guide RNA and the promoter for expression of the second copy of the first guide RNA. In some embodiments, the second vector comprises from 5' to 3' with respect to the plus strand: the reverse complement of a nucleotide sequence encoding a first guide RNA scaffold, the reverse complement of a nucleotide sequence encoding a first guide RNA, the reverse complement of a promoter for expression of a first guide RNA (e.g., a hU6c promoter), a promoter for expression of a second guide RNA (e.g., a hU6c promoter), a nucleotide sequence encoding a second guide RNA, and a nucleotide sequence encoding a second guide RNA scaffold. In some embodiments, the second vector comprises a stuffer sequence (e.g., a 3'UTR desmin sequence) between the reverse complement of the promoter for expression of the first guide RNA and the promoter for expression of the second guide RNA. In particular embodiments, the first guide RNA is different from the second guide RNA. In some embodiments, the first guide RNA comprises a sequence of **Tables 1A-1C** and the second guide RNA comprises a different sequence from **Tables 1A-1C**. In some embodiments, the first guide RNA comprises a sequence of **Table 1A** and the second guide RNA comprises a sequence from **Table 1C**. In some embodiments, the first guide RNA comprises a sequence of **Table 1A** and the second guide RNA

comprises a sequence from **Table 1B**. In some embodiments, the first guide RNA comprises a sequence of **Table 1B** and the second guide RNA comprises a sequence from **Table 1C**.

[00205] In some embodiments, if the composition comprises one or more nucleic acids encoding an RNA-targeted endonuclease and one or more guide RNAs, the one or more nucleic acids are designed such that they express the one or more guide RNAs at an equivalent or higher level (e.g., a greater number of expressed transgene copies) as compared to the expression level of the RNA-targeted endonuclease. In some embodiments, the one or more nucleic acids are designed such that they express (e.g., on average in 100 cells) the one or more guide RNAs at least a 1.1, 1.2, 1.3, 1.4, or 1.5 times higher level (e.g., a greater number of expressed transgene copies) as compared to the expression level of the RNA-targeted endonuclease. In some embodiments, the one or more nucleic acids are designed such that they express the one or more guide RNAs at 1.01-1.5, 1.01-1.4, 1.01-1.3, 1.01-1.2, 1.01-1.1, 1.1-2.0, 1.1-1.8, 1.1-1.6, 1.1-1.4, 1.1-1.3, 1.2-2.0, 1.2-1.8, 1.2-1.6, 1.2-1.4, 1.4-2.0, 1.4-1.8, 1.4-1.6, 1.6-2.0, 1.6-1.8, or 1.8-2.0 times higher level (e.g., a greater number of expressed transgene copies) as compared to the expression level of the RNA-targeted endonuclease. In some embodiments, the one or more guide RNAs are designed to express a higher level than the RNA-targeted endonuclease by: a) utilizing one or more regulatory elements (e.g., promoters or enhancers) that express the one or more guide RNAs at a higher level as compared to the regulatory elements (e.g., promoters or enhancers) for expression of the RNA-targeted endonuclease; and/or b) expressing more copies of one or more of the guide RNAs as compared to the number of copies of the RNA-targeted endonuclease (e.g., 2x or 3x as many copies of the nucleotide sequences encoding the one or more guide RNAs as compared to the number of copies of the nucleotide sequences encoding the RNA-targeted endonuclease). For example, in some embodiments, the composition comprises multiple nucleic acid molecules (e.g., in multiple vectors), wherein for every nucleotide sequence encoding an RNA-targeted endonuclease in the nucleic acid molecules in the composition, there are two or three copies of the nucleotide sequence encoding the guide RNA in the nucleic acid molecules in the composition. In some embodiments, the composition comprises a first guide RNA and a second guide RNA, wherein the first guide RNA and the second guide RNA are not the same (e.g., any of the guide RNA pairs disclosed herein), and for every nucleotide sequence encoding an RNA-targeted endonuclease in the nucleic acid molecules in the composition, there are two or three copies of the nucleotide sequence encoding the first guide RNA and/or the second guide RNA.

Endonucleases

[00206] In some embodiments, any of the nucleic acids disclosed herein encodes an RNA-targeted endonuclease. In some embodiments, the RNA-targeted endonuclease has cleavase activity, which can also be referred to as double-strand endonuclease activity. In some embodiments, the RNA-targeted endonuclease comprises a Cas nuclease. Examples of Cas9 nucleases include those of the type II CRISPR systems.

[00207] In some embodiments, the Cas protein comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 941 (designated herein as SpCas9):

MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEAT
RLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDE
VAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQL
VQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNF
KSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKA
PLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKP
ILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEK
ILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNE
KVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKE
DYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDRE
MIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRN
FMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRH
KPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQ
NGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKK
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRM
NTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKY
PKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIET
NGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDW
DPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE
VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPED
NEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTL
TNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD.

[00208] In some embodiments, the nucleic acid encoding SaCas9 encodes an SaCas9 comprising an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 711:

KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRI
QRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEE
DTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK
AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYA
YNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGY
RVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEE
IEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDD
FILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIR
TTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVL

VKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQ
KDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYK
HHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHI
KDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSP
EKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGN
KLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKC
YEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMN
DKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG.

[00209] In some embodiments, the nucleic acid encoding SaCas9 comprises the nucleic acid of SEQ ID NO: 9014:

[00210] AAGCGCAATTACATCCTGGGCCTGGATATCGGCATCACCTCCGTGGGCTACG
GCATCATCGACTATGAGACACGGGATGTGATCGACGCCGGCGTGAGACTGTTCAAGGAG
GCCAACGTGGAGAACAATGAGGGCCGGCGGAGCAAGAGGGGAGCAAGGCGCCTGAAGC
GGAGAAGGCGCCACAGAATCCAGAGAGTGAAGAAGCTGCTGTTCGATTACAACCTGCTG
ACCGACCACTCCGAGCTGTCTGGCATCAATCCTTATGAGGCCCGGGTGAAGGGCCTGTCC
CAGAAGCTGTCTGAGGAGGAGTTTTCTGCCGCCCTGCTGCACCTGGCAAAGAGGAGAGG
CGTGCACAACGTGAATGAGGTGGAGGAGGACACCGGCAACGAGCTGAGCACAAAGGAG
CAGATCAGCCGCAATTCCAAGGCCCTGGAGGAGAAGTATGTGGCCGAGCTGCAGCTGGA
GCGGCTGAAGAAGGATGGCGAGGTGAGGGGCTCCATCAATCGCTTCAAGACCTCTGACT
ACGTGAAGGAGGCCAAGCAGCTGCTGAAGGTGCAGAAGGCCTACCACCAGCTGGATCAG
AGCTTTATCGATACATATATCGACCTGCTGGAGACCAGGCGCACATACTATGAGGGACC
AGGAGAGGGCTCCCCCTTCGGCTGGAAGGACATCAAGGAGTGGTACGAGATGCTGATGG
GCCACTGCACCTATTTTCCAGAGGAGCTGAGATCCGTGAAGTACGCCTATAACGCCGATC
TGTACAACGCCCTGAATGACCTGAACAACCTGGTCATCACCAGGGATGAGAACGAGAAG
CTGGAGTACTATGAGAAGTTCCAGATCATCGAGAACGTGTTCAAGCAGAAGAAGAAGCC
TACACTGAAGCAGATCGCCAAGGAGATCCTGGTGAACGAGGAGGACATCAAGGGCTACC
GCGTGACCAGCACAGGCAAGCCAGAGTTCACCAATCTGAAGGTGTATCACGATATCAAG
GACATCACAGCCCGGAAGGAGATCATCGAGAACGCCGAGCTGCTGGATCAGATCGCCAA
GATCCTGACCATCTATCAGAGCTCCGAGGACATCCAGGAGGAGCTGACCAACCTGAATA
GCGAGCTGACACAGGAGGAGATCGAGCAGATCAGCAATCTGAAGGGCTACACCGGCAC
ACACAACCTGTCCCTGAAGGCCATCAATCTGATCCTGGATGAGCTGTGGCACACAAACG
ACAATCAGATCGCCATCTTTAACAGGCTGAAGCTGGTGCCAAAGAAGGTGGACCTGAGC
CAGCAGAAGGAGATCCCAACCACACTGGTGGACGATTTCATCCTGTCCCCCGTGGTGAA
GCGGAGCTTCATCCAGAGCATCAAAGTGATCAACGCCATCATCAAGAAGTACGGCCTGC
CCAATGATATCATCATCGAGCTGGCCAGGGAGAAGAACTCTAAGGACGCCCAGAAGATG
ATCAATGAGATGCAGAAGAGGAACCGCCAGACCAATGAGCGGATCGAGGAGATCATCA
GAACCACAGGCAAGGAGAACGCCAAGTACCTGATCGAGAAGATCAAGCTGCACGATAT

GCAGGAGGGCAAGTGTCTGTATAGCCTGGAGGCCATCCCTCTGGAGGACCTGCTGAACA
ATCCATTCAACTACGAGGTGGATCACATCATCCCCCGGAGCGTGAGCTTCGACAATTCCT
TTAACAATAAGGTGCTGGTGAAGCAGGAGGAGAACTCTAAGAAGGGCAATAGGACCCCT
TTCCAGTACCTGTCTAGCTCCGATTCTAAGATCAGCTACGAGACCTTCAAGAAGCACATC
CTGAATCTGGCCAAGGGCAAGGGCCGCATCTCTAAGACCAAGAAGGAGTACCTGCTGGA
GGAGCGGGACATCAACAGATTCAGCGTGCAGAAGGACTTCATCAACCGGAATCTGGTGG
ACACCAGATACGCCACACGCGGCCTGATGAATCTGCTGCGGTCCTATTTCAGAGTGAACA
ATCTGGATGTGAAGGTGAAGAGCATCAACGGCGGCTTCACCTCCTTTCTGCGGAGAAAG
TGGAAGTTTAAGAAGGAGAGAAACAAGGGCTATAAGCACCACGCCGAGGATGCCCTGAT
CATCGCCAATGCCGACTTCATCTTTAAGGAGTGGAAGAAGCTGGACAAGGCCAAGAAAG
TGATGGAGAACCAGATGTTCGAGGAGAAGCAGGCCGAGAGCATGCCCGAGATCGAGAC
CGAGCAGGAGTACAAGGAGATTTTCATCACACCTCACCAGATCAAGCACATCAAGGACT
TCAAGGACTACAAGTATTCCCACAGGGTGGATAAGAAGCCCAACCGCGAGCTGATCAAT
GACACCCTGTATTCTACAAGGAAGGACGATAAGGGCAATACCCTGATCGTGAACAATCT
GAACGGCCTGTACGACAAGGATAATGACAAGCTGAAGAAGCTGATCAACAAGAGCCCC
GAGAAGCTGCTGATGTACCACCACGATCCTCAGACATATCAGAAGCTGAAGCTGATCAT
GGAGCAGTACGGCGACGAGAAGAACCCACTGTATAAGTACTATGAGGAGACCGGCAACT
ACCTGACAAAGTATTCCAAGAAGGATAATGGCCCCGTGATCAAGAAGATCAAGTACTAT
GGCAACAAGCTGAATGCCCACCTGGACATCACCGACGATTACCCCAACAGCCGGAATAA
GGTGGTGAAGCTGAGCCTGAAGCCATACAGGTTCGACGTGTACCTGGACAACGGCGTGT
ATAAGTTTGTGACAGTGAAGAATCTGGATGTGATCAAGAAGGAGAACTACTATGAAGTG
AATAGCAAGTGCTACGAGGAGGCCAAGAAGCTGAAGAAGATCAGCAACCAGGCCGAGT
TCATCGCCTCTTTTTACAACAATGACCTGATCAAGATCAATGGCGAGCTGTATAGAGTGA
TCGGCGTGAACAATGATCTGCTGAACCGCATCGAAGTGAATATGATCGACATCACCTACC
GGGAGTATCTGGAGAACATGAATGATAAGAGGCCCCCTCGCATCATCAAGACCATCGCC
TCTAAGACACAGAGCATCAAGAAGTACTCTACAGACATCCTGGGCAACCTGTATGAGGT
GAAGAGCAAGAAGCACCCTCAGATCATCAAGAAGGGC.In some embodiments comprising a nucleic acid encoding SaCas9, the SaCas9 comprises an amino acid sequence of SEQ ID NO: 711.

[00211] In some embodiments, the SaCas9 is a variant of the amino acid sequence of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an E at the position corresponding to position 781 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an N at the position corresponding to position 967 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an R at the position corresponding to position 1014 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises a K at the position corresponding to position 781 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises a K at the position corresponding to position 967 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an H at the position corresponding to position 1014 of SEQ ID

NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an E at the position corresponding to position 781 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 967 of SEQ ID NO: 711; and an amino acid other than an R at the position corresponding to position 1014 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises a K at the position corresponding to position 781 of SEQ ID NO: 711; a K at the position corresponding to position 967 of SEQ ID NO: 711; and an H at the position corresponding to position 1014 of SEQ ID NO: 711.

[00212] In some embodiments, the SaCas9 comprises an amino acid other than an R at the position corresponding to position 244 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an N at the position corresponding to position 412 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an N at the position corresponding to position 418 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an R at the position corresponding to position 653 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an amino acid other than an R at the position corresponding to position 244 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 412 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 418 of SEQ ID NO: 711; and an amino acid other than an R at the position corresponding to position 653 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 244 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 412 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 418 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 653 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 244 of SEQ ID NO: 711; an A at the position corresponding to position 412 of SEQ ID NO: 711; an A at the position corresponding to position 418 of SEQ ID NO: 711; and an A at the position corresponding to position 653 of SEQ ID NO: 711.

[00213] In some embodiments, the SaCas9 comprises an amino acid other than an R at the position corresponding to position 244 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 412 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 418 of SEQ ID NO: 711; an amino acid other than an R at the position corresponding to position 653 of SEQ ID NO: 711; an amino acid other than an E at the position corresponding to position 781 of SEQ ID NO: 711; an amino acid other than an N at the position corresponding to position 967 of SEQ ID NO: 711; and an amino acid other than an R at the position corresponding to position 1014 of SEQ ID NO: 711. In some embodiments, the SaCas9 comprises an A at the position corresponding to position 244 of SEQ ID NO: 711; an A at the position corresponding to position 412 of SEQ ID NO: 711; an A at the position corresponding to position 418 of SEQ ID NO: 711; an A at the position corresponding to position 653 of SEQ ID NO: 711; a K at

the position corresponding to position 781 of SEQ ID NO: 711; a K at the position corresponding to position 967 of SEQ ID NO: 711; and an H at the position corresponding to position 1014 of SEQ ID NO: 711.

[00214] In some embodiments, the SaCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 715 (designated herein as SaCas9-KKH or SACAS9KKH):

KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRI
QRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEE
DTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK
AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYA
YNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGY
RVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEE
IEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKVDLSQQKEIPTTLVDD
FILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIR
TTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVL
VKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQ
KDFINRNLVDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYK
HHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHI
KDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSP
EKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGN
KLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKC
YEEAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMN
DKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG.

[00215] In some embodiments, the SaCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 716 (designated herein as SaCas9-HF):

KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRI
QRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEE
DTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK
AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELASVKYA
YNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGY
RVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEE
IEQISNLKGYTGTHNLSLKAINLILDELWHTNDAQIAIFARLKLVPKKVDLSQQKEIPTTLVDD
FILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIR
TTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVL
VKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQ
KDFINRNLVDTRYATAGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYK

HHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHI
KDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSP
EKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGN
KLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKC
YEEAKKLKKISNQAEFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMN
DKRPPRIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG.

[00216] In some embodiments, the SaCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 717 (designated herein as SaCas9-KKH-HF):

KRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGARRLKRRRRHRI
QRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSAALLHLAKRRGVHNVNEVEE
DTGNELSTKEQISRNSKALEEKYVAELQLERLKKDGEVRGSINRFKTSDYVKEAKQLLKVQK
AYHQLDQSFIDTYIDLLETRRTYYEGPGEGSPFGWKDIKEWYEMLMGHCTYFPEELASVKYA
YNADLYNALNDLNNLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGY
RVTSTGKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSELTQEE
IEQISNLKGYTGTHNLSLKAINLILDELWHTNDAQIAIFARLKLVPKKVDLSQQKEIPTTLVDD
FILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSKDAQKMINEMQKRNRQTNERIEEIIR
TTGKENAKYLIEKIKLHDMQEGKCLYSLEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVL
VKQEENSKKGNRTPFQYLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQ
KDFINRNLVDTRYATAGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKGYK
HHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQEYKEIFITPHQIKHI
KDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIVNNLNGLYDKDNDKLKKLINKSP
EKLLMYHHDPQTYQKLKLIMEQYGDEKNPLYKYYEETGNYLTKYSKKDNGPVIKKIKYYGN
KLNAHLDITDDYPNSRNKVVKLSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKC
YEEAKKLKKISNQAEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMN
DKRPPHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG.

[00217] In some embodiments, the nucleic acid encoding SluCas9 encodes a SluCas9 comprising an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 712:

NQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLE
RVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDD
VGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFH
QLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKYAY
SADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRI
TKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDK
ENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEF
ILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIG

KYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKV
LVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE
VQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNH
GYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQVQ
DIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPE
KFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNK
LGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDK
LKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEP
RIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00218] In some embodiments, the SluCas9 is a variant of the amino acid sequence of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an Q at the position corresponding to position 781 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an R at the position corresponding to position 1013 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises a K at the position corresponding to position 781 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises a K at the position corresponding to position 966 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an H at the position corresponding to position 1013 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an Q at the position corresponding to position 781 of SEQ ID NO: 712; and an amino acid other than an R at the position corresponding to position 1013 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises a K at the position corresponding to position 781 of SEQ ID NO: 712; a K at the position corresponding to position 966 of SEQ ID NO: 712; and an H at the position corresponding to position 1013 of SEQ ID NO: 712.

[00219] In some embodiments, the SluCas9 comprises an amino acid other than an R at the position corresponding to position 246 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an N at the position corresponding to position 414 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than a T at the position corresponding to position 420 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an R at the position corresponding to position 655 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an amino acid other than an R at the position corresponding to position 246 of SEQ ID NO: 712; an amino acid other than an N at the position corresponding to position 414 of SEQ ID NO: 712; an amino acid other than a T at the position corresponding to position 420 of SEQ ID NO: 712; and an amino acid other than an R at the position corresponding to position 655 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to position 246 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to position 414 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to position 420 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to

position 655 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to position 246 of SEQ ID NO: 712; an A at the position corresponding to position 414 of SEQ ID NO: 712; an A at the position corresponding to position 420 of SEQ ID NO: 712; and an A at the position corresponding to position 655 of SEQ ID NO: 712.

[00220] In some embodiments, the SluCas9 comprises an amino acid other than an R at the position corresponding to position 246 of SEQ ID NO: 712; an amino acid other than an N at the position corresponding to position 414 of SEQ ID NO: 712; an amino acid other than a T at the position corresponding to position 420 of SEQ ID NO: 712; an amino acid other than an R at the position corresponding to position 655 of SEQ ID NO: 712; an amino acid other than an Q at the position corresponding to position 781 of SEQ ID NO: 712; a K at the position corresponding to position 966 of SEQ ID NO: 712; and an amino acid other than an R at the position corresponding to position 1013 of SEQ ID NO: 712. In some embodiments, the SluCas9 comprises an A at the position corresponding to position 246 of SEQ ID NO: 712; an A at the position corresponding to position 414 of SEQ ID NO: 712; an A at the position corresponding to position 420 of SEQ ID NO: 712; an A at the position corresponding to position 655 of SEQ ID NO: 712; a K at the position corresponding to position 781 of SEQ ID NO: 712; a K at the position corresponding to position 966 of SEQ ID NO: 712; and an H at the position corresponding to position 1013 of SEQ ID NO: 712.

[00221] In some embodiments, the SluCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 718 (designated herein as SluCas9-KH or SLUCAS9KH):

NQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLE
RVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDD
VGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFH
QLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKYAY
SADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRI
TKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDK
ENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEF
ILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIG
KYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKV
LVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE
VQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNH
GYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQVQ
DIKDFRNFKYSHRVDKKPNRKLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPE
KFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNK
LGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDK
LKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEP
HIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00222] In some embodiments, the SluCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 719 (designated herein as SluCas9-HF):

NQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLE
RVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDD
VGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFH
QLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELASVKYAY
SADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRI
TKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDK
ENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRAQMEIFAHLNIKPKKINLTAANKIPKAMIDEF
ILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIG
KYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKV
LVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE
VQKEFINRNLVDTRYATAELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNH
GYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQVQ
DIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPE
KFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNK
LGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDK
LKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEP
RIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00223] In some embodiments, the SluCas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 720 (designated herein as SluCas9-HF-KH):

NQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRLE
RVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHKIDVIDSNDD
VGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFH
QLDENFINKYIELVEMRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELASVKYAY
SADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKGYRI
TKSGKPQFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDK
ENIAQLTGYTGTHRLSLKCIRLVLEEQWYSSRAQMEIFAHLNIKPKKINLTAANKIPKAMIDEF
ILSPVVKRTFGQAINLINKIIEKYGVPEDIIIELARENNSKDKQKFINEMQKKNENTRKRINEIIG
KYGNQNAKRLVEKIRLHDEQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKV
LVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE
VQKEFINRNLVDTRYATAELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKERNH
GYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQVQ
DIKDFRNFKYSHRVDKKPNRKLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPE
KFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNK

LGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDK
LKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEP
HIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00224] In some embodiments, the Cas protein is any of the engineered Cas proteins disclosed in Schmidt et al., 2021, Nature Communications, "Improved CRISPR genome editing using small highly active and specific engineered RNA-guided nucleases."

[00225] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7021 (designated herein as sRGN1):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
DRVKHLLAEYDLLDLTNIPKSTNPYQTRVKGLNEKLSKDELVIALLHIAKRRGIHNVDVAAD
KEETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDT
QMQYYPEIDETFKEKYISLVETRREYFEGPGKGSPFGWEGNIKKWFEQMMGHCTYFPEELRS
VKYSYSAELFNALNDLNNLVITRDEDAKLNYGEKFQIIENVFKQKKTPNLKQIAIEIGVHETEI
KGYRVNKSGTPEFTEFKLYHDLKSIVFDKSILENEAILDQIAEILTIYQDEQSIKEELNKLPEILN
EQDKAEIAKLIGYNGTHRLSLKCIHLINEELWQTSRNQMEIFNYLNIKPNKVDLSEQNKIPKD
MVNDFILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRKRI
NEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLKDIPLEDLLRNPNNYDIDHIIPRSVSFDDSM
HNKVLVRREQNAKKNNQTPYQYLTSGYADIKYSVFKQHVLNLAENKDRMTKKKREYLLEE
RDINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKF
KKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFI
IPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQ
FDKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLK
YIGNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPE
QKYDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELN
NIKGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00226] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7022 (designated herein as sRGN2):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKSLLSEYKIISGLAPTNNQPYNIRVKGLTEQLTKDELAVALLHIAKRRGIHKIDVIDSNDD
VGNELSTKEQLNKNSKLLKDKFVCQIQLERMNEGQVRGEKNRFKTADIIKEIIQLLNVQKNFH
QLDENFINKYIELVEMRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYA
YSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYR
ITKSGTPEFTEFKLYHDLKSVLFDQSILENEDVLDQIAEILTIYQDKDSIKSKLTELDILLNEEDK
ENIAQLTGYNGTHRLSLKCIRLVLEEQWYSSRNQMEIFTHLNIKPKKINLTAANKIPKAMIDEF
ILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRKRINEIIGQ

TGNQNAKRIVEKIRLHDQQEGKCLYSLESIALMDLLNNPQNYEVDHIIPRSVAFDNSIHNKVL
VKQIENSKKGNRTPYQYLNSSDAKLSYNQFKQHILNLSKSKDRISKKKKDYLLEERDINKFEV
QKEFINRNLVDTRYATRELTSYLKAYFSANNMDVKVKTINGSFTNHLRKVWRFDKYRNHGY
KHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPKQVQDIK
DFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFL
MYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGS
HLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQKYDKLKL
GKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNIKGEPRIK
KTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00227] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7023 (designated herein as sRGN3):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIALLHLAKRRGIHNVDVAADKE
ETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM
QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSV
KYAYSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIK
GYRITKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLM
SEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGYQRIP
TDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRK
RINEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS
YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEER
DINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFK
KERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFII
PKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQF
DKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLK
YIGNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPE
QKYDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELN
NIKGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00228] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7024 (designated herein as sRGN3.1):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIALLHLAKRRGIHNVDVAADKE
ETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM
QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSV
KYAYSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIK

GYRITKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLM
SEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGYQRIP
TDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRK
RINEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS
YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEER
DINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFK
KERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFII
PKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQF
DKSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLK
YIGNKLGSHLDVTHQFKSSTKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIP
KDKYQELKEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEI
NNIKGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL.

[00229] In some embodiments, the Cas9 comprises an amino acid sequence that is encoded by a nucleic acid molecule at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 918 (an exemplary nucleic acid molecule encoding sRGN3.1):

ATGAATCAGAAATTCATCCTGGGACTGGACATCGGCATTACCTCTGTGGGCTACGGCTTG
ATTGACTACGAGACCAAGAACATCATCGACGCCGGCGTTAGACTGTTTCCTGAGGCCAAT
GTGGAAAACAACGAGGGCAGACGGTCTAAGCGGGGCTCTAGACGACTGAAAAGAAGAA
GAATCCACAGACTGGAAAGAGTGAAGCTGCTGCTGACCGAGTACGACCTGATCAATAAG
GAACAGATCCCTACAAGCAACAACCCCTACCAGATTAGAGTGAAGGGCCTGAGCGAGAT
CCTGAGCAAAGACGAGCTGGCCATCGCCCTGCTGCACCTGGCCAAGCGGAGGGGCATCC
ACAACGTGGATGTGGCCGCCGACAAGGAGGAAACCGCCAGCGACTCCCTGAGCACCAAA
GATCAGATCAACAAGAATGCCAAGTTCCTGGAGAGCAGATACGTGTGCGAGCTGCAGAA
GGAGAGATTGGAGAACGAGGGCCACGTGCGGGGCGTGGAGAATAGATTCCTGACAAAA
GATATCGTGCGGGAAGCCAAGAAGATCATCGACACCCAGATGCAGTACTATCCTGAAAT
CGACGAAACCTTCAAGGAGAAGTACATCAGCCTGGTCGAAACCAGACGCGAGTATTTCG
AGGGCCCCGGACAGGGCTCTCCTTTCGGCTGGAACGGCGATCTGAAGAAGTGGTACGAG
ATGCTGATGGGACACTGCACCTACTTCCCTCAAGAGCTGAGATCTGTGAAGTACGCCTAC
AGCGCCGATCTGTTCAACGCCCTGAACGATCTGAACAACCTTATCATCCAGCGGGACAAT
TCTGAGAAGCTGGAATACCACGAGAAATATCATATCATCGAGAACGTCTTTAAACAAAA
GAAAAAGCCTACCCTGAAGCAGATCGCCAAGGAGATCGGAGTGAATCCTGAGGATATCA
AAGGCTACAGAATCACAAAGTCCGGCACCCCTGAGTTCACCAGCTTTAAGCTGTTCCACG
ACCTGAAGAAGGTCGTGAAAGACCACGCCATCCTCGATGACATCGATCTGCTGAACCAG
ATCGCTGAGATCCTGACAATCTACCAGGACAAAGATTCTATCGTGGCTGAACTGGGACA
GCTGGAATACCTTATGAGCGAGGCCGACAAGCAAAGCATCTCCGAACTGACCGGCTACA
CGGGCACCCATAGCCTGAGCCTGAAGTGTATGAACATGATCATCGATGAGCTGTGGCAC

TCTAGCATGAACCAGATGGAAGTTTTCACCTACCTGAACATGCGGCCTAAGAAGTACGA
GCTGAAGGGCTACCAGAGAATCCCCACCGATATGATCGACGACGCCATCCTGAGCCCCG
TGGTGAAAAGAACATTCATCCAGAGCATCAACGTGATCAACAAGGTGATCGAGAAGTAC
GGCATTCCAGAGGACATCATCATCGAGCTGGCCAGAGAAAACAACAGCGACGATAGAA
AGAAGTTTATCAACAACCTGCAGAAAAAAAACGAGGCCACCCGGAAGAGAATTAATGA
GATCATCGGCCAGACAGGCAACCAGAACGCCAAAAGGATCGTGGAAAAAATCAGACTG
CACGACCAGCAGGAGGGCAAGTGCCTGTACTCTCTGGAAAGCATCCCCCTGGAGGACCT
GCTGAACAATCCAAATCACTACGAGGTGGACCACATCATCCCTAGAAGCGTCAGCTTCG
ACAACAGCTACCACAACAAGGTGCTGGTGAAGCAGAGCGAAAACAGTAAGAAATCCAA
CCTGACACCTTACCAGTACTTTAACAGCGGCAAGAGCAAGCTGAGCTACAACCAGTTCA
AGCAGCACATCCTGAACCTGTCCAAATCTCAGGATAGAATCTCCAAGAAAAAGAAGGAA
TACCTGCTGGAGGAGAGAGATATCAACAAGTTCGAAGTCCAAAAGGAGTTCATCAACAG
GAACCTGGTGGACACCCGGTACGCCACAAGAGAGCTGACAAACTACCTGAAAGCCTACT
TCAGCGCTAACAACATGAACGTGAAGGTGAAAACCATCAATGGAAGTTTCACAGACTAC
CTTCGGAAGGTGTGGAAGTTCAAGAAGGAACGGAATCACGGCTACAAGCACCACGCAGA
GGACGCCCTGATTATAGCTAATGCCGATTTCCTGTTCAAAGAAAACAAGAAGCTGAAAG
CCGTGAACAGCGTTCTGGAAAAGCCTGAAATTGAGACCAAGCAACTGGATATACAGGTG
GACAGCGAGGACAACTACTCCGAGATGTTCATCATCCCTAAACAGGTGCAGGACATCAA
AGACTTCAGAAATTTCAAGTACAGCCACAGAGTGGACAAGAAACCCAACCGGCAGCTGA
TCAATGACACCCTGTATAGCACCCGCAAGAAGGATAACAGCACCTACATCGTCCAGACC
ATCAAGGACATCTACGCTAAGGACAACACCACCCTGAAAAAGCAATTTGATAAGTCCCC
CGAAAAGTTTCTGATGTACCAACACGATCCTAGAACCTTCGAAAAGTTGGAGGTGATCAT
GAAGCAATATGCCAACGAGAAGAACCCACTGGCCAAGTACCATGAGGAGACAGGAGAA
TACCTGACCAAGTATTCTAAGAAGAATAACGGCCCCATCGTGAAGTCCCTGAAGTACATT
GGGAACAAACTCGGAAGCCACCTGGACGTGACGCACCAGTTCAAGAGCAGCACCAAGA
AGCTAGTGAAACTGAGCATCAAGAACTACAGATTCGACGTGTACCTGACAGAAAAGGGC
TACAAATTTGTGACCATCGCTTACCTGAATGTGTTCAAAAAGGACAATTATTACTACATC
CCAAAGGACAAGTACCAGGAGCTTAAAGAGAAAAAAAAGATCAAGGATACCGACCAGT
TTATCGCTAGCTTCTACAAGAACGACCTGATTAAGCTGAACGGCGACCTGTACAAGATCA
TCGGCGTGAACTCTGACGACCGGAACATAATAGAGCTGGATTATTATGACATCAAGTAC
AAGGACTACTGCGAGATCAACAACATCAAGGGCGAGCCTAGAATCAAAAAGACCATCG
GGAAGAAAACCGAGTCTATCGAAAAGTTTACAACAGACGTGCTGGGCAACCTGTACCTG
CACAGCACGGAAAAGGCCCCTCAGCTCATCTTCAAGAGAGGCCTG

[00230] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7025 (designated herein as sRGN3.2):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIALLHLAKRRGIHNVDVAADKE
ETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM
QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSV
KYAYSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIK
GYRITKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLM
SEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGYQRIP
TDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRK
RINEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS
YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEER
DINKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFK
KERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFII
PKQVQDIKDFRNFKFSHRVDKKPNRQLINDTLYSTRMKDEHDYIVQTITDIYGKDNTNLKKQ
FNKNPEKFLMYQNDPKTFEKLSIIMKQYSDEKNPLAKYYEETGEYLTKYSKKNNGPIVKKIK
LLGNKVGNHLDVTNKYENSTKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYI
PKDKYQELKEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYC
EINNIKGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL.

[00231] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7026 (designated herein as sRGN3.3):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIALLHLAKRRGIHNVDVAADKE
ETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQM
QYYPEIDETFKEKYISLVETRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSV
KYAYSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIK
GYRITKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLM
SEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGYQRIP
TDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRK
RINEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNS
YHNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEER
DINKFEVQKEFINRNLVDTRYATRELTSYLKAYFSANNMDVKVKTINGSFTNHLRKVWRFD
KYRNHGYKHHAEDALIIANADFLFKENKKLQNTNKILEKPTIENNTKKVTVEKEEDYNNVFE
TPKLVEDIKQYRDYKFSHRVDKKPNRQLINDTLYSTRMKDEHDYIVQTITDIYGKDNTNLKK
QFNKNPEKFLMYQNDPKTFEKLSIIMKQYSDEKNPLAKYYEETGEYLTKYSKKNNGPIVKKI
KLLGNKVGNHLDVTNKYENSTKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYY
IPKDKYQELKEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYC
EINNIKGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL.

[00232] In some embodiments, the Cas9 comprises an amino acid sequence that is encoded by a nucleic acid molecule at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 919 (an exemplary nucleic acid molecule encoding sRGN3.3):

AACCAGAAGTTTATCCTGGGCCTGGATATCGGCATCACATCCGTGGGCTACGGCCTGATT
GATTACGAAACCAAGAACATCATTGATGCCGGCGTCCGGCTTTTCCCTGAAGCTAACGTG
GAAAACAATGAGGGCAGACGGAGCAAGAGAGGCAGCAGACGGCTGAAGCGGAGAAGA
ATCCATAGACTCGAACGGGTGAAGCTGCTGCTGACCGAGTACGACCTGATCAACAAGGA
GCAGATCCCCACCAGCAACAACCCATACCAGATCAGAGTGAAAGGCCTTTCTGAGATTC
TGAGCAAGGATGAGCTGGCTATCGCTCTGCTCCACCTGGCCAAGAGAAGGGGAATCCAC
AACGTTGACGTGGCCGCCGATAAGGAAGAGACCGCCAGCGATAGCCTGAGCACCAAGG
ACCAGATCAACAAGAACGCCAAGTTCCTGGAAAGCAGATACGTGTGCGAGCTGCAAAAA
GAGAGACTGGAAAATGAGGGCCATGTGCGGGGCGTTGAGAACAGATTCCTGACCAAAG
ACATCGTCAGAGAGGCCAAGAAAATTATTGACACCCAGATGCAGTACTATCCTGAGATA
GACGAGACCTTTAAGGAAAAGTACATCAGCCTGGTGGAAACAAGAAGAGAATACTTCGA
AGGACCTGGCCAGGGCTCCCCTTTCGGCTGGAACGGCGACCTGAAGAAGTGGTACGAGA
TGCTGATGGGCCACTGCACCTACTTCCCCCAGGAGCTGCGGAGCGTGAAGTACGCTTACA
GCGCCGACCTGTTCAATGCCCTGAACGACCTGAACAATCTTATCATCCAAAGAGATAACA
GCGAGAAATTAGAATACCACGAGAAGTACCACATCATCGAGAATGTGTTCAAGCAAAAG
AAGAAGCCTACCCTGAAGCAGATCGCCAAAGAGATCGGCGTGAACCCTGAGGACATCAA
GGGCTATCGGATCACCAAGTCCGGCACCCCTGAATTCACCAGCTTCAAGCTGTTTCACGA
CCTCAAAAAGGTCGTGAAGGACCACGCCATCCTGGACGACATCGATCTGCTGAATCAGA
TCGCCGAGATCCTGACCATCTACCAGGACAAGGACTCTATCGTGGCCGAGCTTGGACAG
CTGGAGTACCTGATGAGCGAGGCTGACAAGCAGAGCATCAGCGAGCTGACCGGCTACAC
CGGAACCCACAGCCTGTCCCTGAAGTGCATGAACATGATCATCGACGAGCTGTGGCACT
CTAGCATGAACCAGATGGAAGTGTTCACCTACCTGAACATGAGACCTAAGAAGTACGAA
CTGAAGGGTTACCAGAGAATCCCAACCGACATGATCGACGACGCCATCCTGAGCCCCGT
GGTGAAGCGGACCTTTATCCAGAGCATCAATGTGATCAACAAGGTGATCGAGAAATACG
GCATCCCCGAGGACATCATCATCGAACTGGCCAGAGAGAATAACTCTGATGACCGGAAG
AAGTTCATCAACAACCTGCAGAAGAAGAACGAAGCCACCAGAAAGCGCATCAACGAGA
TCATCGGCCAAACAGGGAATCAGAACGCCAAGAGGATCGTGGAAAAGATTCGGCTGCAC
GACCAGCAGGAGGGAAAATGCCTGTACAGCCTGGAAAGCATCCCCCTGGAAGATCTACT
GAACAACCCCAACCACTACGAGGTGGATCACATCATCCCTAGAAGCGTGTCCTTTGACA
ACAGTTACCACAACAAGGTGCTGGTGAAGCAATCCGAGAACTCGAAGAAGAGCAACCTG
ACACCTTACCAGTACTTTAACAGCGGCAAGTCCAAGCTGTCTTATAACCAGTTCAAGCAG
CACATCCTCAACCTGTCAAAGTCTCAGGACAGAATCTCTAAGAAGAAGAAGGAGTATCT
GCTGGAAGAGCGGGACATCAACAAGTTCGAGGTGCAGAAAGAGTTCATTAACAGAAACC

TGGTCGACACCCGGTACGCCACACGCGAACTGACAAGCTACCTGAAGGCCTACTTCTCCG
CCAACAATATGGACGTGAAGGTCAAGACCATCAATGGCAGCTTCACAAATCACCTGAGA
AAGGTCTGGCGGTTCGACAAGTACAGAAACCACGGCTACAAGCACCACGCCGAGGATGC
TCTGATTATCGCCAACGCCGACTTCCTGTTCAAGGAAAACAAAAAACTGCAGAACACCA
ACAAGATCCTGGAAAAACCTACAATCGAGAACAACACAAAGAAAGTGACAGTGGAAAA
AGAGGAAGATTACAACAACGTGTTTGAGACACCTAAGCTGGTTGAGGATATCAAGCAGT
ACCGGGACTATAAGTTTAGCCACAGAGTGGACAAGAAACCTAACAGGCAGCTGATCAAC
GACACTCTGTACAGCACAAGAATGAAAGATGAGCACGATTACATCGTGCAGACCATTAC
CGACATCTACGGCAAGGACAACACCAATCTGAAGAAGCAGTTCAACAAAAATCCCGAGA
AGTTCCTGATGTACCAAAATGACCCTAAGACATTCGAGAAGCTGAGCATCATCATGAAA
CAGTACTCTGATGAGAAGAACCCACTGGCCAAGTACTACGAGGAAACAGGCGAATACCT
GACCAAGTACTCTAAGAAGAACAACGGCCCTATCGTGAAGAAGATCAAACTGCTGGGCA
ACAAAGTGGGAAATCATCTGGATGTGACCAATAAATACGAGAACTCTACAAAGAAACTG
GTGAAGCTGAGCATTAAGAACTACAGATTCGACGTCTACCTGACAGAAAAGGGATACAA
GTTCGTGACCATCGCCTACCTGAACGTGTTCAAGAAAGACAACTACTACTACATCCCAAA
AGACAAGTACCAAGAGTTAAAAGAGAAGAAGAAGATAAAGGATACCGACCAGTTTATC
GCTTCTTTCTACAAGAACGACCTGATCAAGCTGAACGGTGATCTGTACAAAATCATCGGA
GTGAATAGCGATGACAGAAATATCATCGAACTGGATTACTATGACATCAAGTACAAAGA
TTATTGTGAAATCAACAACATCAAGGGAGAGCCCAGAATTAAGAAAACCATCGGCAAGA
AAACAGAGAGCATCGAGAAATTCACCACAGATGTGCTGGGCAACCTGTACCTGCACAGC
ACAGAGAAAGCCCCTCAGCTCATCTTCAAGAGAGGCCTG

[00233] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7027 (designated herein as sRGN4):

MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGSRRLKRRRIHRL
ERVKKLLEDYNLLDQSQIPQSTNPYAIRVKGLSEALSKDELVIALLHIAKRRGIHNINVSSEDE
DASNELSTKEQINRNNKLLKDKYVCEVQLQRLKEGQIRGEKNRFKTTDILKEIDQLLKVQKD
YHNLDIDFINQYKEIVETRREYFEGPGKGSPYGWEGDPKAWYETLMGHCTYFPDELRSVKY
AYSADLFNALNDLNNLVIQRDGLSKLEYHEKYHIIENVFKQKKKPTLKQIANEINVNPEDIKG
YRITKSGKPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLEYLMS
EADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGYQRIPT
DMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRKR
INEIIGQTGNQNAKRIVEKIRLHDQQEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSY
HNKVLVKQSENSKKSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDI
NKFEVQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKVWKFKKE
RNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDIQVDSEDNYSEMFIIPK
QVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKKDNSTYIVQTIKDIYAKDNTTLKKQFD

KSPEKFLMYQHDPRTFEKLEVIMKQYANEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYI
GNKLGSHLDVTHQFKSSTKKLVKLSIKPYRFDVYLTDKGYKFITISYLDVLKKDNYYYIPEQK
YDKLKLGKAIDKNAKFIASFYKNDLIKLDGEIYKIIGVNSDTRNMIELDLPDIRYKEYCELNNI
KGEPRIKKTIGKKVNSIEKLTTDVLGNVFTNTQYTKPQLLFKRGN.

[00234] In some embodiments, the Cas9 comprises an amino acid sequence that is encoded by a nucleic acid molecule at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 920 (an exemplary nucleic acid molecule encoding sRGN4):

ATGAATCAAAAGTTTATCCTGGGTCTGGACATCGGCATCACATCTGTGGGCTACGGCCTT
ATCGATTACGAGACCAAGAATATCATTGATGCTGGCGTACGGCTGTTCCCTGAGGCTAAC
GTGGAAAACAACGAGGGTAGACGGAGCAAGAGAGGCAGCAGACGGCTGAAACGGCGTA
GAATCCACCGGCTGGAGAGAGTGAAGAAGTTGCTGGAAGATTACAACTTGCTGGATCAA
TCCCAGATCCCCCAGAGCACTAATCCTTATGCTATCCGGGTGAAGGGCCTGTCTGAAGCC
CTGAGCAAAGACGAGCTGGTGATTGCCCTGCTGCACATCGCGAAGAGAAGAGGCATCCA
CAATATCAATGTGTCCTCTGAGGATGAGGATGCCAGCAACGAGCTGAGCACTAAGGAAC
AGATCAATCGGAACAACAAGCTGCTGAAGGACAAGTACGTGTGTGAAGTGCAGCTGCAG
AGACTGAAGGAAGGCCAGATAAGAGGCGAAAAGAACAGATTCAAGACAACAGACATCC
TGAAAGAAATCGACCAGCTGCTGAAGGTCCAGAAGGACTACCACAACCTCGACATCGAT
TTCATTAACCAGTACAAGGAAATCGTGGAAACCAGGAGAGAGTACTTCGAGGGCCCTGG
CAAGGGCTCCCCATACGGCTGGGAGGGCGACCCCAAGGCCTGGTACGAAACCCTGATGG
GCCACTGCACCTACTTCCCCGACGAACTGAGAAGCGTCAAGTACGCCTACAGCGCCGAT
CTGTTCAACGCCCTGAACGACCTGAACAACCTGGTGATCCAGCGGGACGGCCTGAGCAA
ACTGGAGTACCATGAAAAGTATCATATCATCGAGAACGTGTTCAAGCAGAAGAAAAAAC
CTACCCTGAAGCAGATCGCCAACGAGATCAACGTGAACCCTGAGGACATTAAAGGCTAC
AGAATCACCAAAAGCGGCAAGCCAGAGTTCACCAGCTTCAAGCTGTTTCACGACCTGAA
GAAGGTCGTGAAAGACCACGCCATCCTGGACGACATCGATCTGCTTAACCAGATCGCTG
AAATCCTCACAATCTACCAGGACAAGGACTCTATCGTGGCCGAGCTGGGACAGCTGGAA
TACCTGATGAGCGAGGCCGATAAGCAGAGCATCAGCGAGCTGACCGGCTACACCGGAAC
CCACAGCCTGAGCCTGAAGTGTATGAACATGATCATCGACGAGCTGTGGCACAGCTCTAT
GAACCAGATGGAAGTATTCACCTACCTGAACATGAGACCTAAGAAGTACGAACTGAAGG
GCTATCAGAGAATCCCTACAGACATGATCGACGATGCCATCCTGTCTCCTGTGGTGAAGA
GAACCTTCATCCAGTCTATCAACGTGATCAACAAGGTGATCGAAAAGTACGGAATCCCT
GAAGATATCATCATCGAACTGGCCAGAGAGAACAACTCCGACGACAGAAAGAAATTCAT
CAACAACCTGCAGAAGAAGAATGAGGCCACACGGAAGCGGATTAATGAGATCATCGGC
CAAACCGGCAACCAGAACGCCAAAAGAATCGTGGAAAAGATCCGGCTGCACGATCAGC
AGGAGGGCAAATGCCTGTACAGCCTGGAGAGCATCCCCCTGGAGGACCTGCTCAACAAC
CCCAACCACTACGAGGTGGATCACATCATCCCAAGATCTGTTAGCTTCGACAACAGCTAC

CACAACAAGGTGCTGGTGAAGCAAAGCGAAAACTCTAAGAAATCTAACCTGACACCTTA
CCAGTACTTTAACAGCGGCAAGTCCAAGCTGTCTTATAACCAGTTTAAGCAGCACATCCT
GAACCTGAGCAAGTCCCAGGATAGAATCAGCAAAAAAAAGAAGGAATACCTGCTGGAG
GAACGCGACATCAATAAATTTGAGGTGCAAAAGGAGTTCATCAACCGGAACCTGGTGGA
CACCCGGTACGCCACCAGAGAACTGACCAACTACCTGAAAGCCTACTTCAGCGCCAACA
ACATGAACGTGAAGGTGAAAACCATCAACGGAAGCTTCACCGACTACCTGCGGAAGGTG
TGGAAGTTCAAGAAAGAGCGGAATCACGGCTATAAGCACCACGCTGAGGACGCTCTGAT
CATCGCCAATGCCGATTTCCTGTTCAAGGAAAACAAGAAGTTAAAGGCCGTGAACTCTGT
CCTGGAGAAGCCCGAGATCGAGACAAAGCAGCTGGACATCCAAGTGGACTCAGAGGAC
AATTACTCTGAGATGTTCATCATCCCCAAGCAGGTGCAGGACATCAAGGATTTTAGAAAT
TTCAAGTACAGCCATAGAGTGGACAAGAAGCCCAATAGACAGCTGATCAACGATACACT
GTACAGCACCAGAAAGAAGGACAACAGCACATATATCGTCCAGACCATCAAGGACATTT
ACGCAAAGGATAACACCACACTGAAGAAGCAGTTCGACAAAAGCCCTGAGAAGTTCCTG
ATGTACCAACACGACCCTCGGACCTTCGAGAAGTTAGAGGTTATCATGAAACAGTACGC
CAACGAGAAAAACCCTCTGGCCAAGTACCACGAGGAAACCGGAGAATACCTGACAAAA
TATAGCAAGAAGAACAACGGCCCCATCGTGAAAAGCCTGAAGTACATCGGCAACAAGCT
GGGCAGCCACCTGGACGTGACCCACCAGTTCAAGAGCAGCACCAAGAAGCTGGTCAAGC
TGAGCATCAAGCCTTATAGGTTCGACGTGTACCTGACAGATAAGGGATACAAGTTCATCA
CCATCAGCTACCTGGATGTTCTGAAAAAGGACAATTACTACTACATCCCTGAGCAGAAGT
ACGACAAACTCAAGCTGGGCAAGGCCATCGATAAGAATGCCAAGTTCATCGCATCTTTTT
ACAAGAACGACCTGATCAAACTGGACGGCGAGATCTACAAGATCATAGGAGTGAACAGC
GACACCAGGAATATGATCGAGCTCGATCTGCCTGACATCAGATACAAGGAATACTGCGA
GCTGAACAACATCAAGGGAGAGCCTAGAATCAAGAAAACCATCGGCAAGAAGGTGAAC
AGCATCGAGAAACTTACAACAGATGTGCTCGGCAACGTGTTCACCAACACCCAGTACAC
CAAGCCACAGCTGCTGTTTAAGCGGGGGAAC

[00235] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7028 (designated herein as *Staphylococcus hyicus* Cas9 or ShyCas9):

MNNYILGLDIGITSVGYGIVDSDTREIKDAGVRLFPEANVDNNEGRRSKRGARRLKR
RRIHRLDRVKHLLAEYDLLDLTNIPKSTNPYQTRVKGLNEKLSKDELVIALLHIAKRRGIHNV
NVMMDDNDSGNELSTKDQLKKNAKALSDKYVCELQLERFEQDYKVRGEKNRFKTEDFVRE
ARKLLETQSKFFEIDQTFIMRYIELIETRREYFEGPGKGSPFGWEGNIKKWFEQMMGHCTYFP
EELRSVKYSYSAELFNALNDLNNLVITRDEDAKLNYGEKFQIIENVFKQKKTPNLKQIAIEIGV
HETEIKGYRVNKSGKPEFTQFKLYHDLKNIFKDPKYLNDIQLMDNIAEIITIYQDAESIIKELNQ
LPELLSEREKEKISALSGYSGTHRLSLKCINLLLDDLWESSLNQMELFTKLNLKPKKIDLSQQH
KIPSKLVDDFILSPVVKRAFIQSIQVVNAIIDKYGLPEDIIIELARENNSDDRRKFLNQLQKQNE
ETRKQVEKVLREYGNDNAKRIVQKIKLHNMQEGKCLYSLKDIPLEDLLRNPHHYEVDHIIPRS

VAFDNSMHNKVLVRADENSKKGNRTPYQYLNSSESSLSYNEFKQHILNLSKTKDRITKKKRE
YLLEERDINKFDVQKEFINRNLVDTRYATRELTSLLKAYFSANNLDVKVKTINGSFTNYLRKV
WKFDKDRNKGYKHHAEDALIIANADFLFKHNKKLRNINKVLDAPSKEVDKKRVTVQSEDEY
NQIFEDTQKAQAIKKFEIRKFSHRVDKKPNRQLINDTLYSTRNIDGIEYVVESIKDIYSVNNDK
VKTKFKKDPHRLLMYRNDPQTFEKFEKVFKQYESEKNPFAKYYEETGEKIRKFSKTGQGPYI
NKIKYLRERLGRHCDVTNKYINSRNKIVQLKIYSYRFDIYQYGNNYKMITISYIDLEQKSNYY
YISREKYEQKKKDKQIDDSYKFIGSFYKNDIINYNGEMYRVIGVNDSEKNKIQLDMIDISIKDY
MELNNIKKTGVIYKTIGKSTTHIEKYTTDILGNLYKAAPPKKPQLIFK.

[00236] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7029 (designated herein as *Staphylococcus microti* Cas9 or Smi Cas9):
MEKDYILGLDIGIGSVGYGLIDYDTKSIIDAGVRLFPEANADNNLGRRAKRGARRLKRRRIHR
LERVKSLLSEYKIISGLAPTNNQPYNIRVKGLTEQLTKDELAVALLHIAKRRGIHNVDVAADK
EETASDSLSTKDQINKNAKFLESRYVCELQKERLENEGHVRGVENRFLTKDIVREAKKIIDTQ
MQYYPEIDETFKEKYISLVETRREYYEGPGKGSPYGWDADVKKWYQLMMGHCTYFPVEFRS
VKYAYTADLYNALNDLNNLTIARDDNPKLEYHEKYHIIENVFKQKRNPTLKQIAKEIGVNDI
NISGYRVTKSGKPQFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQLE
YLMSEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYLNMRPKKYELKGY
QRIPTDMIDDAILSPVVKRSFKQAIGVVNAIIKKYGLPKDIIIELARESNSAEKSRYLRAIQKKN
EKTRERIEAIIKEYGNENAKGLVQKIKLHDAQEGKCLYSLKDIPLEDLLRNPNNYDIDHIIPRS
VSFDDSMHNKVLVRREQNAKKNNQTPYQYLTSGYADIKYSVFKQHVLNLAENKDRMTKKK
REYLLEERNINKYDVQKEFINRNLVDTRYTTRELTTLLKTYFTINNLDVKVKTINGSFTDFLR
KRWGFKKNRDEGYKHHAEDALIIANADYLFKEHKLLKEIKDVSDLAGDERNSNVKDEDQYE
EVFGGYFKIEDIKKYKIKKFSHRVDKKPNRQLINDTIYSTRVKDDKRYLINTLKNLYDKSNGD
LKERMQKDPESLLMYHHDPQTFEKLKIVMSQYENEKNPLAKYFEETGQYLTKYAKHDNGPA
IHKIKYYGNKLVEHLDITKNYHNPQNKVVQLSQKSFRFDVYQTDKGYKFISIAYLTLKNEKN
YYAISQEKYDQLKSEKKISNNAVFIGSFYTSDIIEINNEKFRVIGVNSDKNNLIEVDRIDIRQKEF
IELEEEKKNNRIKVTIGRKTTNIEKFHTDILGNMYKSKRPKAPQLVFKKG.

[00237] In some embodiments, the Cas9 comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7030 (designated herein as *Staphylococcus pasteuri* Cas9 or Spa Cas9):
MKEKYILGLDLGITSVGYGIINFETKKIIDAGVRLFPEANVDNNEGRRSKRGSRRLKRRRIHRL
ERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIALLHLAKRRGIHNINVSSEDED
ASNELSTKEQINRNNKLLKDKYVCEVQLQRLKEGQIRGEKNRFKTTDILKEIDQLLKVQKDY
HNLDIDFINQYKEIVETRREYFEGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYA
YSADLFNALNDLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYR
ITKSGTPQFTEFKLYHDLKSIVFDKSILENEAILDQIAEILTIYQDEQSIKEELNKLPEILNEQDK

AEIAKLIGYNGTHRLSLKCIHLINEELWQTSRNQMEIFNYLNIKPNKVDLSEQNKIPKDMVND
FILSPVVKRTFIQSINVINKVIEKYGIPEDIIIELARENNSDDRKKFINNLQKKNEATRKRINEIIG
QTGNQNAKRIVEKIRLHDQQEGKCLYSLESIALMDLLNNPQNYEVDHIIPRSVAFDNSIHNKV
LVKQIENSKKGNRTPYQYLNSSDAKLSYNQFKQHILNLSKSKDRISKKKKDYLLEERDINKFE
VQKEFINRNLVDTRYATRELTSYLKAYFSANNMDVKVKTINGSFTNHLRKVWRFDKYRNHG
YKHHAEDALIIANADFLFKENKKLQNTNKILEKPTIENNTKKVTVEKEEDYNNVFETPKLVED
IKQYRDYKFSHRVDKKPNRQLINDTLYSTRMKDEHDYIVQTITDIYGKDNTNLKKQFNKNPE
KFLMYQNDPKTFEKLSIIMKQYSDEKNPLAKYYEETGEYLTKYSKKNNGPIVKKIKLLGNKV
GNHLDVTNKYENSTKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQ
ELKEKKKIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEINNIKG
EPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL.

[00238] In some embodiments, the Cas protein comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7031 (designated herein as Cas12i1):

MSNKEKNASETRKAYTTKMIPRSHDRMKLLGNFMDYLMDGTPIFFELWNQFGGGIDRDIISG
TANKDKISDDLLLAVNWFKVMPINSKPQGVSPSNLANLFQQYSGSEPDIQAQEYFASNFDTE
KHQWKDMRVEYERLLAELQLSRSDMHHDLKLMYKEKCIGLSLSTAHYITSVMFGTGAKNN
RQTKHQFYSKVIQLLEESTQINSVEQLASIILKAGDCDSYRKLRIRCSRKGATPSILKIVQDYEL
GTNHDDEVNVPSLIANLKEKLGRFEYECEWKCMEKIKAFLASKVGPYYLGSYSAMLENALS
PIKGMTTKNCKFVLKQIDAKNDIKYENEPFGKIVEGFFDSPYFESDTNVKWVLHPHHIGESNI
KTLWEDLNAIHSKYEEDIASLSEDKKEKRIKVYQGDVCQTINTYCEEVGKEAKTPLVQLLRY
LYSRKDDIAVDKIIDGITFLSKKHKVEKQKINPVIQKYPSFNFGNNSKLLGKIISPKDKLKHNL
KCNRNQVDNYIWIEIKVLNTKTMRWEKHHYALSSTRFLEEVYYPATSENPPDALAARFRTKT
NGYEGKPALSAEQIEQIRSAPVGLRKVKKRQMRLEAARQQNLLPRYTWGKDFNINICKRGN
NFEVTLATKVKKKKEKNYKVVLGYDANIVRKNTYAAIEAHANGDGVIDYNDLPVKPIESGF
VTVESQVRDKSYDQLSYNGVKLLYCKPHVESRRSFLEKYRNGTMKDNRGNNIQIDFMKDFE
AIADDETSLYYFNMKYCKLLQSSIRNHSSQAKEYREEIFELLRDGKLSVLKLSSLSNLSFVMF
KVAKSLIGTYFGHLLKKPKNSKSDVKAPPITDEDKQKADPEMFALRLALEEKRLNKVKSKKE
VIANKIVAKALELRDKYGPVLIKGENISDTTKKGKKSSTNSFLMDWLARGVANKVKEMVM
MHQGLEFVEVNPNFTSHQDPFVHKNPENTFRARYSRCTPSELTEKNRKEILSFLSDKPSKRPT
NAYYNEGAMAFLATYGLKKNDVLGVSLEKFKQIMANILHQRSEDQLLFPSRGGMFYLATYK
LDADATSVNWNGKQFWVCNADLVAAYNVGLVDIQKDFKKK.

[00239] In some embodiments, the Cas protein comprises an amino acid sequence that is at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the sequence of SEQ ID NO: 7032 (designated herein as Cas12i2):

MSSAIKSYKSVLRPNERKNQLLKSTIQCLEDGSAFFFKMLQGLFGGITPEIVRFSTEQEKQQQD
IALWCAVNWFRPVSQDSLTHTIASDNLVEKFEEYYGGTASDAIKQYFSASIGESYYWNDCRQ

QYYDLCRELGVEVSDLTHDLEILCREKCLAVATESNQNNSIISVLFGTGEKEDRSVKLRITKKI
LEAISNLKEIPKNVAPIQEIILNVAKATKETFRQVYAGNLGAPSTLEKFIAKDGQKEFDLKKLQ
TDLKKVIRGKSKERDWCCQEELRSYVEQNTIQYDLWAWGEMFNKAHTALKIKSTRNYNFA
KQRLEQFKEIQSLNNLLVVKKLNDFFDSEFFSGEETYTICVHHLGGKDLSKLYKAWEDDPAD
PENAIVVLCDDLKNNFKKEPIRNILRYIFTIRQECSAQDILAAAKYNQQLDRYKSQKANPSVL
GNQGFTWTNAVILPEKAQRNDRPNSLDLRIWLYLKLRHPDGRWKKHHIPFYDTRFFQEIYAA
GNSPVDTCQFRTPRFGYHLPKLTDQTAIRVNKKHVKAAKTEARIRLAIQQGTLPVSNLKITEIS
ATINSKGQVRIPVKFDVGRQKGTLQIGDRFCGYDQNQTASHAYSLWEVVKEGQYHKELGCF
VRFISSGDIVSITENRGNQFDQLSYEGLAYPQYADWRKKASKFVSLWQITKKNKKKEIVTVE
AKEKFDAICKYQPRLYKFNKEYAYLLRDIVRGKSLVELQQIRQEIFRFIEQDCGVTRLGSLSLS
TLETVKAVKGIIYSYFSTALNASKNNPISDEQRKEFDPELFALLEKLELIRTRKKKQKVERIAN
SLIQTCLENNIKFIRGEGDLSTTNNATKKKANSRSMDWLARGVFNKIRQLAPMHNITLFGCGS
LYTSHQDPLVHRNPDKAMKCRWAAIPVKDIGDWVLRKLSQNLRAKNIGTGEYYHQGVKEF
LSHYELQDLEEELLKWRSDRKSNIPCWVLQNRLAEKLGNKEAVVYIPVRGGRIYFATHKVAT
GAVSIVFDQKQVWVCNADHVAAANIALTVKGIGEQSSDEENPDGSRIKLQLTS.

Modified guide RNAs

[00240] In some embodiments, the guide RNA is chemically modified. A guide RNA comprising one or more modified nucleosides or nucleotides is called a "modified" guide RNA or "chemically modified" guide RNA, to describe the presence of one or more non-naturally and/or naturally occurring components or configurations that are used instead of or in addition to the canonical A, G, C, and U residues. In some embodiments, a modified guide RNA is synthesized with a non-canonical nucleoside or nucleotide, is here called "modified." Modified nucleosides and nucleotides can include one or more of: (i) alteration, e.g., replacement, of one or both of the non-linking phosphate oxygens and/or of one or more of the linking phosphate oxygens in the phosphodiester backbone linkage (an exemplary backbone modification); (ii) alteration, e.g., replacement, of a constituent of the ribose sugar, e.g., of the 2' hydroxyl on the ribose sugar (an exemplary sugar modification); (iii) wholesale replacement of the phosphate moiety with "dephospho" linkers (an exemplary backbone modification); (iv) modification or replacement of a naturally occurring nucleobase, including with a non-canonical nucleobase (an exemplary base modification); (v) replacement or modification of the ribose-phosphate backbone (an exemplary backbone modification); (vi) modification of the 3' end or 5' end of the oligonucleotide, e.g., removal, modification or replacement of a terminal phosphate group or conjugation of a moiety, cap or linker (such 3' or 5' cap modifications may comprise a sugar and/or backbone modification); and (vii) modification or replacement of the sugar (an exemplary sugar modification).

[00241] Chemical modifications such as those listed above can be combined to provide modified guide RNAs comprising nucleosides and nucleotides (collectively "residues") that can have two,

three, four, or more modifications. For example, a modified residue can have a modified sugar and a modified nucleobase, or a modified sugar and a modified phosphodiester. In some embodiments, every base of a guide RNA is modified, *e.g.*, all bases have a modified phosphate group, such as a phosphorothioate group. In certain embodiments, all, or substantially all, of the phosphate groups of a guide RNA molecule are replaced with phosphorothioate groups. In some embodiments, modified guide RNAs comprise at least one modified residue at or near the 5' end of the RNA. In some embodiments, modified guide RNAs comprise at least one modified residue at or near the 3' end of the RNA.

[00242] In some embodiments, the guide RNA comprises one, two, three or more modified residues. In some embodiments, at least 5% (*e.g.*, at least 5%, at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or 100%) of the positions in a modified guide RNA are modified nucleosides or nucleotides.

[00243] Unmodified nucleic acids can be prone to degradation by, *e.g.*, intracellular nucleases or those found in serum. For example, nucleases can hydrolyze nucleic acid phosphodiester bonds. Accordingly, in one aspect the guide RNAs described herein can contain one or more modified nucleosides or nucleotides, *e.g.*, to introduce stability toward intracellular or serum-based nucleases. In some embodiments, the modified guide RNA molecules described herein can exhibit a reduced innate immune response when introduced into a population of cells, both *in vivo* and *ex vivo*. The term "innate immune response" includes a cellular response to exogenous nucleic acids, including single stranded nucleic acids, which involves the induction of cytokine expression and release, particularly the interferons, and cell death.

[00244] In some embodiments of a backbone modification, the phosphate group of a modified residue can be modified by replacing one or more of the oxygens with a different substituent. Further, the modified residue, *e.g.*, modified residue present in a modified nucleic acid, can include the wholesale replacement of an unmodified phosphate moiety with a modified phosphate group as described herein. In some embodiments, the backbone modification of the phosphate backbone can include alterations that result in either an uncharged linker or a charged linker with unsymmetrical charge distribution.

[00245] Examples of modified phosphate groups include, phosphorothioate, phosphoroselenates, borano phosphates, borano phosphate esters, hydrogen phosphonates, phosphoroamidates, alkyl or aryl phosphonates and phosphotriesters. The phosphorous atom in an unmodified phosphate group is achiral. However, replacement of one of the non-bridging oxygens with one of the above atoms or groups of atoms can render the phosphorous atom chiral. The stereogenic phosphorous atom can possess either the "R" configuration (herein Rp) or the "S" configuration (herein Sp). The backbone

can also be modified by replacement of a bridging oxygen, (*i.e.*, the oxygen that links the phosphate to the nucleoside), with nitrogen (bridged phosphoroamidates), sulfur (bridged phosphorothioates) and carbon (bridged methylenephosphonates). The replacement can occur at either linking oxygen or at both of the linking oxygens.

[00246] The phosphate group can be replaced by non-phosphorus containing connectors in certain backbone modifications. In some embodiments, the charged phosphate group can be replaced by a neutral moiety. Examples of moieties which can replace the phosphate group can include, without limitation, *e.g.*, methyl phosphonate, hydroxylamino, siloxane, carbonate, carboxymethyl, carbamate, amide, thioether, ethylene oxide linker, sulfonate, sulfonamide, thioformacetal, formacetal, oxime, methyleneimino, methylenemethylimino, methylenehydrazo, methylenedimethylhydrazo and methyleneoxymethylimino.

[00247] Scaffolds that can mimic nucleic acids can also be constructed wherein the phosphate linker and ribose sugar are replaced by nuclease resistant nucleoside or nucleotide surrogates. Such modifications may comprise backbone and sugar modifications. In some embodiments, the nucleobases can be tethered by a surrogate backbone. Examples can include, without limitation, the morpholino, cyclobutyl, pyrrolidine and peptide nucleic acid (PNA) nucleoside surrogates.

[00248] The modified nucleosides and modified nucleotides can include one or more modifications to the sugar group, *i.e.* at sugar modification. For example, the 2' hydroxyl group (OH) can be modified, *e.g.* replaced with a number of different "oxy" or "deoxy" substituents. In some embodiments, modifications to the 2' hydroxyl group can enhance the stability of the nucleic acid since the hydroxyl can no longer be deprotonated to form a 2'-alkoxide ion.

[00249] Examples of 2' hydroxyl group modifications can include alkoxy or aryloxy (OR, wherein "R" can be, *e.g.*, alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or a sugar); polyethyleneglycols (PEG), $O(CH_2CH_2O)_nCH_2CH_2OR$ wherein R can be, *e.g.*, H or optionally substituted alkyl, and n can be an integer from 0 to 20 (*e.g.*, from 0 to 4, from 0 to 8, from 0 to 10, from 0 to 16, from 1 to 4, from 1 to 8, from 1 to 10, from 1 to 16, from 1 to 20, from 2 to 4, from 2 to 8, from 2 to 10, from 2 to 16, from 2 to 20, from 4 to 8, from 4 to 10, from 4 to 16, and from 4 to 20). In some embodiments, the 2' hydroxyl group modification can be 2'-O-Me. In some embodiments, the 2' hydroxyl group modification can be a 2'-fluoro modification, which replaces the 2' hydroxyl group with a fluoride. In some embodiments, the 2' hydroxyl group modification can include "locked" nucleic acids (LNA) in which the 2' hydroxyl can be connected, *e.g.*, by a C_{1-6} alkylene or C_{1-6} heteroalkylene bridge, to the 4' carbon of the same ribose sugar, where exemplary bridges can include methylene, propylene, ether, or amino bridges; O-amino (wherein amino can be, *e.g.*, NH_2; alkylamino, dialkylamino, heterocyclyl, arylamino, diarylamino, heteroarylamino, or diheteroarylamino, ethylenediamine, or polyamino) and aminoalkoxy, $O(CH_2)_n$-amino, (wherein amino can be, *e.g.*, NH_2; alkylamino, dialkylamino,

heterocyclyl, arylamino, diarylamino, heteroarylamino, or diheteroarylamino, ethylenediamine, or polyamino). In some embodiments, the 2' hydroxyl group modification can include "unlocked" nucleic acids (UNA) in which the ribose ring lacks the C2'-C3' bond. In some embodiments, the 2' hydroxyl group modification can include the methoxyethyl group (MOE), ($OCH_2CH_2OCH_3$, *e.g.*, a PEG derivative).

[00250] "Deoxy" 2' modifications can include hydrogen (*i.e.* deoxyribose sugars, *e.g.*, at the overhang portions of partially dsRNA); halo (*e.g.*, bromo, chloro, fluoro, or iodo); amino (wherein amino can be, *e.g.*, NH_2; alkylamino, dialkylamino, heterocyclyl, arylamino, diarylamino, heteroarylamino, diheteroarylamino, or amino acid); $NH(CH_2CH_2NH)_nCH2CH_2$- amino (wherein amino can be, *e.g.*, as described herein), -NHC(O)R (wherein R can be, *e.g.*, alkyl, cycloalkyl, aryl, aralkyl, heteroaryl or sugar), cyano; mercapto; alkyl-thio-alkyl; thioalkoxy; and alkyl, cycloalkyl, aryl, alkenyl and alkynyl, which may be optionally substituted with *e.g.*, an amino as described herein.

[00251] The sugar modification can comprise a sugar group which may also contain one or more carbons that possess the opposite stereochemical configuration than that of the corresponding carbon in ribose. Thus, a modified nucleic acid can include nucleotides containing *e.g.*, arabinose, as the sugar. The modified nucleic acids can also include abasic sugars. These abasic sugars can also be further modified at one or more of the constituent sugar atoms. The modified nucleic acids can also include one or more sugars that are in the L form, *e.g.* L- nucleosides.

[00252] The modified nucleosides and modified nucleotides described herein, which can be incorporated into a modified nucleic acid, can include a modified base, also called a nucleobase. Examples of nucleobases include, but are not limited to, adenine (A), guanine (G), cytosine (C), and uracil (U). These nucleobases can be modified or wholly replaced to provide modified residues that can be incorporated into modified nucleic acids. The nucleobase of the nucleotide can be independently selected from a purine, a pyrimidine, a purine analog, or pyrimidine analog. In some embodiments, the nucleobase can include, for example, naturally-occurring and synthetic derivatives of a base.

[00253] In embodiments employing a dual guide RNA, each of the crRNA and the tracr RNA can contain modifications. Such modifications may be at one or both ends of the crRNA and/or tracr RNA. In embodiments comprising sgRNA, one or more residues at one or both ends of the sgRNA may be chemically modified, and/or internal nucleosides may be modified, and/or the entire sgRNA may be chemically modified. Certain embodiments comprise a 5' end modification. Certain embodiments comprise a 3' end modification.

[00254] Modifications of 2'-O-methyl are encompassed.

[00255] Another chemical modification that has been shown to influence nucleotide sugar rings is halogen substitution. For example, 2'-fluoro (2'-F) substitution on nucleotide sugar rings can increase

oligonucleotide binding affinity and nuclease stability. Modifications of 2'-fluoro (2'-F) are encompassed.

[00256] Phosphorothioate (PS) linkage or bond refers to a bond where a sulfur is substituted for one nonbridging phosphate oxygen in a phosphodiester linkage, for example in the bonds between nucleotides bases. When phosphorothioates are used to generate oligonucleotides, the modified oligonucleotides may also be referred to as S-oligos.

[00257] Abasic nucleotides refer to those which lack nitrogenous bases.

[00258] Inverted bases refer to those with linkages that are inverted from the normal 5' to 3' linkage (i.e., either a 5' to 5' linkage or a 3' to 3' linkage).

[00259] An abasic nucleotide can be attached with an inverted linkage. For example, an abasic nucleotide may be attached to the terminal 5' nucleotide via a 5' to 5' linkage, or an abasic nucleotide may be attached to the terminal 3' nucleotide via a 3' to 3' linkage. An inverted abasic nucleotide at either the terminal 5' or 3' nucleotide may also be called an inverted abasic end cap.

[00260] In some embodiments, one or more of the first three, four, or five nucleotides at the 5' terminus, and one or more of the last three, four, or five nucleotides at the 3' terminus are modified. In some embodiments, the modification is a 2'-O-Me, 2'-F, inverted abasic nucleotide, PS bond, or other nucleotide modification well known in the art to increase stability and/or performance.

[00261] In some embodiments, the first four nucleotides at the 5' terminus, and the last four nucleotides at the 3' terminus are linked with phosphorothioate (PS) bonds.

[00262] In some embodiments, the first three nucleotides at the 5' terminus, and the last three nucleotides at the 3' terminus comprise a 2'-O-methyl (2'-O-Me) modified nucleotide. In some embodiments, the first three nucleotides at the 5' terminus, and the last three nucleotides at the 3' terminus comprise a 2'-fluoro (2'-F) modified nucleotide.

Ribonucleoprotein complex

[00263] In some embodiments, a composition is encompassed comprising: a) one or more guide RNAs comprising one or more guide sequences or one or more guide pairs from **Tables 1A-1F** and b) SluCas9. In some embodiments, the guide RNA together with a Cas9 is called a ribonucleoprotein complex (RNP).

[00264] In some embodiments, the disclosure provides for an RNP complex, wherein the guide RNA (*e.g.*, any of the guide RNAs disclosed herein) binds to or is capable of binding to a target sequence in the dystrophin gene.

[00265] In some embodiments, chimeric Cas9 (SaCas9 or SluCas9) nucleases are used, where one domain or region of the protein is replaced by a portion of a different protein. In some embodiments, a Cas9 nuclease domain may be replaced with a domain from a different nuclease such as Fok1. In some embodiments, a Cas9 nuclease may be a modified nuclease.

[00266] In some embodiments, the Cas9 is modified to contain only one functional nuclease domain. For example, the agent protein may be modified such that one of the nuclease domains is mutated or fully or partially deleted to reduce its nucleic acid cleavage activity.

[00267] In some embodiments, a conserved amino acid within a Cas9 protein nuclease domain is substituted to reduce or alter nuclease activity. In some embodiments, a Cas9 nuclease may comprise an amino acid substitution in the RuvC or RuvC-like nuclease domain. Exemplary amino acid substitutions in the RuvC or RuvC-like nuclease domain include D10A (based on the S. *pyogenes* Cas9 protein). *See*, *e.g.*, Zetsche et al. (2015) *Cell* Oct 22:163(3): 759-771. In some embodiments, the Cas9 nuclease may comprise an amino acid substitution in the HNH or HNH-like nuclease domain. Exemplary amino acid substitutions in the HNH or HNH-like nuclease domain include E762A, H840A, N863A, H983A, and D986A (based on the S. *pyogenes* Cas9 protein). *See*, *e.g.*, Zetsche et al. (2015). Further exemplary amino acid substitutions include D917A, E1006A, and D1255A (based on the *Francisella novicida* U112 Cpf1 (FnCpf1) sequence (UniProtKB - A0Q7Q2 (CPF1_FRATN)). Further exemplary amino acid substitutions include D10A and N580A (based on the *S. aureus* Cas9 protein). *See, e.g.*, Friedland et al., 2015, Genome Biol., 16:257.

[00268] In some embodiments, the Cas9 lacks cleavase activity. In some embodiments, the Cas9 comprises a dCas DNA-binding polypeptide. A dCas polypeptide has DNA-binding activity while essentially lacking catalytic (cleavase/nickase) activity. In some embodiments, the dCas polypeptide is a dCas9 polypeptide. In some embodiments, the Cas9 lacking cleavase activity or the dCas DNA-binding polypeptide is a version of a Cas nuclease (e.g., a Cas9 nuclease discussed above) in which its endonucleolytic active sites are inactivated, e.g., by one or more alterations (e.g., point mutations) in its catalytic domains. See, e.g., US 2014/0186958 A1; US 2015/0166980 A1.

[00269] In some embodiments, the Cas9 comprises one or more heterologous functional domains (e.g., is or comprises a fusion polypeptide).

[00270] In some embodiments, the heterologous functional domain may facilitate transport of the Cas9 into the nucleus of a cell. For example, the heterologous functional domain may be a nuclear localization signal (NLS). In some embodiments, the Cas9 may be fused with 1-10 NLS(s). In some embodiments, the Cas9 may be fused with 1-5 NLS(s). In some embodiments, the Cas9 may be fused with 1-3 NLS(s). In some embodiments, the Cas9 may be fused with one NLS. Where one NLS is used, the NLS may be attached at the N-terminus or the C-terminus of the Cas9 sequence, and may be directly fused/attached. In some embodiments, where more than one NLS is used, one or more NLS may be attached at the N-terminus and/or one or more NLS may be attached at the C-terminus. In some embodiments, one or more NLSs are directly attached to the Cas9. In some embodiments, one or more NLSs are attached to the Cas9 by means of a linker. In some embodiments, the linker is between 3-25 amino acids in length. In some embodiments, the linker is between 3-6 amino acids in length. In some embodiments, the linker comprises glycine and serine. In some embodiments, the linker comprises the sequence of GSVD (SEQ ID NO: 550) or GSGS (SEQ ID NO: 551). It may also

be inserted within the Cas9 sequence. In other embodiments, the Cas9 may be fused with more than one NLS. In some embodiments, the Cas9 may be fused with 2, 3, 4, or 5 NLSs. In some embodiments, the Cas9 may be fused with two NLSs. In certain circumstances, the two NLSs may be the same (*e.g.*, two SV40 NLSs) or different. In some embodiments, the Cas9 protein is fused with one or more SV40 NLSs. In some embodiments, the SV40 NLS comprises the amino acid sequence of SEQ ID NO: 713 (PKKKRKV). In some embodiments, the Cas9 protein (e.g., the SaCas9 or SluCas9 protein) is fused to one or more nucleoplasmin NLSs. In some embodiments, the Cas protein is fused to one or more c-myc NLSs. In some embodiments, the Cas protein is fused to one or more E1A NLSs. In some embodiments, the Cas protein is fused to one or more BP (bipartite) NLSs. In some embodiments, the nucleoplasmin NLS comprises the amino acid sequence of SEQ ID NO: 714 (KRPAATKKAGQAKKKK). In some embodiments, the Cas9 protein is fused with a c-Myc NLS. In some embodiments, the c-Myc NLS comprises the amino acid sequence of SEQ ID NO: 942 (PAAKKKKLD) and/or is encoded by the nucleic acid sequence of SEQ ID NO: 722 (CCGGCAGCTAAGAAAAAGAAACTGGAT). In some embodiments, the Cas9 is fused to two SV40 NLS sequences linked at the carboxy terminus. In some embodiments, the Cas9 may be fused with two NLSs, one linked at the N-terminus and one at the C-terminus. In some embodiments, the Cas9 may be fused with 3 NLSs. In some embodiments, the Cas9 may be fused with 3 NLSs, two linked at the N-terminus and one linked at the C-terminus. In some embodiments, the Cas9 may be fused with 3 NLSs, one linked at the N-terminus and two linked at the C-terminus. In some embodiments, the Cas9 may be fused with no NLS. In some embodiments, the Cas9 may be fused with one NLS. In some embodiments, the Cas9 may be fused with an NLS on the C-terminus and does not comprise an NLS fused on the N-terminus. In some embodiments, the Cas9 may be fused with an NLS on the N-terminus and does not comprise an NLS fused on the C-terminus. In some embodiments, the Cas9 protein is fused to an SV40 NLS and to a nucleoplasmin NLS. In some embodiments, the Cas9 protein is fused to an SV40 NLS and to a c-Myc NLS. In some embodiments, the SV40 NLS is fused to the C-terminus of the Cas9, while the nucleoplasmin NLS is fused to the N-terminus of the Cas9 protein. In some embodiments, the SV40 NLS is fused to the C-terminus of the Cas9, while the c-Myc NLS is fused to the N-terminus of the Cas9 protein. In some embodiments, the SV40 NLS is fused to the N-terminus of the Cas9, while the nucleoplasmin NLS is fused to the C-terminus of the Cas9 protein. In some embodiments, the SV40 NLS is fused to the N-terminus of the Cas9, while the c-Myc NLS is fused to the C-terminus of the Cas9 protein. In some embodiments, the SV40 NLS is fused to the Cas9 protein by means of a linker. In some embodiments, the SV40 NLS and linker is encoded by the nucleic acid sequence of SEQ ID NO: 723 (ATGATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCC). In some embodiments, the nucleoplasmin NLS is fused to the Cas9 protein by means of a linker. In some embodiments, the c-Myc NLS is fused to the Cas9 protein by means of a linker. In some embodiments, an additional domain may be: a) fused to the N- or C-terminus of the Cas protein (e.g.,

a Cas9 protein), b) fused to the N-terminus of an NLS fused to the N-terminus of a Cas protein, or c) fused to the C-terminus of an NLS fused to the C-terminus of a Cas protein. In some embodiments, an NLS is fused to the N- and/or C-terminus of the Cas protein by means of a linker. In some embodiments, an NLS is fused to the N-terminus of an N-terminally-fused NLS on a Cas protein by means of a linker, and/or an NLS is fused to the C-terminus of a C-terminally fused NLS on a Cas protein by means of a linker. In some embodiments, the linker is GSVD (SEQ ID NO: 550) or GSGS (SEQ ID NO: 551). In some embodiments, the Cas protein comprises a c-Myc NLS fused to the N-terminus of the Cas protein (or to an N-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises an SV40 NLS fused to the C-terminus of the Cas protein (or to a C-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises a nucleoplasmin NLS fused to the C-terminus of the Cas protein (or to a C-terminally-fused NLS on the Cas protein), optionally by means of a linker. In some embodiments, the Cas protein comprises: a) a c-Myc NLS fused to the N-terminus of the Cas protein, optionally by means of a linker, b) an SV40 NLS fused to the C-terminus of the Cas protein, optionally by means of a linker, and c) a nucleoplasmin NLS fused to the C-terminus of the SV40 NLS, optionally by means of a linker. In some embodiments, the Cas protein comprises: a) a c-Myc NLS fused to the N-terminus of the Cas protein, optionally by means of a linker, b) a nucleoplasmin NLS fused to the C-terminus of the Cas protein, optionally by means of a linker, and c) an SV40 NLS fused to the C-terminus of the nucleoplasmin NLS, optionally by means of a linker. In some embodiments, a c-myc NLS is fused to the N-terminus of the Cas9 and an SV40 NLS and/or nucleoplasmin NLS is fused to the C-terminus of the Cas9. In some embodiments, a c-myc NLS is fused to the N-terminus of the Cas9 (e.g., by means of a linker such as GSVD), an SV40 NLS is fused to the C-terminus of the Cas9 (e.g., by means of a linker such as GSGS), and a nucleoplasmin NLS is fused to the C-terminus of the SV-40 NLS (e.g., by means of a linker such as GSGS).

[00271] In some embodiments, the heterologous functional domain may be capable of modifying the intracellular half-life of the Cas9. In some embodiments, the half-life of the Cas9 may be increased. In some embodiments, the half-life of the Cas9 may be reduced. In some embodiments, the heterologous functional domain may be capable of increasing the stability of the Cas9. In some embodiments, the heterologous functional domain may be capable of reducing the stability of the Cas9. In some embodiments, the heterologous functional domain may act as a signal peptide for protein degradation. In some embodiments, the protein degradation may be mediated by proteolytic enzymes, such as, for example, proteasomes, lysosomal proteases, or calpain proteases. In some embodiments, the heterologous functional domain may comprise a PEST sequence. In some embodiments, the Cas9 may be modified by addition of ubiquitin or a polyubiquitin chain. In some embodiments, the ubiquitin may be a ubiquitin-like protein (UBL). Non-limiting examples of ubiquitin-like proteins include small ubiquitin-like modifier (SUMO), ubiquitin cross-reactive protein

(UCRP, also known as interferon-stimulated gene-15 (ISG15)), ubiquitin-related modifier-1 (URM1), neuronal-precursor-cell-expressed developmentally downregulated protein-8 (NEDD8, also called Rub1 in *S. cerevisiae*), human leukocyte antigen F-associated (FAT10), autophagy-8 (ATG8) and -12 (ATG12), Fau ubiquitin-like protein (FUB1), membrane-anchored UBL (MUB), ubiquitin fold-modifier-1 (UFM1), and ubiquitin-like protein-5 (UBL5).

[00272] In some embodiments, the heterologous functional domain may be a marker domain. Non-limiting examples of marker domains include fluorescent proteins, purification tags, epitope tags, and reporter gene sequences. In some embodiments, the marker domain may be a fluorescent protein. Non-limiting examples of suitable fluorescent proteins include green fluorescent proteins (*e.g.*, GFP, GFP-2, tagGFP, turboGFP, sfGFP, EGFP, Emerald, Azami Green, Monomeric Azami Green, CopGFP, AceGFP, ZsGreen1), yellow fluorescent proteins (*e.g.*, YFP, EYFP, Citrine, Venus, YPet, PhiYFP, ZsYellow1), blue fluorescent proteins (*e.g.*, EBFP, EBFP2, Azurite, mKalamal, GFPuv, Sapphire, T-sapphire,), cyan fluorescent proteins (*e.g.*, ECFP, Cerulean, CyPet, AmCyan1, Midoriishi-Cyan), red fluorescent proteins (*e.g.*, mKate, mKate2, mPlum, DsRed monomer, mCherry, mRFP1, DsRed-Express, DsRed2, DsRed-Monomer, HcRed-Tandem, HcRed1, AsRed2, eqFP611, mRasberry, mStrawberry, Jred), and orange fluorescent proteins (mOrange, mKO, Kusabira-Orange, Monomeric Kusabira-Orange, mTangerine, tdTomato) or any other suitable fluorescent protein. In other embodiments, the marker domain may be a purification tag and/or an epitope tag. Non-limiting exemplary tags include glutathione-S-transferase (GST), chitin binding protein (CBP), maltose binding protein (MBP), thioredoxin (TRX), poly(NANP), tandem affinity purification (TAP) tag, myc, AcV5, AU1, AU5, E, ECS, E2, FLAG, HA, nus, Softag 1, Softag 3, Strep, SBP, Glu-Glu, HSV, KT3, S, S1, T7, V5, VSV-G, 6xHis, 8xHis, biotin carboxyl carrier protein (BCCP), poly-His, and calmodulin. Non-limiting exemplary reporter genes include glutathione-S-transferase (GST), horseradish peroxidase (HRP), chloramphenicol acetyltransferase (CAT), beta-galactosidase, beta-glucuronidase, luciferase, or fluorescent proteins.

[00273] In additional embodiments, the heterologous functional domain may target the Cas9 to a specific organelle, cell type, tissue, or organ. In some embodiments, the heterologous functional domain may target the Cas9 to muscle.

[00274] In further embodiments, the heterologous functional domain may be an effector domain. When the Cas9 is directed to its target sequence, *e.g.*, when a Cas9 is directed to a target sequence by a guide RNA, the effector domain may modify or affect the target sequence. In some embodiments, the effector domain may be chosen from a nucleic acid binding domain or a nuclease domain (e.g., a non-Cas nuclease domain). In some embodiments, the heterologous functional domain is a nuclease, such as a FokI nuclease. See, e.g., US Pat. No. 9,023,649.

[00275] In some embodiments, any of the compositions disclosed herein comprising any of the guides and/or endonucleases disclosed herein is sterile and/or substantially pyrogen-free. In particular embodiments, any of the compositions disclosed herein comprise a pharmaceutically acceptable

carrier. The phrase "pharmaceutically or pharmacologically acceptable" refers to molecular entities and compositions that do not produce an adverse, allergic, or other untoward reaction when administered to an animal or human. As used herein "pharmaceutically acceptable carrier" includes any and all solvents (e.g., water), dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like that are physiologically compatible, including pharmaceutically acceptable cell culture media. Pharmaceutically acceptable carriers include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In some embodiments, the composition comprises a preservative to prevent the growth of microorganisms.

Determination of efficacy of guide RNAs

[00276] In some embodiments, the efficacy of a guide RNA is determined when delivered or expressed together with other components forming an RNP. In some embodiments, the guide RNA is expressed together with a SaCas9 or SluCas9 or sRGN. In some embodiments, the guide RNA is delivered to or expressed in a cell line that already stably expresses an SaCas9 or SluCas9. In some embodiments the guide RNA is delivered to a cell as part of an RNP. In some embodiments, the guide RNA is delivered to a cell along with a nucleic acid (e.g., mRNA) encoding SaCas9 or SluCas9.

[00277] In some embodiments, the efficacy of particular guide RNAs is determined based on *in vitro* models. In some embodiments, the *in vitro* model is a cell line.

[00278] In some embodiments, the efficacy of particular guide RNAs is determined across multiple *in vitro* cell models for a guide RNA selection process. In some embodiments, a cell line comparison of data with selected guide RNAs is performed. In some embodiments, cross screening in multiple cell models is performed.

[00279] In some embodiments, the efficacy of particular guide RNAs is determined based on *in vivo* models. In some embodiments, the *in vivo* model is a rodent model. In some embodiments, the rodent model is a mouse which expresses a mutated dystrophin gene. In some embodiments, the *in vivo* model is a non-human primate, for example cynomolgus monkey.

III. Methods of Gene Editing and Treating DMD

[00280] This disclosure provides methods for gene editing and treating Duchenne Muscular Dystrophy (DMD). In some embodiments, any of the compositions described herein may be administered to a subject in need thereof for use in excising all or a portion (e.g., less than about 400 nucleotides) of exon 53 of the dystrophin (DMD) gene and to treat DMD. In some embodiments, pairs of guide RNAs described herein, in any of the vector configurations described herein, may be administered to a subject in need thereof to excise all or a portion of exon 53 of the DMD gene, and treat DMD. In some embodiments, any of the compositions described herein may be administered to a subject in need thereof for use in treating DMD. In some embodiments, a nucleic acid molecule

comprising a first nucleic acid encoding one or more guide RNAs of **Tables 1A-1C** and a second nucleic acid encoding SluCas9 or another Cas protein (e.g., a sRGN) is administered to a subject to treat DMD. In some embodiments, a single nucleic acid molecule (which may be a vector, such as an AAV vector) comprising a first nucleic acid encoding one or more guide RNAs of **Tables 1A-1C** and a second nucleic acid encoding either SluCas9 is administered to a subject to treat DMD. In some embodiments, more than one nucleic acid molecules (which may be a vector, such as an AAV vectors) are administered to a subject to treat DMD, wherein a first nucleic acid encoding one or more guide RNAs of **Tables 1A-1C** and a second nucleic acid encoding either SluCas9 or another Cas protein (e.g., a sRGN) are together on one nucleic acid molecule or separated on different nucleic acid molecules.

[00281] In some embodiments, any of the compositions described herein is administered to a subject in need thereof to treat DMD.

[00282] In some embodiments, any of the compositions described herein is administered to a subject in need thereof to induce a double or single strand break in exon 53 of the dystrophin gene.

[00283] In some embodiments, any of the compositions described herein is administered to a subject in need thereof to delete all or a portion (e.g., excise a portion) of exon 53 of the dystrophin gene, such as all of exon 53 of the dystrophin gene, a portion of exon 53 flanking a splice acceptor site, or a portion of exon 53 flanking a splice donor site.

[00284] In some embodiments, a method of treating DMD is provided, the method comprising delivering to a cell any one of the compositions described herein, wherein the cell comprises a mutation in the dystrophin gene that is known to be associated with DMD.

[00285] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising one or more guide RNAs wherein each guide RNA comprises a guide sequence of **Tables 1A-1C**, or comprises a guide sequence comprising at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, or is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to guide sequence selected from **Tables 1A-1C**. In each instance, the composition may comprise a nucleic acid encoding the guide RNA(s). In some embodiments, a method for treating DMD is provided comprising administering a composition comprising one or more nucleic acid molecules encoding one or more guide RNAs, wherein each guide RNA comprises a guide sequence of **Tables 1A-1C**, or at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, or is at least 90% identical to guide sequence selected from **Tables 1A-1C**.

[00286] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising a guide RNA wherein the guide RNA comprises a guide sequence of **Tables 1A-1C**, or at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C,** or is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least

96%, at least 97%, at least 98%, at least 99%, or 100% identical to guide sequence of **Tables 1A-1C**. In each instance, the composition may comprise a nucleic acid encoding the guide RNA.

[00287] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising a guide RNA comprising no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, or is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C**. In each instance, the composition may comprise a nucleic acid encoding the guide RNA.

[00288] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising two or more guide RNAs wherein each guide RNA comprises a guide sequence of **Tables 1A-1C**, or at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, or is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to guide sequence selected from **Tables 1A-1C**. In each instance, the composition may comprise a nucleic acid encoding the guide RNA.

[00289] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising two or more guide RNAs wherein at least one of the two or more guide RNAs, optionally each guide RNA, comprises no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence of **Tables 1A-1C**, is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 contiguous nucleotides of a guide sequence selected from **Tables 1A-1C**. In each instance, the composition may comprise a nucleic acid encoding the guide RNA.

[00290] In some embodiments, a method for treating DMD is provided comprising administering a composition comprising a SluCas9 or sRGN protein or a nucleic acid encoding a SluCas9 or sRGN protein and a pair of guide RNAs, wherein the pair of guide RNAs comprise or consist of any one of the pairs of guide sequences of any one of **Tables 1D-1F**.

[00291] In some embodiments, a method for treating DMD is provided comprising administering a SluCas9 or sRGN protein or a nucleic acid encoding a SluCas9 or sRGN protein and a composition comprising one or more nucleic acid molecules encoding a pair of guide RNAs, wherein the pair of guide RNAs comprise or consist of one or more nucleic acid molecules 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% identical to any one of the pairs of guide sequences of any one of **Tables 1D-1F**.

[00292] In some embodiments, methods are provided for treating DMD, the method comprising delivering to a cell at least one nucleic acid molecule comprising a pair of guide RNAs comprising a first and second guide RNA, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 1-64; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 88-143.

[00293] In some embodiments, methods are provided for treating DMD, the method comprising delivering to a cell at least one nucleic acid molecule comprising a pair of guide RNAs comprising a first and second spacer sequence, wherein the pair of first and spacer sequences are 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% identical to the sequences of any one of the following pairs:

a. a pair of guide sequences selected from Table 1D; or
b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42; and

a nucleic acid encoding a SluCas9, wherein the nucleic acid encoding the SluCas9 may be on the same or different nucleic acid molecule as the pair of guide RNAs.

[00294] In some embodiments, methods are provided for treating DMD, the method comprising delivering to a cell at least one nucleic acid molecule comprising a pair of guide RNAs comprising a

first and second guide RNA, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 1-64; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 65-87. In some embodiments, methods are provided for treating DMD, the method comprising delivering to a cell at least one nucleic acid molecule comprising a pair of guide RNAs comprising a first and second guide RNA, wherein the first guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 65-87; and the second guide RNA comprises a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical any one of SEQ ID NOs: 88-143.

[00295] In some embodiments, methods are provided for treating DMD, the method comprising delivering to a cell at least one nucleic acid molecule comprising a pair of guide RNAs comprising a first and second spacer sequence, wherein the pair of first and spacer sequences are 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% identical to the sequences of any one of the following pairs:

a. a pair of guide sequences selected from Table 1E or Table 1F.
b. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

c. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81; and

a nucleic acid encoding a SluCas9, wherein the nucleic acid encoding the SluCas9 may be on the same or different nucleic acid molecule as the pair of guide RNAs.

[00296] Also provided are methods of excising a fragment of a DMD gene, comprising delivering to a cell a composition comprising (a) a pair of guide RNA molecules or a nucleic acid encoding a pair of RNA molecules, wherein the first guide RNA targets a region upstream of a splice acceptor site or a splice donor site in a DMD gene and wherein the second guide RNA targets a region downstream of a splice acceptor site or a splice donor site in the DMD gene, and (b) an endonuclease or a nucleic acid encoding an endonuclease. In some embodiments, the endonuclease is a Staphylococcus lugdunensis Cas9 (SluCas9). In one particular embodiment, the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an exon of the DMD gene. In another particular embodiment, the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an intron of the DMD gene. In another particular embodiment, the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an exon of the DMD gene. In another particular embodiment, the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an intron of the DMD gene. In some embodiments, the pair of guide RNAs and the endonuclease excise a fragment of the DMD gene comprising the splice acceptor site or the splice donor site, wherein the fragment is between 3 and 400 nucleotides in length. In some embodiments, the excised fragment of the DMD gene comprises a splice acceptor site. In other embodiments, the excised fragment of the DMD gene comprises a splice donor site. In some embodiments, the excised fragment is between 3-200, 3-150, 3-100, 3-50, 30-250, 30-200, 30-150, 30-100, 30-50, 75-250, 75-200, 75-150, 75-100, 100-250, 100-200, 100-150, 150-250, 150-200, 200-250, 250-400, 300-400, or 350-400 nucleotides in length.

[00297] In some embodiments, the subject is a mammal. In some embodiments, the subject is human.

[00298] For treatment of a subject (e.g., a human), any of the compositions disclosed herein may be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective. The compositions may be readily administered in a variety of dosage forms, such as injectable solutions. For parenteral administration in an aqueous solution, for example, the solution will generally be suitably buffered and the liquid diluent first rendered isotonic with, for example, sufficient saline or glucose. Such aqueous solutions may be used, for example, for intravenous, intramuscular, subcutaneous, and/or intraperitoneal administration.

Combination Therapy

[00299] In some embodiments, the invention comprises combination therapies comprising any of the methods or uses described herein together with an additional therapy suitable for ameliorating DMD.

Delivery of Guide RNA Compositions

[00300] The methods and uses disclosed herein may use any suitable approach for delivering the guide RNAs and compositions described herein. Exemplary delivery approaches include vectors, such as viral vectors; lipid nanoparticles (LNPs); liposomes; transfection; and electroporation. In some embodiments, vectors, such as viral vectors, LNPs, or liposomes associated with the single-vector guide RNAs/Cas9's disclosed herein are for use in preparing a medicament for treating DMD.

[00301] Lipid nanoparticles (LNPs) are a known means for delivery of nucleotide and protein cargo, and may be used for delivery of the guide RNAs, compositions, or pharmaceutical formulations disclosed herein. In some embodiments, the LNPs deliver nucleic acid, protein, or nucleic acid together with protein.

[00302] Electroporation is a well-known means for delivery of cargo, and any electroporation methodology may be used for delivering the single vectors disclosed herein.

[00303] In some embodiments, the invention comprises a method for delivering any one of the single vectors disclosed herein to an ex vivo cell, wherein the guide RNA is encoded by a vector, associated with an LNP or a liposome, or in aqueous solution. In some embodiments, the guide RNA/LNP, guide RNA/liposome, or guide RNA is also associated with a Cas9 (such as a SluCas9) or sequence encoding Cas9 (e.g., in the same vector (such as the same viral vector, LNP, or liposome), or solution).

[00304] In some embodiments, the disclosure provides for methods of using any of the guides, endonucleases, cells, or compositions disclosed herein in research methods. For example, any of the guides or endonucleases disclosed herein may be used alone or in combination in experiments under

various parameters (e.g., temperatures, pH, types of cells) or combined with other reagents to evaluate the activity of the guides and/or endonucleases.

EXAMPLES

[00305] The following examples are provided to illustrate certain disclosed embodiments and are not to be construed as limiting the scope of this disclosure in any way.

Example 1: Exemplary DMD sgRNAs

[00306] Guide RNAs comprising the guide sequences shown in **Tables 1A-1C** (SEQ ID NOs: 1-143) are prepared according to standard methods in a single guide (sgRNA) format. A single AAV vector, or two AAV vectors, are prepared that express one or more of the guide RNAs and a SluCas9. The AAV vector is administered to cells *in vitro* to assess the ability of the AAV to express the one or more guide RNAs and SluCas9, edit the targeted region of exon 53, and thereby treat DMD.

Example 2: Exemplary DMD sgRNA pairs

[00307] Guide RNAs comprising the guide sequences shown in **Tables 1A-1C** (SEQ ID NOs: 1-143) are prepared according to standard methods in a single guide (sgRNA) format. A single AAV vector, or two AAV vectors, are prepared that express one or more guide RNA pairs selected from **Tables 1D-1F** (see, **Figure 4**), and a SluCas9. The AAV vector is administered to cells *in vitro* to assess the ability of the AAV to express the one or more guide RNA pairs and SluCas9, excise the targeted region of exon 53, and thereby treat DMD.

Example 3: Evaluation of sgRNA Pairs

[00308] Immortalized human skeletal muscle myoblast cells (iHsMM) comprising either the full DMD gene sequence (WT13) or with the DMD exon 52 deleted (ΔE52) were used for *in vitro* evaluation of sgRNA pairs. Cells were transfected with SluCas9 mRNA (or in some cases sRGN3.3 mRNA) along with synthetic sgRNAs using the Lipofectamine MessengerMAX reagent.

[00309] For qPCR, cells were seeded into 96-well plates after transfection and were harvested after 72 hours. Genomic DNA (gDNA) was extracted from each sample using the MagMAX DNA Ultra 2.0 kit, followed by qPCR analysis. qPCR was performed on each gDNA sample separately with an "Editing" primer pair that amplified a portion of exon 53 and a "Control" primer pair that amplified a portion of intron 52. The differences in the cycle number of the "Editing" pair and the "Control" pair was used to calculate the percentage of exon 53 deletion for each gDNA sample.

[00310] For dystrophin/Jess protein analyses, cells were seeded into 12-well plates coated with Matrigel after transfection. After 48 hours, cells were then maintained in Myocult media for 12 days to induce differentiation into myotubes and to induce expression of dystrophin. Cells were then

harvested and lysed using MSD buffer and the protein concentration was measured using Pierce BCA (ThermoFisher, 23227) assay according to the manufacturer's protocol. Next, samples were prepared for Jess Separation module ("Jess"), according to the manufacturer's protocol. Primary antibody (ab154168, Abcam) was used for dystrophin protein detection at 1:250 dilution, and secondary antibody (ProteinSimple, 042-206) and Total Protein Detection Module DM-TP01 were used for normalizing the samples during analysis. Samples were run using 24-well cartridges and 66-440 kDa kits for Jess analysis. The data were acquired using the capillary gel electrophoresis system ProteinSimple "Jess" and analyzed using Compass for Simple Western software.

[00311] **Figure 1** shows that tested guide pairs targeting intron 52 and intron 53 of the dystrophin gene result in different excision fragment sizes, e.g., from about 500-600 base pairs in length to about 200-300 bp in length. **Figure 2** shows the editing frequencies of selected SluCas9 guide pairs targeting intron 52 and intron 53 of the dystrophin gene, for excision of exon 53 in the immortalized HsMM ΔE52 cells. Editing frequencies for the experimental pairs ranged from approximately 15% to more than 40%. **Figures 3A and 3B** show dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected SluCas9 sgRNA pairs. **Figures 3A and 3B** detection of dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected SluCas9 sgRNA pairs that result in either precise reframing deletion or deletion of the entire exon 53 of the dystrophin gene, using the Jess protein assay (**Figure 3A**) or qPCR (**Figure 3B**). All guide pairs tested restored dystrophin levels to 30-50% of control levels on day 12. Each bar in **Figure 3B** represents a sgRNA pair and the bar height depicts normalized dystrophin protein signal of the sample as a percentage of normalized dystrophin expression in untreated WT13 cells. **Figures 5 and 6** show dystrophin restoration in immortalized HsMM ΔE52 cells treated with selected SluCas9 or sRGN sgRNA pairs that result in either precise reframing deletion, deletion of the entire exon 53 of the dystrophin gene, or skipping of exon 53. Each bar represents a sgRNA pair or triplet and the bar height depicts dystrophin protein signal normalized to the total protein signal, as determined by Jess protein assay.

What is claimed is:

1. A composition comprising one or more guide RNAs or a nucleic acid encoding one or more guide RNAs, wherein the one or more guide RNAs comprise i) a guide sequence of any one of the guide sequences shown in **Tables 1A or 1C**; ii) at least 16, 17, 18, 19, or 20 contiguous nucleotides of any one of the guide sequences shown in **Tables 1A or 1C**; iii) a guide sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of the guide sequences shown in **Tables 1A or 1C**; or iv) a pair of guide RNAs comprising any of the guide sequence pairs shown in **Table 1D**, optionally further comprising a *Staphylococcus lugdunensis* Cas9 (SluCas9) or a nucleic acid encoding a SluCas9.

2. A composition comprising a first guide RNA and a second guide RNA, wherein
    a. the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and
    b. the second guide RNA is selected from any one of SEQ ID NOs: 88-143.

3. A composition comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprise or consist of a first and a second guide sequence selected from any of the following pairs of first and second guide sequences:
    a. SEQ ID NOs: 88 and 1; 88 and 2; 88 and 3; 88 and 4; 88 and 5; 88 and 6; 88 and 7; 88 and 8; 88 and 9; 88 and 10; 88 and 11; 88 and 12; 88 and 13; 88 and 14; 88 and 15; 88 and 16; 88 and 17; 88 and 18; 88 and 19; 88 and 20; 88 and 21; 88 and 22; 88 and 23; 88 and 24; 88 and 25; 88 and 26; 88 and 27; 88 and 28; 88 and 29; 88 and 30; 88 and 31; 88 and 32; 88 and 33; 88 and 34; 88 and 35; 88 and 36; 88 and 37; 88 and 38; 88 and 39; 88 and 40; 88 and 41; 88 and 42; 88 and 43; 88 and 44; 88 and 45; 88 and 46; 88 and 47; 88 and 48; 88 and 49; 88 and 50; 88 and 51; 88 and 52; 88 and 53; 88 and 54; 88 and 55; 88 and 56; 88 and 57; 88 and 58; 88 and 59; 88 and 60; 88 and 61; 88 and 62; 88 and 63; 88 and 64; 89 and 1; 89 and 2; 89 and 3; 89 and 4; 89 and 5; 89 and 6; 89 and 7; 89 and 8; 89 and 9; 89 and 10; 89 and 11; 89 and 12; 89 and 13; 89 and 14; 89 and 15; 89 and 16; 89 and 17; 89 and 18; 89 and 19; 89 and 20; 89 and 21; 89 and 22; 89 and 23; 89 and 24; 89 and 25; 89 and 26; 89 and 27; 89 and 28; 89 and 29; 89 and 30; 89 and 31; 89 and 32; 89 and 33; 89 and 34; 89 and 35; 89 and 36; 89 and 37; 89 and 38; 89 and 39; 89 and 40; 89 and 41; 89 and 42; 89 and 43; 89 and 44; 89 and 45; 89 and 46; 89 and 47; 89 and 48; 89 and 49; 89 and 50; 89 and 51; 89 and 52; 89 and 53; 89 and 54; 89 and 55; 89 and 56; 89 and 57; 89 and 58; 89 and 59; 89 and 60; 89 and 61; 89 and 62; 89 and 63; 89 and 64; 90 and 1; 90 and 2; 90

and 3; 90 and 4; 90 and 5; 90 and 6; 90 and 7; 90 and 8; 90 and 9; 90 and 10; 90 and 11; 90 and 12; 90 and 13; 90 and 14; 90 and 15; 90 and 16; 90 and 17; 90 and 18; 90 and 19; 90 and 20; 90 and 21; 90 and 22; 90 and 23; 90 and 24; 90 and 25; 90 and 26; 90 and 27; 90 and 28; 90 and 29; 90 and 30; 90 and 31; 90 and 32; 90 and 33; 90 and 34; 90 and 35; 90 and 36; 90 and 37; 90 and 38; 90 and 39; 90 and 40; 90 and 41; 90 and 42; 90 and 43; 90 and 44; 90 and 45; 90 and 46; 90 and 47; 90 and 48; 90 and 49; 90 and 50; 90 and 51; 90 and 52; 90 and 53; 90 and 54; 90 and 55; 90 and 56; 90 and 57; 90 and 58; 90 and 59; 90 and 60; 90 and 61; 90 and 62; 90 and 63; 90 and 64; 91 and 1; 91 and 2; 91 and 3; 91 and 4; 91 and 5; 91 and 6; 91 and 7; 91 and 8; 91 and 9; 91 and 10; 91 and 11; 91 and 12; 91 and 13; 91 and 14; 91 and 15; 91 and 16; 91 and 17; 91 and 18; 91 and 19; 91 and 20; 91 and 21; 91 and 22; 91 and 23; 91 and 24; 91 and 25; 91 and 26; 91 and 27; 91 and 28; 91 and 29; 91 and 30; 91 and 31; 91 and 32; 91 and 33; 91 and 34; 91 and 35; 91 and 36; 91 and 37; 91 and 38; 91 and 39; 91 and 40; 91 and 41; 91 and 42; 91 and 43; 91 and 44; 91 and 45; 91 and 46; 91 and 47; 91 and 48; 91 and 49; 91 and 50; 91 and 51; 91 and 52; 91 and 53; 91 and 54; 91 and 55; 91 and 56; 91 and 57; 91 and 58; 91 and 59; 91 and 60; 91 and 61; 91 and 62; 91 and 63; 91 and 64; 92 and 1; 92 and 2; 92 and 3; 92 and 4; 92 and 5; 92 and 6; 92 and 7; 92 and 8; 92 and 9; 92 and 10; 92 and 11; 92 and 12; 92 and 13; 92 and 14; 92 and 15; 92 and 16; 92 and 17; 92 and 18; 92 and 19; 92 and 20; 92 and 21; 92 and 22; 92 and 23; 92 and 24; 92 and 25; 92 and 26; 92 and 27; 92 and 28; 92 and 29; 92 and 30; 92 and 31; 92 and 32; 92 and 33; 92 and 34; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 92 and 43; 92 and 44; 92 and 45; 92 and 46; 92 and 47; 92 and 48; 92 and 49; 92 and 50; 92 and 51; 92 and 52; 92 and 53; 92 and 54; 92 and 55; 92 and 56; 92 and 57; 92 and 58; 92 and 59; 92 and 60; 92 and 61; 92 and 62; 92 and 63; 92 and 64; 93 and 1; 93 and 2; 93 and 3; 93 and 4; 93 and 5; 93 and 6; 93 and 7; 93 and 8; 93 and 9; 93 and 10; 93 and 11; 93 and 12; 93 and 13; 93 and 14; 93 and 15; 93 and 16; 93 and 17; 93 and 18; 93 and 19; 93 and 20; 93 and 21; 93 and 22; 93 and 23; 93 and 24; 93 and 25; 93 and 26; 93 and 27; 93 and 28; 93 and 29; 93 and 30; 93 and 31; 93 and 32; 93 and 33; 93 and 34; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; 93 and 42; 93 and 43; 93 and 44; 93 and 45; 93 and 46; 93 and 47; 93 and 48; 93 and 49; 93 and 50; 93 and 51; 93 and 52; 93 and 53; 93 and 54; 93 and 55; 93 and 56; 93 and 57; 93 and 58; 93 and 59; 93 and 60; 93 and 61; 93 and 62; 93 and 63; 93 and 64; 94 and 1; 94 and 2; 94 and 3; 94 and 4; 94 and 5; 94 and 6; 94 and 7; 94 and 8; 94 and 9; 94 and 10; 94 and 11; 94 and 12; 94 and 13; 94 and 14; 94 and 15; 94 and 16; 94 and 17; 94 and 18; 94 and 19; 94 and 20; 94 and 21; 94 and 22; 94 and 23; 94 and 24; 94 and 25; 94 and 26; 94 and 27; 94 and 28; 94 and 29; 94 and 30; 94 and 31; 94 and 32; 94 and 33; 94 and

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b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

4. A composition comprising one or more nucleic acid molecules encoding:
    a. a *Staphylococcus lugdunensis* Cas9 (SluCas9); and
    b. at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first guide sequence and a second guide sequence selected from any of the pairs of guide sequences shown in Table 1D.

5. A composition comprising:
    a. a single nucleic acid molecule comprising:
        i. a nucleic acid encoding *Staphylococcus lugdunensis* (SluCas9) and at least one, at least two, or at least three guide RNAs; or
        ii. a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
        iii. a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs;

    wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Table 1D**, and further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence; or
    b. two nucleic acid molecules comprising:
        i. a first nucleic acid encoding SluCas9; and

        a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:
            1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
            2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
            3. from one to six guide RNAs;
        ii. a first nucleic acid encoding SluCas9 and
            1. at least one, at least two, or at least three guide RNAs; or
            2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
            3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

iii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and
a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

iv. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and
a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A or 1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from the pairs of guide sequences shown in **Table 1D**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

6. A composition comprising a single nucleic acid molecule encoding at least one pair of guide RNAs and a Cas9, wherein the single nucleic acid molecule comprises:
   a. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences shown in Table 1D; and a second nucleic acid encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9); or
   b. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and

16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42; and a second nucleic acid encoding a SluCas9.

7. A composition comprising a first and a second nucleic acid molecule, wherein the first nucleic acid molecule encodes a *Staphylococcus lugdunensis* (SluCas9) endonuclease and optionally a first or a first and second guide RNA, and the second nucleic acid molecule comprises a first or a first and second guide RNA, wherein the first guide RNA comprises a first guide sequence and the second guide RNA comprises a second guide sequence selected from any one the following pairs of first and second guide sequences:
   a. any one of the pairs of first and second guide sequences shown in Table 1D; or
   b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115 and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and

58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

8. A composition comprising one or more nucleic acid molecules encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9) and at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide RNA, and wherein the first guide RNA targets a sequence in intron 53 of a DMD gene and the second guide RNA targets a sequence in intron 52 of the DMD gene.

9. The composition of any one of claims 1-8, comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising at least a portion of exon 53 of the DMD gene.

10. The composition of any one of claims 1-9, comprising at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first and a second guide sequence selected from any one of the following pairs of first and second guide sequences:
    a. any one of the pairs of first and second guide sequences shown in Table 1D; or
    b. SEQ ID NOs: 113 and 1; 113 and 2; 113 and 3; 113 and 5; 113 and 6; 113 and 28; 113 and 35; 113 and 36; 113 and 37; 113 and 38; 113 and 39; 113 and 40; 113 and 41; 113 and 42; 113 and 9; 113 and 44; 113 and 10; 113 and 45; 113 and 46; 113 and 11; 113 and 47; 113 and 12; 113 and 48; 113 and 13; 113 and 53; 113 and 54; 113 and 55; 113 and 56; 113 and 14; 113 and 15; 113 and 16; 113 and 17; 113 and 57; 113 and 18; 113 and 58; 113 and 19; 113 and 20; 113 and 59; 113 and 23; 113 and 24; 113 and 60; 113 and 62; 113 and 63; 113 and 64; 113 and 25; 113 and 26; 115 and 1; 115 and 2; 115 and 3; 115 and 5; 115 and 6; 115 and 28; 115 and 35; 115 and 36; 115 and 37; 115 and 38; 115 and 39; 115 and 40; 115 and 41; 115 and 42; 115 and 9; 115 and 44; 115 and 10; 115 and 45; 115 and 46; 115 and 11; 115 and 47; 115

and 12; 115 and 48; 115 and 13; 115 and 53; 115 and 54; 115 and 55; 115 and 56; 115 and 14; 115 and 15; 115 and 16; 115 and 17; 115 and 57; 115 and 18; 115 and 58; 115 and 19; 115 and 20; 115 and 59; 115 and 23; 115 and 24; 115 and 60; 115 and 62; 115 and 63; 115 and 64; 115 and 25; 115 and 26; 116 and 1; 116 and 2; 116 and 3; 116 and 5; 117 and 1; 117 and 2; 117 and 3; 117 and 5; 118 and 1; 118 and 2; 118 and 3; 118 and 5; 120 and 1; 120 and 2; 120 and 3; 120 and 5; 120 and 6; 121 and 1; 121 and 2; 121 and 3; 121 and 5; 121 and 6; 122 and 1; 122 and 2; 122 and 3; 122 and 5; 122 and 6; 122 and 28; 92 and 1; 92 and 2; 92 and 3; 92 and 5; 92 and 6; 92 and 28; 92 and 35; 92 and 36; 92 and 37; 92 and 38; 92 and 39; 92 and 40; 92 and 41; 92 and 42; 93 and 1; 93 and 2; 93 and 3; 93 and 5; 93 and 6; 93 and 28; 93 and 35; 93 and 36; 93 and 37; 93 and 38; 93 and 39; 93 and 40; 93 and 41; or 93 and 42.

11. The composition of any one of claims 1-10, wherein:
    i) the first guide RNA comprises the sequence of SEQ ID NO: 115 and the second guide RNA comprises the sequence of SEQ ID NO: 2;
    ii) the first guide RNA comprises the sequence of SEQ ID NO: 115, and the second guide RNA comprises the sequence of SEQ ID NO: 3; or
    iii) the first guide RNA comprises the sequence of SEQ ID NO: 113, and the second guide RNA comprises the sequence of SEQ ID NO: 3.

12. A composition comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of exon 53 of the DMD gene, and wherein
    i. the fragment comprises a splice donor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice donor site, and a second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice donor site; or
    ii. the fragment comprises a splice acceptor site, a first guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases upstream of the splice acceptor site, and a second guide RNA of the at least one pair of guide RNAs targets a sequence within 200 nucleobases downstream of the splice acceptor site.

13. The composition of claim 12, wherein
    i. the first guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice acceptor site, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice acceptor site; or

ii. the first guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases upstream of the splice donor site, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within 190, 180, 170, 160, 150, 140, 130, 120, 110, or 100 nucleobases downstream of the splice donor site.

14. The composition of claim 12 or claim 13, wherein
    a. the fragment of the DMD gene comprises a splice donor site and further comprises a portion of intron 53 and an adjoining portion of exon 53 of the DMD gene; or
    b. the fragment of the DMD gene comprises a splice acceptor site and further comprises a portion of exon 53 and an adjoining portion of intron 52 of the DMD gene.

15. The composition of any one of claims 12-14, wherein
    a. the first guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 1-200 of SEQ ID NO: 144, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 201-400 of SEQ ID NO: 144; or
    b. the first guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 1-200 of SEQ ID NO: 145, and the second guide RNA of the at least one pair of guide RNAs targets a sequence within nucleotides 201-400 of SEQ ID NO: 145.

16. The composition of any one of claims 12-15, further comprising a SluCas9 or a nucleic acid encoding a SluCas9.

17. A composition comprising one or more guide RNAs or a nucleic acid encoding one or more guide RNAs, wherein the one or more guide RNAs comprise i) a guide sequence of any one of the guide sequences shown in **Tables 1A-1C**; ii) at least 16, 17, 18, 19, or 20 contiguous nucleotides of a guide sequence of any one of the guide sequences shown in **Tables 1A-1C**; iii) a guide sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to any one of the guide sequences shown in **Tables 1A-1C**; or iv) a pair of guide RNAs comprising any two of the guide sequence pairs shown in **Tables 1E or 1F**; optionally further comprising a SluCas9 or a nucleic acid encoding a SluCas9.

18. A composition comprising a first guide RNA and a second guide RNA, wherein

a. the first guide RNA is selected from any one of SEQ ID NOs: 1-64; and the second guide RNA is selected from any one of SEQ ID NOs: 65-87; or
b. the first guide RNA is selected from any one of SEQ ID NOs: 65-87; and the second guide RNA is selected from any one of SEQ ID NOs: 88-143.

19. A composition comprising at least one pair of guide RNAs or a nucleic acid encoding at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprise or consist of a first and a second guide sequence selected from any of the following pairs of first and second guide sequences:
    a. SEQ ID NOs: 1 and 65; 1 and 66; 1 and 67; 1 and 68; 1 and 69; 1 and 70; 1 and 71; 1 and 72; 1 and 73; 1 and 74; 1 and 75; 1 and 76; 1 and 77; 1 and 78; 1 and 79; 1 and 80; 1 and 81; 1 and 82; 1 and 83; 1 and 84; 1 and 85; 1 and 86; 1 and 87; 2 and 65; 2 and 66; 2 and 67; 2 and 68; 2 and 69; 2 and 70; 2 and 71; 2 and 72; 2 and 73; 2 and 74; 2 and 75; 2 and 76; 2 and 77; 2 and 78; 2 and 79; 2 and 80; 2 and 81; 2 and 82; 2 and 83; 2 and 84; 2 and 85; 2 and 86; 2 and 87; 3 and 65; 3 and 66; 3 and 67; 3 and 68; 3 and 69; 3 and 70; 3 and 71; 3 and 72; 3 and 73; 3 and 74; 3 and 75; 3 and 76; 3 and 77; 3 and 78; 3 and 79; 3 and 80; 3 and 81; 3 and 82; 3 and 83; 3 and 84; 3 and 85; 3 and 86; 3 and 87; 4 and 65; 4 and 66; 4 and 67; 4 and 68; 4 and 69; 4 and 70; 4 and 71; 4 and 72; 4 and 73; 4 and 74; 4 and 75; 4 and 76; 4 and 77; 4 and 78; 4 and 79; 4 and 80; 4 and 81; 4 and 82; 4 and 83; 4 and 84; 4 and 85; 4 and 86; 4 and 87; 5 and 65; 5 and 66; 5 and 67; 5 and 68; 5 and 69; 5 and 70; 5 and 71; 5 and 72; 5 and 73; 5 and 74; 5 and 75; 5 and 76; 5 and 77; 5 and 78; 5 and 79; 5 and 80; 5 and 81; 5 and 82; 5 and 83; 5 and 84; 5 and 85; 5 and 86; 5 and 87; 6 and 65; 6 and 66; 6 and 67; 6 and 68; 6 and 69; 6 and 70; 6 and 71; 6 and 72; 6 and 73; 6 and 74; 6 and 75; 6 and 76; 6 and 77; 6 and 78; 6 and 79; 6 and 80; 6 and 81; 6 and 82; 6 and 83; 6 and 84; 6 and 85; 6 and 86; 6 and 87; 7 and 65; 7 and 66; 7 and 67; 7 and 68; 7 and 69; 7 and 70; 7 and 71; 7 and 72; 7 and 73; 7 and 74; 7 and 75; 7 and 76; 7 and 77; 7 and 78; 7 and 79; 7 and 80; 7 and 81; 7 and 82; 7 and 83; 7 and 84; 7 and 85; 7 and 86; 7 and 87; 8 and 65; 8 and 66; 8 and 67; 8 and 68; 8 and 69; 8 and 70; 8 and 71; 8 and 72; 8 and 73; 8 and 74; 8 and 75; 8 and 76; 8 and 77; 8 and 78; 8 and 79; 8 and 80; 8 and 81; 8 and 82; 8 and 83; 8 and 84; 8 and 85; 8 and 86; 8 and 87; 9 and 65; 9 and 66; 9 and 67; 9 and 68; 9 and 69; 9 and 70; 9 and 71; 9 and 72; 9 and 73; 9 and 74; 9 and 75; 9 and 76; 9 and 77; 9 and 78; 9 and 79; 9 and 80; 9 and 81; 9 and 82; 9 and 83; 9 and 84; 9 and 85; 9 and 86; 9 and 87; 10 and 65; 10 and 66; 10 and 67; 10 and 68; 10 and 69; 10 and 70; 10 and 71; 10 and 72; 10 and 73; 10 and 74; 10 and 75; 10 and 76; 10 and 77; 10 and 78; 10 and 79; 10 and 80; 10 and 81; 10 and 82; 10 and 83; 10 and 84; 10 and 85; 10 and 86; 10 and 87; 11 and 65; 11 and 66; 11 and 67; 11 and

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79; 117 and 80; 117 and 81; 117 and 82; 117 and 83; 117 and 84; 117 and 85; 117 and 86; 117 and 87; 118 and 65; 118 and 66; 118 and 67; 118 and 68; 118 and 69; 118 and 70; 118 and 71; 118 and 72; 118 and 73; 118 and 74; 118 and 75; 118 and 76; 118 and 77; 118 and 78; 118 and 79; 118 and 80; 118 and 81; 118 and 82; 118 and 83; 118 and 84; 118 and 85; 118 and 86; 118 and 87; 119 and 65; 119 and 66; 119 and 67; 119 and 68; 119 and 69; 119 and 70; 119 and 71; 119 and 72; 119 and 73; 119 and 74; 119 and 75; 119 and 76; 119 and 77; 119 and 78; 119 and 79; 119 and 80; 119 and 81; 119 and 82; 119 and 83; 119 and 84; 119 and 85; 119 and 86; 119 and 87; 120 and 65; 120 and 66; 120 and 67; 120 and 68; 120 and 69; 120 and 70; 120 and 71; 120 and 72; 120 and 73; 120 and 74; 120 and 75; 120 and 76; 120 and 77; 120 and 78; 120 and 79; 120 and 80; 120 and 81; 120 and 82; 120 and 83; 120 and 84; 120 and 85; 120 and 86; 120 and 87; 121 and 65; 121 and 66; 121 and 67; 121 and 68; 121 and 69; 121 and 70; 121 and 71; 121 and 72; 121 and 73; 121 and 74; 121 and 75; 121 and 76; 121 and 77; 121 and 78; 121 and 79; 121 and 80; 121 and 81; 121 and 82; 121 and 83; 121 and 84; 121 and 85; 121 and 86; 121 and 87; 122 and 65; 122 and 66; 122 and 67; 122 and 68; 122 and 69; 122 and 70; 122 and 71; 122 and 72; 122 and 73; 122 and 74; 122 and 75; 122 and 76; 122 and 77; 122 and 78; 122 and 79; 122 and 80; 122 and 81; 122 and 82; 122 and 83; 122 and 84; 122 and 85; 122 and 86; 122 and 87; 123 and 65; 123 and 66; 123 and 67; 123 and 68; 123 and 69; 123 and 70; 123 and 71; 123 and 72; 123 and 73; 123 and 74; 123 and 75; 123 and 76; 123 and 77; 123 and 78; 123 and 79; 123 and 80; 123 and 81; 123 and 82; 123 and 83; 123 and 84; 123 and 85; 123 and 86; 123 and 87; 124 and 65; 124 and 66; 124 and 67; 124 and 68; 124 and 69; 124 and 70; 124 and 71; 124 and 72; 124 and 73; 124 and 74; 124 and 75; 124 and 76; 124 and 77; 124 and 78; 124 and 79; 124 and 80; 124 and 81; 124 and 82; 124 and 83; 124 and 84; 124 and 85; 124 and 86; 124 and 87; 125 and 65; 125 and 66; 125 and 67; 125 and 68; 125 and 69; 125 and 70; 125 and 71; 125 and 72; 125 and 73; 125 and 74; 125 and 75; 125 and 76; 125 and 77; 125 and 78; 125 and 79; 125 and 80; 125 and 81; 125 and 82; 125 and 83; 125 and 84; 125 and 85; 125 and 86; 125 and 87; 126 and 65; 126 and 66; 126 and 67; 126 and 68; 126 and 69; 126 and 70; 126 and 71; 126 and 72; 126 and 73; 126 and 74; 126 and 75; 126 and 76; 126 and 77; 126 and 78; 126 and 79; 126 and 80; 126 and 81; 126 and 82; 126 and 83; 126 and 84; 126 and 85; 126 and 86; 126 and 87; 127 and 65; 127 and 66; 127 and 67; 127 and 68; 127 and 69; 127 and 70; 127 and 71; 127 and 72; 127 and 73; 127 and 74; 127 and 75; 127 and 76; 127 and 77; 127 and 78; 127 and 79; 127 and 80; 127 and 81; 127 and 82; 127 and 83; 127 and 84; 127 and 85; 127 and 86; 127 and 87; 128 and 65; 128 and 66; 128 and 67; 128 and 68; 128 and 69; 128 and 70; 128 and 71; 128 and 72; 128

and 73; 128 and 74; 128 and 75; 128 and 76; 128 and 77; 128 and 78; 128 and 79; 128 and 80; 128 and 81; 128 and 82; 128 and 83; 128 and 84; 128 and 85; 128 and 86; 128 and 87; 129 and 65; 129 and 66; 129 and 67; 129 and 68; 129 and 69; 129 and 70; 129 and 71; 129 and 72; 129 and 73; 129 and 74; 129 and 75; 129 and 76; 129 and 77; 129 and 78; 129 and 79; 129 and 80; 129 and 81; 129 and 82; 129 and 83; 129 and 84; 129 and 85; 129 and 86; 129 and 87; 130 and 65; 130 and 66; 130 and 67; 130 and 68; 130 and 69; 130 and 70; 130 and 71; 130 and 72; 130 and 73; 130 and 74; 130 and 75; 130 and 76; 130 and 77; 130 and 78; 130 and 79; 130 and 80; 130 and 81; 130 and 82; 130 and 83; 130 and 84; 130 and 85; 130 and 86; 130 and 87; 131 and 65; 131 and 66; 131 and 67; 131 and 68; 131 and 69; 131 and 70; 131 and 71; 131 and 72; 131 and 73; 131 and 74; 131 and 75; 131 and 76; 131 and 77; 131 and 78; 131 and 79; 131 and 80; 131 and 81; 131 and 82; 131 and 83; 131 and 84; 131 and 85; 131 and 86; 131 and 87; 132 and 65; 132 and 66; 132 and 67; 132 and 68; 132 and 69; 132 and 70; 132 and 71; 132 and 72; 132 and 73; 132 and 74; 132 and 75; 132 and 76; 132 and 77; 132 and 78; 132 and 79; 132 and 80; 132 and 81; 132 and 82; 132 and 83; 132 and 84; 132 and 85; 132 and 86; 132 and 87; 133 and 65; 133 and 66; 133 and 67; 133 and 68; 133 and 69; 133 and 70; 133 and 71; 133 and 72; 133 and 73; 133 and 74; 133 and 75; 133 and 76; 133 and 77; 133 and 78; 133 and 79; 133 and 80; 133 and 81; 133 and 82; 133 and 83; 133 and 84; 133 and 85; 133 and 86; 133 and 87; 134 and 65; 134 and 66; 134 and 67; 134 and 68; 134 and 69; 134 and 70; 134 and 71; 134 and 72; 134 and 73; 134 and 74; 134 and 75; 134 and 76; 134 and 77; 134 and 78; 134 and 79; 134 and 80; 134 and 81; 134 and 82; 134 and 83; 134 and 84; 134 and 85; 134 and 86; 134 and 87; 135 and 65; 135 and 66; 135 and 67; 135 and 68; 135 and 69; 135 and 70; 135 and 71; 135 and 72; 135 and 73; 135 and 74; 135 and 75; 135 and 76; 135 and 77; 135 and 78; 135 and 79; 135 and 80; 135 and 81; 135 and 82; 135 and 83; 135 and 84; 135 and 85; 135 and 86; 135 and 87; 136 and 65; 136 and 66; 136 and 67; 136 and 68; 136 and 69; 136 and 70; 136 and 71; 136 and 72; 136 and 73; 136 and 74; 136 and 75; 136 and 76; 136 and 77; 136 and 78; 136 and 79; 136 and 80; 136 and 81; 136 and 82; 136 and 83; 136 and 84; 136 and 85; 136 and 86; 136 and 87; 137 and 65; 137 and 66; 137 and 67; 137 and 68; 137 and 69; 137 and 70; 137 and 71; 137 and 72; 137 and 73; 137 and 74; 137 and 75; 137 and 76; 137 and 77; 137 and 78; 137 and 79; 137 and 80; 137 and 81; 137 and 82; 137 and 83; 137 and 84; 137 and 85; 137 and 86; 137 and 87; 138 and 65; 138 and 66; 138 and 67; 138 and 68; 138 and 69; 138 and 70; 138 and 71; 138 and 72; 138 and 73; 138 and 74; 138 and 75; 138 and 76; 138 and 77; 138 and 78; 138 and 79; 138 and 80; 138 and 81; 138 and 82; 138 and 83; 138 and 84; 138 and 85; 138 and 86; 138 and 87; 139 and 65; 139 and 66;

139 and 67; 139 and 68; 139 and 69; 139 and 70; 139 and 71; 139 and 72; 139 and 73; 139 and 74; 139 and 75; 139 and 76; 139 and 77; 139 and 78; 139 and 79; 139 and 80; 139 and 81; 139 and 82; 139 and 83; 139 and 84; 139 and 85; 139 and 86; 139 and 87; 140 and 65; 140 and 66; 140 and 67; 140 and 68; 140 and 69; 140 and 70; 140 and 71; 140 and 72; 140 and 73; 140 and 74; 140 and 75; 140 and 76; 140 and 77; 140 and 78; 140 and 79; 140 and 80; 140 and 81; 140 and 82; 140 and 83; 140 and 84; 140 and 85; 140 and 86; 140 and 87; 141 and 65; 141 and 66; 141 and 67; 141 and 68; 141 and 69; 141 and 70; 141 and 71; 141 and 72; 141 and 73; 141 and 74; 141 and 75; 141 and 76; 141 and 77; 141 and 78; 141 and 79; 141 and 80; 141 and 81; 141 and 82; 141 and 83; 141 and 84; 141 and 85; 141 and 86; 141 and 87; 142 and 65; 142 and 66; 142 and 67; 142 and 68; 142 and 69; 142 and 70; 142 and 71; 142 and 72; 142 and 73; 142 and 74; 142 and 75; 142 and 76; 142 and 77; 142 and 78; 142 and 79; 142 and 80; 142 and 81; 142 and 82; 142 and 83; 142 and 84; 142 and 85; 142 and 86; 142 and 87; 143 and 65; 143 and 66; 143 and 67; 143 and 68; 143 and 69; 143 and 70; 143 and 71; 143 and 72; 143 and 73; 143 and 74; 143 and 75; 143 and 76; 143 and 77; 143 and 78; 143 and 79; 143 and 80; 143 and 81; 143 and 82; 143 and 83; 143 and 84; 143 and 85; 143 and 86; or 143 and 87;

c. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

d. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

20. A composition comprising one or more nucleic acid molecules encoding
    a. a *Staphylococcus lugdunensis* Cas9 (SluCas9); and
    b. at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first guide sequence and a second guide sequence selected from any of the pairs of guide sequences shown in Tables 1E or 1F.

21. A composition comprising:
    a. a single nucleic acid molecule comprising:
        i. a nucleic acid encoding *Staphylococcus lugdunensis* (SluCas9) and at least one, at least two, or at least three guide RNAs; or
        ii. a nucleic acid encoding SluCas9 and from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
        iii. a nucleic acid encoding SluCas9 and 1, 2, or 3 guide RNAs;

    wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide sequence selected from the pairs of guide sequences shown in **Tables 1E or 1F**, and

further optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence; or

b. two nucleic acid molecules comprising:

i. a first nucleic acid encoding SluCas9; and

a second nucleic acid that does not encode a SluCas9 and encodes any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

ii. a first nucleic acid encoding SluCas9 and

1. at least one, at least two, or at least three guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. 1, 2, or 3 guide RNAs; and

a second nucleic acid that does not encode a SluCas9, optionally wherein the second nucleic acid comprises any one of the following:

1. at least one, at least two, at least three, at least four, at least five, or at least six guide RNAs; or
2. from one to n guide RNAs, wherein n is no more than the maximum number of guide RNAs that can be expressed from said nucleic acid; or
3. from one to six guide RNAs;

iii. a first nucleic acid encoding SluCas9 and at least one, at least two, or at least three guide RNAs; and

a second nucleic acid that does not encode a SluCas9 and encodes from one to six guide RNAs; or

iv. a first nucleic acid encoding SluCas9 and at least two guide RNAs, and

a second nucleic acid that does not encode a SluCas9 and encodes at least one additional copy of each of the guide RNAs encoded in the first nucleic acid;

wherein each guide RNA comprises a guide sequence selected from any one of the guide sequences of **Tables 1A-1C**, optionally wherein the composition comprises at least one pair

of guide RNAs, wherein the at least one pair of guide RNAs comprises a guide sequence selected from the pairs of guide sequences shown in **Tables 1E or 1F**, and optionally wherein a first guide RNA of the at least one pair of guide RNAs binds upstream of a target sequence and a second guide RNA of the at least one pair of guide RNAs binds downstream of the target sequence.

22. A composition comprising a single nucleic acid molecule encoding at least one pair of guide RNAs and a Cas9, wherein the single nucleic acid molecule comprises:
    a. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences shown in Table 1E or 1F; and a second nucleic acid encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9);
    b. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; and a second nucleic acid encoding a SluCas9; or
    c. a first nucleic acid encoding the at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a pair of guide sequences selected from any one of the pairs of guide sequences of: SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82;

118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81; and a second nucleic acid encoding a SluCas9.

23. A composition comprising a first and a second nucleic acid molecule, wherein the first nucleic acid molecule encodes a *Staphylococcus lugdunensis* Cas9 (SluCas9) and optionally a first or a first and second guide RNA, and the second nucleic acid molecule comprises a first or a first and second guide RNA, wherein the first guide RNA comprises a first guide sequence and the second guide RNA comprises a second guide sequence selected from any one the following pairs of first and second guide sequences:
    a. any one of the pairs of first and second guide sequences shown in Tables 1E or 1F;
    b. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19

and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or

c. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121 and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

24. A composition comprising one or more nucleic acid molecules encoding a *Staphylococcus lugdunensis* Cas9 (SluCas9) and at least one pair of guide RNAs, wherein the at least one pair of guide RNAs comprises a first and a second guide RNA, wherein the first guide RNA targets a sequence in intron 53 of a DMD gene and the second guide RNA targets a sequence in exon 53 of the DMD gene, or the first guide RNA targets a sequence in exon 53 of a DMD gene and the second guide RNA targets a sequence in intron 52 of the DMD gene.

25. The composition of any one of claims 12-24, comprising at least one pair of guide RNAs, wherein the at least one pair of guide RNAs is capable of excising a fragment of the DMD gene, wherein the fragment comprises a splice donor site or a splice acceptor site, and optionally wherein the fragment is between 5 and 400 nucleotides in length.

26. The composition of any one of claims 12-15 or 25, wherein the excised fragment of the DMD gene does not comprise an entire exon of the DMD gene.

27. The composition of any one of claims 12-26, comprising at least one pair of guide RNAs, wherein the first and the second guide RNAs of the at least one pair of guide RNAs each comprise a sequence that is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% identical to a first and a second guide sequence selected from any one of the following pairs of first and second guide sequences:
    a. any one of the pairs of first and second guide sequences shown in Tables 1E or 1F;
    b. SEQ ID NOs: 2 and 85; 2 and 71; 2 and 84; 2 and 70; 2 and 83; 2 and 82; 2 and 81; 2 and 80; 2 and 69; 2 and 68; 2 and 76; 2 and 75; 2 and 74; 2 and 73; 35 and 85; 35 and 71; 35 and 84; 36 and 85; 36 and 71; 36 and 84; 35 and 70; 37 and 85; 37 and 71; 37 and 84; 36 and 70; 37 and 70; 38 and 85; 38 and 71; 39 and 85; 39 and 71; 38 and 84; 39 and 84; 35 and 83; 38 and 70; 39 and 70; 36 and 83; 37 and 83; 35 and 82; 35 and 81; 36 and 82; 38 and 83; 39 and 83; 36 and 81; 37 and 82; 35 and 80; 37 and 81; 36 and 80; 38 and 82; 39 and 82; 37 and 80; 38 and 81; 39 and 81; 38 and 80; 39 and 80; 35 and 69; 35 and 68; 36 and 69; 35 and 76; 37 and 69; 36 and 68; 35 and 75; 36 and 76; 35 and 74; 35 and 73; 37 and 68; 36 and 75; 37 and 76; 36 and 74; 38 and 69; 36 and 73; 39 and 69; 37 and 75; 37 and 74; 37 and 73; 38 and 68; 39 and 68; 38 and 76; 39 and 76; 38 and 75; 39 and 75; 38 and 74; 38 and 73; 39 and 74; 39 and 73; 57 and 85; 57 and 71; 58 and 85; 19 and 85; 58 and 71; 19 and 71; 57 and 84; 58 and 84; 19 and 84; 57 and 70; 58 and 70; 19 and 70; 20 and 85; 20 and 71; 20 and 84; 20 and 70; 57 and 83; 58 and 83; 19 and 83; 57 and 82; 58 and 82; 19 and 82; 20 and 83; 57 and 81; 58 and 81; 19 and 81; 57 and 80; 58 and 80; 19 and 80; 20 and 82; 20 and 81; 20 and 80; 57 and 69; 58 and 69; 19 and 69; 57 and 68; 58 and 68; 19 and 68; 57 and 76; 58 and 76; 19 and 76; 57 and 75; 58 and 75; 19 and 75; 20 and 69; 57 and 74; 57 and 73; 58 and 74; 19 and 74; 58 and 73; 19 and 73; 20 and 68; 20 and 76; 20 and 75; 20 and 74; or 20 and 73; or
    c. SEQ ID NOs: 115 and 82; 116 and 82; 117 and 82; 118 and 82; 119 and 82; 120 and 82; 121 and 82; 90 and 82; 115 and 83; 116 and 83; 117 and 83; 118 and 83; 119 and 83; 120 and 83; 121 and 83; 90 and 83; 115 and 84; 116 and 84; 117 and 84; 118 and 84; 119 and 84; 120 and 84; 121 and 84; 90 and 84; 115 and 85; 116 and 85; 117 and 85; 118 and 85; 119 and 85; 120 and 85; 121 and 85; 90 and 85; 115 and 68; 116 and 68; 117 and 68; 118 and 68; 119 and 68; 120 and 68; 121 and 68; 90 and 68; 115 and 69; 116 and 69; 117 and 69; 118 and 69; 119 and 69; 120 and 69; 121 and 69; 90 and 69; 115 and 70; 116 and 70; 117 and 70; 118 and 70; 119 and 70; 120 and 70; 121

and 70; 90 and 70; 115 and 71; 116 and 71; 117 and 71; 118 and 71; 119 and 71; 120 and 71; 121 and 71; 90 and 71; 115 and 73; 116 and 73; 117 and 73; 118 and 73; 119 and 73; 120 and 73; 121 and 73; 90 and 73; 115 and 74; 116 and 74; 117 and 74; 118 and 74; 119 and 74; 120 and 74; 121 and 74; 90 and 74; 115 and 75; 116 and 75; 117 and 75; 118 and 75; 119 and 75; 120 and 75; 121 and 75; 90 and 75; 115 and 76; 116 and 76; 117 and 76; 118 and 76; 119 and 76; 120 and 76; 121 and 76; 90 and 76; 115 and 80; 116 and 80; 117 and 80; 118 and 80; 119 and 80; 120 and 80; 121 and 80; 90 and 80; 115 and 81; 116 and 81; 117 and 81; 118 and 81; 119 and 81; 120 and 81; 121 and 81; or 90 and 81.

28. The composition of any one of claims 12-26, wherein:
    i) the first guide RNA comprises the sequence of SEQ ID NO: 70 and the second guide RNA comprises the sequence of SEQ ID NO: 2;
    ii) the first guide RNA comprises the sequence of SEQ ID NO: 76, and the second guide RNA comprises the sequence of SEQ ID NO: 2; or
    iii) the first guide RNA comprises the sequence of SEQ ID NO: 115, and the second guide RNA comprises the sequence of SEQ ID NO: 70.

29. The composition of any one of the preceding claims, comprising at least one pair of guide RNAs, wherein once expressed in vitro or in vivo in combination with a SluCas9 endonuclease, the at least one pair of guide RNAs (i) excises exon 53 of a DMD gene, (ii) excises a fragment of the DMD gene comprising a portion of intron 53 and an adjoining portion of exon 53, wherein the excised fragment of the DMD gene comprises a splice donor site, or (iii) excises a fragment of the DMD gene comprising a portion of exon 53 and an adjoining portion of intron 52, wherein the excised fragment of the DMD gene comprises a splice acceptor site; wherein the size of the excised fragment of the DMD gene is between 5 and 400 nucleotides in length.

30. The composition of any one of claims 12-15 or 25-29, wherein the size of the excised fragment of the DMD gene is between 5 and 400, 5 and 375, 5 and 350, 5 and 325, 5 and 300, 5 and 275, 5 and 250, 5 and 225, 5 and 200, 5 and 175, 5 and 150, 5 and 125, 5 and 100, 20 and 400, 20 and 375, 20 and 350, 20 and 325, 20 and 300, 20 and 275, 20 and 250, 20 and 225, 20 and 200, 20 and 175, 20 and 150, 20 and 125, 20 and 100, 50 and 400, 50 and 375, 50 and 350, 50 and 325, 50 and 300, 50 and 275, 50 and 250, 50 and 225, 50 and 200, 50 and 175, 50 and 150, 50 and 125, or 50 and 100 nucleotides in length.

31. The composition of any one of the preceding claims, wherein the one or more guide RNAs is an sgRNA, the first and/or second guide RNA is an sgRNA, or the at least one pair of guide RNAs is a pair of sgRNAs.

32. The composition of any one of the preceding claims, wherein the one or more guide RNAs is modified, the first and/or second guide RNA is modified, or the at least one pair of guide RNAs is a pair of modified guide RNAs.

33. The composition of any one of the preceding claims, wherein the one or more guide RNAs, the first and/or second guide RNA, the at least one pair of guide RNAs, or the nucleic acid is in a vector.

34. The composition of claim 33, wherein the vector is a lipid nanoparticle or a liposome.

35. The composition of claim 33, wherein the vector is a viral vector.

36. The composition of claim 35, wherein the viral vector is an AAV vector.

37. The composition of claim 36, wherein the AAV vector is an AAV9 vector.

38. The composition of any one of the preceding claims, wherein a promoter for the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs is hU6c.

39. The composition of any one of the preceding claims, wherein the one or more guide RNAs is a guide RNA for SluCas9, the first and/or second guide RNA is a guide RNA for SluCas9, or the at least one pair of guide RNAs is a pair of guide RNAs for SluCas9; and the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs comprise a scaffold comprising the sequence of any one of SEQ ID NOs: 600, 601, or 900-917.

40. The composition of the immediately preceding claim, wherein the scaffold comprises the sequence of SEQ ID NO: 901.

41. The composition of any one of the preceding claims, wherein the one or more guide RNAs, the first and/or second guide RNA, or the at least one pair of guide RNAs is in an AAV vector, wherein the vector comprises from 5' to 3' with respect to the plus strand: the reverse

complement of a first guide RNA scaffold sequence; the reverse complement of a nucleic acid encoding a first guide RNA sequence; the reverse complement of a promoter for expression of the nucleic acid encoding the first guide RNA sequence; a promoter for expression of a nucleic acid encoding SluCas9; a nucleic acid encoding a SluCas9; a polyadenylation sequence; a promoter for expression of a second guide RNA sequence in the same direction as the promoter for SluCas9; a second RNA guide sequence; and a second guide RNA scaffold sequence.

42. The composition of any one of the preceding claims, wherein the one or more guide RNAs, or the first and/or second guide RNA, is no more than 16, no more than 17, no more than 18, no more than 19, no more than 20, no more than 21, or no more than 22 nucleotides in length.

43. A method of treating Duchenne Muscular Dystrophy (DMD), the method comprising delivering to a cell the composition of any one of claims 1-42.

44. A method of excising a DMD gene or a fragment of the DMD gene, the method comprising delivering to a cell the composition of any one of claims 1-42, wherein the size of the excised portion of the DMD gene is less than about 400 nucleotides.

45. A composition comprising:
a) a pair of guide RNA molecules or a nucleic acid encoding a pair of RNA molecules, wherein the first guide RNA targets a region upstream of a splice acceptor site or a splice donor site in a DMD gene and wherein the second guide RNA targets a region downstream of a splice acceptor site or a splice donor site in the DMD gene; and
b) an endonuclease or a nucleic acid encoding an endonuclease, optionally wherein the endonuclease is a *Staphylococcus lugdunensis* Cas9 (SluCas9).

46. The composition of claim 45, wherein the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an exon of the DMD gene.

47. The composition of claim 45, wherein the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an intron of the DMD gene.

48. The composition of claim 45, wherein the first guide RNA is in an exon of the DMD gene and the second guide RNA is in an exon of the DMD gene.

49. The composition of claim 45, wherein the first guide RNA is in an intron of the DMD gene and the second guide RNA is in an intron of the DMD gene.

50. The composition of any one of claims 45-49, wherein the splice acceptor site or splice donor site is in intron 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, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, or 78 of the DMD gene.

51. The composition of any one of claims 45-50, wherein the splice acceptor site or splice donor site is in intron 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56 or 57 of the DMD gene.

52. The composition of any one of claims 45-51, wherein the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides upstream of the splice acceptor or splice donor site.

53. The composition of any one of claims 45-52, wherein the first guide RNA targets a region within 1-200, 1-150, 1-100, 1-50, 30-200, 30-150, 30-100, 30-50, 75-200, 75-150, 75-100, 100-200, 100-150, or 150-200 nucleotides downstream of the splice acceptor or splice donor site.

54. A method of excising a fragment of a DMD gene, the method comprising delivering to a cell the composition of any one of claims 45-53, wherein the pair of guide RNAs and the endonuclease excise a fragment of the DMD gene comprising the splice acceptor site or the splice donor site, wherein the fragment is between 3 and 400 nucleotides in length.

55. The method of claim 54, wherein the excised fragment of the DMD gene comprises a splice acceptor site.

56. The method of claim 54, wherein the excised fragment of the DMD gene comprises a splice donor site.

57. The method of any one of claims 54-56, wherein the excised fragment is between 3-200, 3-150, 3-100, 3-50, 30-250, 30-200, 30-150, 30-100, 30-50, 75-250, 75-200, 75-150, 75-100, 100-250, 100-200, 100-150, 150-250, 150-200, 200-250, 250-400, 300-400, or 350-400 nucleotides in length.