MODULATORS OF DNM2 EXPRESSION

Sequence Listing

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled BIOL0322WOSEQ_ST25.txt created January 10, 2019 which is 784 kb in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety.

Field

The present embodiments provide methods, compounds, and compositions useful for inhibiting DNM2 expression, which can be useful for treating, preventing, or ameliorating a disease associated with DNM2.

Background

Dynamin 2 (DNM2) is a large GTPase that is involved in membrane trafficking and microtubule dynamics (*See, e.g.,* Durieux et al. *J Mol Med*, 88, 339 (2010)). Mutations in DNM2 are associated with several diseases, including centronuclear myopathy (CNM) and Charcot-Marie-Tooth disease. DNM2 is also associated with Duchenne's Muscular Dystrophy (*See, e.g.*, WO 2015/055859 and WO 2016/170162). CNM and CNM-like myopathy are also associated with mutations in MTM1, BIN1, RYR1, TTN, CCDC78, and MTMR14

Summary

Certain embodiments provided herein are directed to potent and tolerable compounds and compositions useful for inhibiting DNM2 expression, which can be useful for treating, preventing, ameliorating, or slowing progression of diseases, such as centronuclear myopathy (CNM), Charcot-Marie-Tooth disease (CMT), and Duchenne's Muscular Dystrophy (DMD). Certain embodiments provided herein comprise modified oligonucleotides complementary to a DNM2 nucleic acid that potently reduce DNM2 expression in animals.

One object of the present invention is a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 9 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 9 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 10 to 50 linked

nucleosides in length having a nucleobase sequence comprising at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 11 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 12 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 12, at least 13, at least 14, or at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 7-3134. Another object of the present invention is a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length complementary within nucleobases 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1, wherein said modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1. Another object of the present invention is a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length having a nucleobase sequence comprising a portion of at least 8 contiguous nucleobases 100% complementary to an equal length portion of nucleobases 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1. Another object of the present invention is a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length complementary within nucleobases 83,573-87,287 or 87,359-90,915 of SEQ ID NO: 1, wherein said modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to intron 1 of a human DNM2 pre-mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to intron 11 of a human DNM2 pre-mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to intron 12 of a human DNM2 pre-mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to intron 13 of a human DNM2 pre-mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to intron 14 of a human DNM2 pre-mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to exon 10 of a human DNM2 pre-mRNA or human DNM2 mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide complementary to the 3'-UTR of a human DNM2 pre-mRNA or human DNM2 mRNA. Another object of the present invention is a compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any of SEQ ID NOs: 2879, 3056, 2123, 2189,

2453, 2160, or 2232. Another object of the present invention is a compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. Another object of the present invention is a compound comprising a modified oligonucleotide having a nucleobase sequence comprising SEQ ID NO: 2879.

Another object of the present invention is a compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises:

a gap segment consisting of 8-12 linked 2'-deoxynucleosides;

a 5' wing segment consisting of 1-7 linked nucleosides; and

a 3' wing segment consisting of 1-7 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each terminal wing nucleoside comprises a modified sugar.

Another object of the present invention is a compound comprising a modified oligonucleotide 16 linked nucleosides in length having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises

a gap segment consisting of 10 linked 2'-deoxynucleosides;

a 5' wing segment consisting of 3 linked nucleosides; and

a 3' wing segment consisting of 3 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of each wing segment comprises a cEt sugar moiety; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

In one embodiment, the oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to any of SEQ ID NO: 1, 2, 3, or 3135. In one embodiment, the modified oligonucleotide comprises at least one modified internucleoside linkage. In one embodiment, the at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage. In one embodiment, the modified oligonucleotide comprises at least one bicyclic sugar. In one embodiment, the at least one bicyclic sugar is selected from the group consisting of LNA, ENA, and cEt. In one embodiment, the at least one bicyclic sugar moiety is a cEt sugar moiety.

In one embodiment, the modified oligonucleotide comprises at least one 5-methylcytosine. In one embodiment, the modified oligonucleotide comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar moiety.

In one embodiment, the compound is single-stranded. In one embodiment, the compound is double-stranded.

In one embodiment, the compound comprises at least one unmodified ribosyl sugar moiety. In one embodiment, the compound comprises at least one unmodified 2'-deoxyribosyl sugar moiety.

In one embodiment, the modified oligonucleotide consists of 10 to 30 linked nucleosides. In one embodiment, the modified oligonucleotide consists of 12 to 30 linked nucleosides. In one embodiment, the modified oligonucleotide consists of 15 to 30 linked nucleosides. In one embodiment, the modified oligonucleotide consists of 16 to 20 linked nucleosides.

Another object of the present invention is a compound comprising a modified oligonucleotide according to the following formula: Gks Tks Tks Tds Ads Tds Tds Ads Tds Ads Gds Gds Gds mCks Tks Tk; wherein,

A = an adenine,

mC = a 5-methylcytosine

G = a guanine,

T = a thymine,

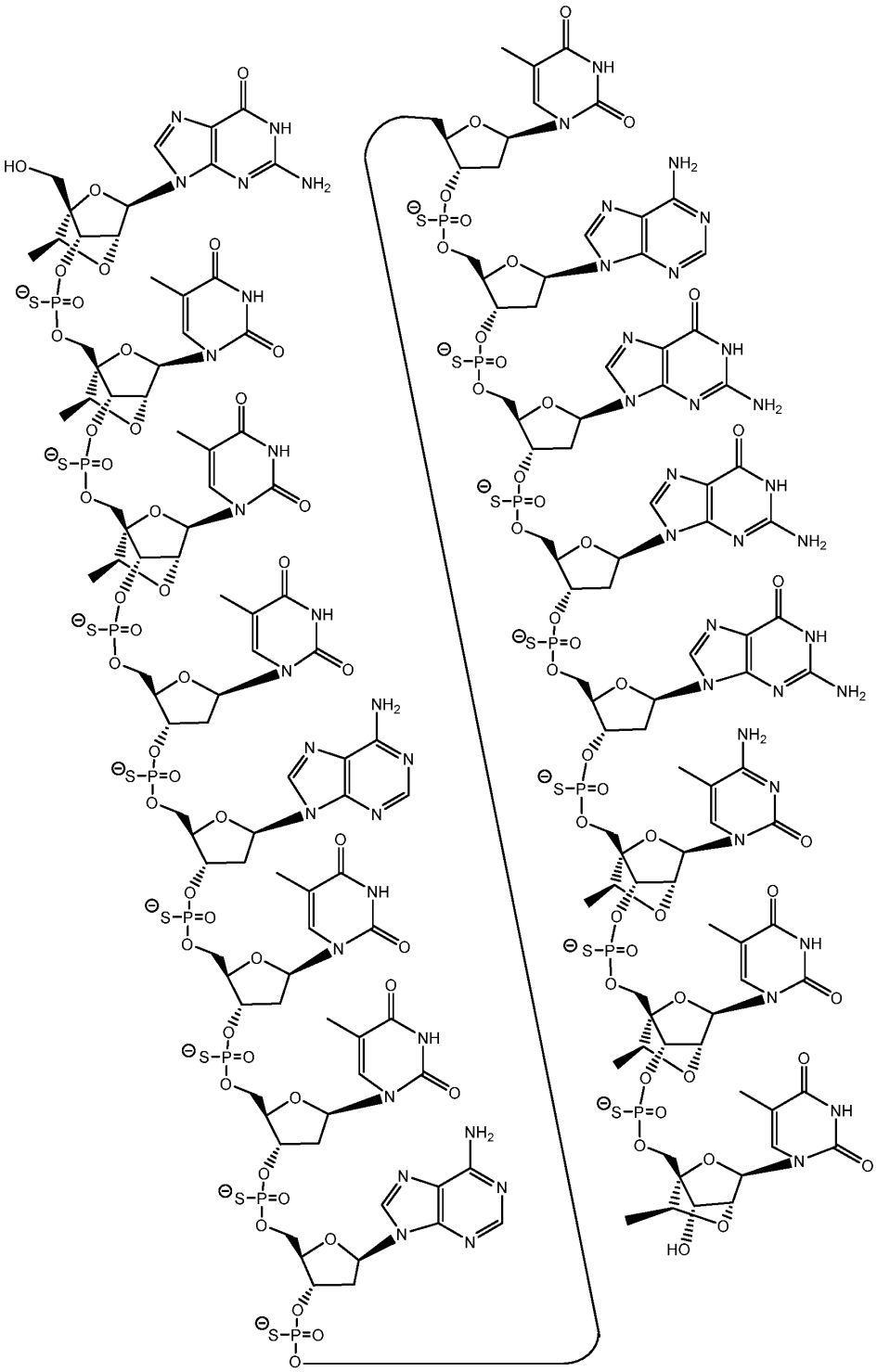
k = a cEt sugar moiety,

d = a 2'-deoxyribosyl sugar moiety, and

s = a phosphorothioate internucleoside linkage.

In one embodiment, the compound of the invention comprises a conjugate group. In one embodiment, the compound of the invention consists of the modified oligonucleotide and the conjugate group.

Another object of the present invention is a compound according to the following formula:



[SEQ ID NO: 2879] or a salt thereof.

In one embodiment, the compound consists of the modified oligonucleotide.

The present invention further relates to a compound consisting of a pharmaceutically acceptable salt form of any one of the compounds described herein. In one embodiment, the pharmaceutically acceptable salt is a sodium salt. In one embodiment, the pharmaceutically acceptable salt is a potassium salt.

The present invention also relates to a pharmaceutical composition comprising a compound as described herein and at least one pharmaceutically acceptable carrier or diluent.

The present invention further relates to a chirally enriched population of the compounds described herein, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration. In one embodiment, the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*S*p) configuration. In one embodiment, the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*R*p) configuration. In one embodiment, the population is enriched for modified oligonucleotides having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage. In one embodiment, the population is enriched for modified oligonucleotides having the (*S*p) configuration at each phosphorothioate internucleoside linkage. In one embodiment, the population is enriched for modified oligonucleotides having the (*R*p) configuration at each phosphorothioate internucleoside linkage. In one embodiment, the population is enriched for modified oligonucleotides having the (*R*p) configuration at one particular phosphorothioate internucleoside linkage and the (*S*p) configuration at each of the remaining phosphorothioate internucleoside linkages. In one embodiment, the population is enriched for modified oligonucleotides having at least 3 contiguous phosphorothioate internucleoside linkages in the *S*p, *S*p, and *R*p configurations, in the 5' to 3' direction. In one embodiment, all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

The present invention further relates to a pharmaceutical composition comprising the population of compounds described herein and at least one pharmaceutically acceptable diluent or carrier.

The present invention further relates to a compound described herein, a pharmaceutical composition comprising said compound and at least one pharmaceutically acceptable carrier or diluent, or a pharmaceutical composition comprising the population of compounds described herein and at least one pharmaceutically acceptable carrier or diluent, for use in therapy.

The present invention further relates to a compound described herein, a pharmaceutical composition comprising said compound and at least one pharmaceutically acceptable carrier or diluent, or a pharmaceutical composition comprising the population of compounds described herein and at least one pharmaceutically acceptable carrier or diluent, for use in treating, preventing, or ameliorating centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

The present invention also relates to a method of treating, preventing, or ameliorating a disease associated with DNM2 in an individual comprising administering to the individual a compound or composition described herein, thereby treating, preventing, or ameliorating the disease.

The present invention also relates to a method of treating, preventing, or ameliorating a disease associated with DNM2 in an individual comprising administering to the individual a compound comprising a modified oligonucleotide 100% complementary to an exon 10, an intron, or the 3'-UTR of a DNM2 nucleic acid transcript, thereby treating, preventing, or ameliorating the disease.

In one embodiment, the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease. In one embodiment, the compound is single-stranded. In one embodiment, the DNM2 nucleic acid transcript is a pre-mRNA. In one embodiment, the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy. In one embodiment, the individual has at least one mutation in at least one gene selected from among MTM1, BIN1, and DNM2. In one embodiment, the administering increases body weight or muscle strength.

The present invention further relates to a method of inhibiting expression of DNM2 in a cell comprising contacting the cell with a single-stranded compound comprising a modified oligonucleotide 100% complementary to exon 10, an intron, or the 3'-UTR of a DNM2 nucleic acid transcript, thereby inhibiting expression of DNM2 in the cell. In one embodiment, the method is an in vitro method. In one embodiment, the cell is in the muscle of an individual. In one embodiment, the individual has, or is at risk of having, a centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

The present invention further relates to a method of increasing body weight or muscle strength in an individual having, or at risk of having, a disease associated with DNM2 comprising administering a single-stranded compound comprising a modified oligonucleotide 100% complementary to a DNM2 nucleic acid transcript to the individual, thereby increasing body weight or muscle strength in the individual. In one embodiment, the individual has, or is at risk of having, centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

In one embodiment, the compound is a compound as described herein. In one embodiment, the compound is a member of the chirally enriched population described herein. In one embodiment, the compound is a component of the pharmaceutical composition described herein.

In one embodiment, the compound is administered to the individual via subcutaneous injection. In one embodiment, the compound is administered to the individual via intramuscular injection. In one embodiment, the compound is administered to the individual via intravenous injection.

The present invention further relates to the use of a single-stranded compound comprising a modified oligonucleotide 100% complementary to exon 10, intron 1, intron 11, intron, 12, intron 13, intron 14, or the 3'-UTR of a DNM2 nucleic acid transcript for treating, preventing, or ameliorating a disease associated with

DNM2. In one embodiment, the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

The present invention further relates to the use of the compound described herein or the composition described herein for treating, preventing, or ameliorating a disease associated with DNM2.

The present invention further relates to the use of the compound described herein or the composition described herein in the manufacture of a medicament for treating, preventing, or ameliorating a disease associated with DNM2.

In one embodiment, the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease. In one embodiment, the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy. In one embodiment, the disease is associated with a mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

The present invention further relates to the use of the compound described herein or the composition described herein in the preparation of a medicament for treating, preventing, or ameliorating a disease associated with DNM2. In one embodiment, the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease. In one embodiment, the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy. In one embodiment, the the disease is associated with a mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

Detailed Description

It is to be understood that both the foregoing general description and the following detailed description are exemplary and explanatory only and are not restrictive of the embodiments, as claimed. Herein, the use of the singular includes the plural unless specifically stated otherwise. As used herein, the use of "or" means "and/or" unless stated otherwise. Furthermore, the use of the term "including" as well as other forms, such as "includes" and "included", is not limiting.

The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described. All documents, or portions of documents, cited in this application, including, but not limited to, patents, patent applications, articles, books, treatises, and GenBank and NCBI reference sequence records are hereby expressly incorporated by reference for the portions of the document discussed herein, as well as in their entirety.

It is understood that the sequence set forth in each SEQ ID NO contained herein is independent of any modification to a sugar moiety, an internucleoside linkage, or a nucleobase. As such, compounds defined by a SEQ ID NO may comprise, independently, one or more modifications to a sugar moiety, an internucleoside

linkage, or a nucleobase.

As used herein, “2’-deoxynucleoside” means a nucleoside comprising 2’-H(H) ribosyl sugar moiety, as found in naturally occurring deoxyribonucleic acids (DNA). In certain embodiments, a 2’-deoxynucleoside may comprise a modified nucleobase or may comprise an RNA nucleobase (uracil).

As used herein, “2’-substituted nucleoside” or “2-modified nucleoside” means a nucleoside comprising a 2’-substituted or 2’-modified sugar moiety. As used herein, “2’-substituted” or “2-modified” in reference to a furanosyl sugar moiety means a sugar moiety comprising at least one 2'-substituent group other than H or OH.

As used herein, "administration" or "administering" refers to routes of introducing a compound or composition provided herein to an individual to perform its intended function. An example of a route of administration that can be used includes, but is not limited to, administration by inhalation.

As used herein, “administered concomitantly” or “co-administration” means administration of two or more compounds in any manner in which the pharmacological effects of both are manifest in the patient. Concomitant administration does not require that both compounds be administered in a single pharmaceutical composition, in the same dosage form, by the same route of administration, or at the same time. The effects of both compounds need not manifest themselves at the same time. The effects need only be overlapping for a period of time and need not be coextensive. Concomitant administration or co-administration encompasses administration in parallel or sequentially.

As used herein, “animal” refers to a human or non-human animal, including, but not limited to, mice, rats, rabbits, dogs, cats, pigs, and non-human primates, including, but not limited to, monkeys and chimpanzees.

As used herein, “antisense activity” means any detectable and/or measurable change attributable to the hybridization of an antisense compound to its target nucleic acid. In certain embodiments, antisense activity is a decrease in the amount or expression of a target nucleic acid or protein encoded by such target nucleic acid compared to target nucleic acid levels or target protein levels in the absence of the antisense compound.

As used herein, “antisense compound” means a compound comprising an antisense oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group.

As used herein, “antisense oligonucleotide” means an oligonucleotide having a nucleobase sequence that is at least partially complementary to a target nucleic acid.

As used herein, “ameliorate” in reference to a treatment means improvement in at least one symptom relative to the same symptom in the absence of the treatment. In certain embodiments, amelioration is the reduction in the severity or frequency of a symptom or the delayed onset or slowing of progression in the severity or frequency of a symptom.

As used herein, “bicyclic nucleoside” or “BNA” means a nucleoside comprising a bicyclic sugar moiety. As used herein, “bicyclic sugar” or “bicyclic sugar moiety” means a modified sugar moiety comprising

two rings, wherein the second ring is formed via a bridge connecting two of the atoms in the first ring thereby forming a bicyclic structure. In certain embodiments, the first ring of the bicyclic sugar moiety is a furanosyl moiety. In certain embodiments, the bicyclic sugar moiety does not comprise a furanosyl moiety.

As used herein, "cEt" or "constrained ethyl" means a bicyclic sugar moiety, wherein the first ring of the bicyclic sugar moiety is a ribosyl sugar moiety, the second ring of the bicyclic sugar is formed via a bridge connecting the 4'-carbon and the 2'-carbon, the bridge has the formula 4'-$CH(CH_3)$-O-2', and the methyl group of the bridge is in the *S* configuration. A cEt bicyclic sugar moiety is in the β-D configuration.

As used herein, "chirally enriched population" means a plurality of molecules of identical molecular formula, wherein the number or percentage of molecules within the population that contain a particular stereochemical configuration at a particular chiral center is greater than the number or percentage of molecules expected to contain the same particular stereochemical configuration at the same particular chiral center within the population if the particular chiral center were stereorandom. Chirally enriched populations of molecules having multiple chiral centers within each molecule may contain one or more sterorandom chiral centers. In certain embodiments, the molecules are modified oligonucleotides. In certain embodiments, the molecules are compounds comprising modified oligonucleotides.

As used herein, "complementary" in reference to an oligonucleotide means that at least 70% of the nucleobases of such oligonucleotide or one or more regions thereof and the nucleobases of another nucleic acid or one or more regions thereof are capable of hydrogen bonding with one another when the nucleobase sequence of the oligonucleotide and the other nucleic acid are aligned in opposing directions. Complementary nucleobases are nucleobase pairs that are capable of forming hydrogen bonds with one another. Complementary nucleobase pairs include adenine (A) and thymine (T), adenine (A) and uracil (U), cytosine (C) and guanine (G), 5-methyl cytosine (^{m}C) and guanine (G). Complementary oligonucleotides and/or nucleic acids need not have nucleobase complementarity at each nucleoside. Rather, some mismatches are tolerated. As used herein, "fully complementary" or "100% complementary" in reference to oligonucleotides means that such oligonucleotides are complementary to another oligonucleotide or nucleic acid at each nucleoside of the oligonucleotide.

As used herein, "conjugate group" means a group of atoms that is directly or indirectly attached to an oligonucleotide. Conjugate groups include a conjugate moiety and a conjugate linker that attaches the conjugate moiety to the oligonucleotide.

As used herein, "conjugate linker" means a group of atoms comprising at least one bond that connects a conjugate moiety to an oligonucleotide.

As used herein, "conjugate moiety" means a group of atoms that is attached to an oligonucleotide via a conjugate linker.

As used herein, "contiguous" in the context of an oligonucleotide refers to nucleosides, nucleobases, sugar moieties, or internucleoside linkages that are immediately adjacent to each other. For example,

"contiguous nucleobases" means nucleobases that are immediately adjacent to each other in a sequence.

As used herein, "double-stranded antisense compound" means an antisense compound comprising two oligomeric compounds that are complementary to each other and form a duplex, and wherein one of the two said oligomeric compounds comprises an antisense oligonucleotide.

As used herein, "effective amount" means the amount of compound sufficient to effectuate a desired physiological outcome in an individual in need of the compound. The effective amount may vary among individuals depending on the health and physical condition of the individual to be treated, the taxonomic group of the individuals to be treated, the formulation of the composition, assessment of the individual's medical condition, and other relevant factors.

As used herein, "efficacy" means the ability to produce a desired effect.

As used herein "DNM2" means any Dynamin 2 nucleic acid or protein. "DNM2 nucleic acid" means any nucleic acid encoding DNM2. For example, in certain embodiments, a DNM2 nucleic acid includes a DNA chromosomal region encoding DNM2, an RNA transcribed from DNA encoding DNM2 (*e.g.*, a pre-mRNA transcript), and an mRNA transcript encoding DNM2.

As used herein, "expression" includes all the functions by which a gene's coded information is converted into structures present and operating in a cell. Such structures include, but are not limited to, the products of transcription and translation. Methods for measuring expression levels (such as a transcription level or a translation level) are well-known in the field and include, but are not limited to, RT-PCR, RT-qPCR, Northern Blot, hybridization techniques such as, for example, use of microarrays, and combinations thereof including but not limited to, hybridization of amplicons obtained by RT-PCR, sequencing such as, for example, next-generation DNA sequencing (NGS) or RNA-seq (also known as "Whole Transcriptome Shotgun Sequencing") and the like, immunohistochemistry, Multiplex methods (Luminex), western blot, enzyme-linked immunosorbent assay (ELISA), sandwich ELISA, multiplex ELISA, electrochemiluminescence (ECL) (Elecsys®, Roche Diagnostics), enzyme-linked fluorescent assay (ELFA) (such as VIDAS®, Biomérieux), fluorescent-linked immunosorbent assay (FLISA), enzyme immunoassay (EIA), radioimmunoassay (RIA), flow cytometry (FACS), surface plasmon resonance (SPR), biolayer interferometry (BLI), immunochromatographic assay (ICA) (such as NEXUS IB10, Sphingotech) and mass spectrometry-based approaches.

As used herein, "gapmer" means an oligonucleotide, such as an antisense oligonucleotide, comprising an internal segment having a plurality of nucleosides that support RNase H cleavage positioned between external segments, each having one or more nucleosides, wherein the nucleosides comprising the internal segment are chemically distinct from the immediately adjacent nucleoside or nucleosides comprising the external segments. The internal segment may be referred to as the "gap" or "gap segment" and the external segments may be referred to as the "wings" or "wing segments".

As used herein, "hybridization" means the pairing or annealing of complementary oligonucleotides and/or nucleic acids. While not limited to a particular mechanism, the most common mechanism of hybridization involves hydrogen bonding, which may be, for example, Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleobases.

As used herein, “individual” means a human or non-human animal selected for treatment or therapy.

As used herein, "inhibiting the expression or activity" refers to a reduction or blockade of the expression or activity relative to the expression or activity in an untreated or control sample and does not necessarily indicate a total elimination of expression or activity. In one embodiment, inhibiting the expression or activity refers to a reduction or blockade of the expression or activity relative to the expression or activity in an untreated or control sample of at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90%. In one embodiment, inhibiting the expression or activity refers to a reduction or blockade of the expression or activity relative to the expression or activity in an untreated or control sample of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99%.

As used herein, the term “about” preceding a figure means plus or less 10% of the value of said figure.

As used herein, the terms “internucleoside linkage” means a group or bond that forms a covalent linkage between adjacent nucleosides in an oligonucleotide. As used herein “modified internucleoside linkage” means any internucleoside linkage other than a naturally occurring, phosphate internucleoside linkage. Non-phosphate linkages are referred to herein as modified internucleoside linkages. “Phosphorothioate linkage” means a modified phosphate linkage in which one of the non-bridging oxygen atoms is replaced with a sulfur atom. A phosphorothioate internucleoside linkage is a modified internucleoside linkage. Modified internucleoside linkages include linkages that comprise abasic nucleosides. As used herein, “abasic nucleoside” means a sugar moiety in an oligonucleotide or oligomeric compound that is not directly connected to a nucleobase. In certain embodiments, an abasic nucleoside is adjacent to one or two nucleosides in an oligonucleotide.

As used herein, “linker-nucleoside” means a nucleoside that links, either directly or indirectly, an oligonucleotide to a conjugate moiety. Linker-nucleosides are located within the conjugate linker of an oligomeric compound. Linker-nucleosides are not considered part of the oligonucleotide portion of an oligomeric compound even if they are contiguous with the oligonucleotide.

As used herein, “non-bicyclic modified sugar” or “non-bicyclic modified sugar moiety” means a modified sugar moiety that comprises a modification, such as a substituent, that does not form a bridge between two atoms of the sugar to form a second ring.

As used herein, “linked nucleosides” are nucleosides that are connected in a continuous sequence (*i.e.* no additional nucleosides are present between those that are linked).

As used herein, “mismatch” or “non-complementary” means a nucleobase of a first oligonucleotide

that is not complementary with the corresponding nucleobase of a second oligonucleotide or target nucleic acid when the first and second oligomeric compound are aligned.

As used herein, “modulating” refers to changing or adjusting a feature in a cell, tissue, organ or organism. For example, modulating DNM2 expression can mean to increase or decrease the level of an DNM2 RNA and/or a DNM2 protein in a cell, tissue, organ or organism. A “modulator” effects the change in the cell, tissue, organ or organism. For example, a compound that modulates DNM2 expression can be a modulator that decreases the amount of a DNM2 RNA and/or a DNM2 protein in a cell, tissue, organ or organism.

As used herein, “MOE” means methoxyethyl. ”2’-MOE” or “2’-O-methoxyethyl” means a 2’-$OCH_2CH_2OCH_3$ group in place of the 2’-OH group of a ribosyl ring.

As used herein, “motif” means the pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages, in an oligonucleotide.

As used herein, “naturally occurring” means found in nature.

As used herein, "nucleobase" means an unmodified nucleobase or a modified nucleobase. As used herein an “unmodified nucleobase” is adenine (A), thymine (T), cytosine (C), uracil (U), and guanine (G). As used herein, a modified nucleobase is a group of atoms capable of pairing with at least one unmodified nucleobase. A universal base is a nucleobase that can pair with any one of the five unmodified nucleobases.

As used herein, “nucleobase sequence” means the order of contiguous nucleobases in a nucleic acid or oligonucleotide independent of any sugar or internucleoside linkage modification.

As used herein, “nucleoside” means a moiety comprising a nucleobase and a sugar moiety. The nucleobase and sugar moiety are each, independently, unmodified or modified. As used herein, “modified nucleoside” means a nucleoside comprising a modified nucleobase and/or a modified sugar moiety.

As used herein, "oligomeric compound" means a compound consisting of an oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group.

As used herein, "oligonucleotide" means a strand of linked nucleosides connected via internucleoside linkages, wherein each nucleoside and internucleoside linkage may be modified or unmodified. Unless otherwise indicated, oligonucleotides consist of 8-50 linked nucleosides. As used herein, “modified oligonucleotide” means an oligonucleotide, wherein at least one nucleoside or internucleoside linkage is modified. As used herein, “unmodified oligonucleotide” means an oligonucleotide that does not comprise any nucleoside modifications or internucleoside modifications.

As used herein, “pharmaceutically acceptable carrier or diluent” means any substance suitable for use in administering to an animal. Certain such carriers enable pharmaceutical compositions to be formulated as, for example, liquids, powders, or suspensions that can be aerosolized or otherwise dispersed for inhalation by a subject. In certain embodiments, a pharmaceutically acceptable carrier or diluent is sterile water; sterile saline; or sterile buffer solution. In one embodiment, the pharmaceutically acceptable carrier or diluent does not produce an adverse, allergic or other untoward reaction when administered to an animal, preferably a

human. It includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. For human administration, preparations should meet sterility, pyrogenicity, general safety and purity standards as required by regulatory offices, such as, for example, FDA Office or EMA.

As used herein "pharmaceutically acceptable salts" means physiologically and pharmaceutically acceptable salts of compounds, such as oligomeric compounds, *i.e.*, salts that retain the desired biological activity of the parent compound and do not impart undesired toxicological effects thereto.

As used herein "pharmaceutical composition" means a mixture of substances suitable for administering to a subject. For example, a pharmaceutical composition may comprise an antisense compound and an aqueous solution.

As used herein, "phosphorus moiety" means a group of atoms comprising a phosphorus atom. In certain embodiments, a phosphorus moiety comprises a mono-, di-, or tri-phosphate, or phosphorothioate.

As used herein "prodrug" means a therapeutic agent in a form outside the body that is converted to a differentform within the body or cells thereof. Typically conversion of a prodrug within the body is facilitated by the action of an enzymes (e.g., endogenous or viral enzyme) or chemicals present in cells or tissues and/or by physiologic conditions.

As used herein, "RNAi compound" means an antisense compound that acts, at least in part, through RISC or Ago2 to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. RNAi compounds include, but are not limited to double-stranded siRNA, single-stranded RNA (ssRNA), and microRNA, including microRNA mimics. In certain embodiments, an RNAi compound modulates the amount, activity, and/or splicing of a target nucleic acid. The term RNAi compound excludes antisense oligonucleotides that act through RNase H.

As used herein, the term "single-stranded" in reference to an antisense compound means such a compound consisting of one oligomeric compound that is not paired with a second oligomeric compound to form a duplex. "Self-complementary" in reference to an oligonucleotide means an oligonucleotide that at least partially hybridizes to itself. A compound consisting of one oligomeric compound, wherein the oligonucleotide of the oligomeric compound is self-complementary, is a single-stranded compound. A single-stranded antisense or oligomeric compound may be capable of binding to a complementary oligomeric compound to form a duplex, in which case the compound would no longer be single-stranded.

As used herein, "standard cell assay" means any of the assays described in Examples 1-9, and reasonable variations thereof.

As used herein, "standard in vivo experiment" means the procedure described in Example 10 and reasonable variations thereof.

As used herein, "stereorandom chiral center" in the context of a population of molecules of identical molecular formula means a chiral center having a random stereochemical configuration. For example, in a

population of molecules comprising a stereorandom chiral center, the number of molecules having the (*S*) configuration of the stereorandom chiral center may be but is not necessarily the same as the number of molecules having the (*R*) configuration of the stereorandom chiral center. The stereochemical configuration of a chiral center is considered random when it is the result of a synthetic method that is not designed to control the stereochemical configuration.In certain embodiments, a stereorandom chiral center is a stereorandom phosphorothioate internucleoside linkage.

As used herein, "sugar moiety" means an unmodified sugar moiety or a modified sugar moiety. As used herein, "unmodified sugar moiety" means a 2'-OH(H) ribosyl moiety, as found in RNA (an "unmodified RNA sugar moiety"), or a 2'-H(H) moiety, as found in DNA (an "unmodified DNA sugar moiety"). As used herein, "modified sugar moiety" or "modified sugar" means a modified furanosyl sugar moiety or a sugar surrogate. As used herein, modified furanosyl sugar moiety means a furanosyl sugar comprising a non-hydrogen substituent in place of at least one hydrogen of an unmodified sugar moiety. In certain embodiments, a modified furanosyl sugar moiety is a 2'-substituted sugar moiety. Such modified furanosyl sugar moieties include bicyclic sugars and non-bicyclic sugars. As used herein, "sugar surrogate" means a modified sugar moiety having other than a furanosyl moiety that can link a nucleobase to another group, such as an internucleoside linkage, conjugate group, or terminal group in an oligonucleotide. Modified nucleosides comprising sugar surrogates can be incorporated into one or more positions within an oligonucleotide and such oligonucleotides are capable of hybridizing to complementary oligomeric compounds or nucleic acids.

As used herein, "target nucleic acid," "target RNA," "target RNA transcript" and "nucleic acid target" mean a nucleic acid that an antisense compound is designed to affect.

As used herein, "target region" means a portion of a target nucleic acid to which an antisense compound is designed to hybridize.

As used herein, "terminal group" means a chemical group or group of atoms that is covalently linked to a terminus of an oligonucleotide.

As used herein, "terminal wing nucleoside" means a nucleoside that is located at the terminus of a wing segment of a gapmer. Any wing segment that comprises or consists of at least two nucleosides has two termini: one that is immediately adjacent to the gap segment; and one that is at the end opposite the gap segment. Thus, any wing segment that comprises or consists of at least two nucleosides has two terminal nucleosides, one at each terminus.

As used herein, "therapeutically effective amount" means an amount of a compound, pharmaceutical agent, or composition that provides a therapeutic benefit to an individual. In certain embodiments, the therapeutically effective amount refers to the level or amount of a compound that treats or ameliorates symptoms of a disease associated with DNM2. In certain embodiments, the therapeutically effective amount may be administered prior to the onset of the disease associated with DNM2or may be administered after initiation of the disease associated with DNM2.

As used herein, "treat" refers to administering a compound or pharmaceutical composition to an animal in order to effect an alteration or improvement of a disease, disorder, or condition in the animal. In one embodiment, a subject is successfully treated if, after receiving a therapeutically effective amount of a compound according to the present invention, the subject shows observable and/or measurable reduction or relief to some extent of one or more of the symptoms associated with the specific disease associated with DNM2, such as but not limited to reduced morbidity and mortality, improvement in quality of life issues, increased body weight, preservation or increase in muscle strength, decrease in time taken to rise from the floor, decrease in nine-meter walking time, decrease in time taken to climb four stairs, increased ability to lift weight, increased distance of a 6 minute walk, increased leg function grade, improved pulmonary function and/or cardiac function. Parameters for assessing successful treatment and improvement in the disease are readily measurable by routine procedures familiar to a physician.

Certain Embodiments

Certain embodiments provide methods, compounds and compositions for inhibiting DNM2 expression.

Certain embodiments provide methods, compounds and compositions for inhibiting DNM2 expression as compared to an untreated or control sample. In one embodiment, said inhibition is an inhibition of DNM2 expression of at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90%. In one embodiment, inhibiting the expression or activity refers to a reduction or blockade of the expression or activity relative to the expression or activity in an untreated or control sample of at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% as compared to an untreated or control sample.

Certain embodiments provide compounds comprising or consisting of oligonucleotides complementary to a DNM2 nucleic acid. In certain embodiments, the DNM2 nucleic acid has the sequence set forth in RefSeq or GenBank Accession No. NC_000019.10 truncated from nucleosides 10715001 to 10835000 (disclosed herein as SEQ ID NO: 1), NM_004945.3 (disclosed herein as SEQ ID NO: 2), NM_001005361.2 (disclosed herein as SEQ ID NO: 3), or NM_001005360.2 (disclosed herein as SEQ ID NO: 3135). In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded.

Certain embodiments provide a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134.

As used herein, the term "identity" refers to the subunit sequence identity between two nucleic acid molecules, such as, two DNA molecules or two RNA molecules. When a subunit position in both of the two

molecules is occupied by the same monomeric subunit; *e.g.*, if a position in each of two DNA molecules is occupied by adenine, then they are identical (or homologous) at that position. The homology between two sequences is a direct function of the number of matching or homologous positions; *e.g.*, if half (*e.g.*, five positions in a polymer ten subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (*e.g.*, 9 of 10), are matched or homologous, the two sequences are 90% homologous. Thus, the term "homologous" or "identical", when used in a relationship between the sequences of two or more nucleic acid molecules, refers to the degree of sequence relatedness between nucleic acid molecules, as determined by the number of matches between strings of two or more nucleotide residues. "Identity" measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (*i.e.*, "algorithms"). Identity of related polypeptides can be readily calculated by known methods. Such methods include, but are not limited to, those described in Computational Molecular Biology, Lesk, A. M., ed., Oxford University Press, New York, 1988; Biocomputing: Informatics and Genome Projects, Smith, D. W., ed., Academic Press, New York, 1993; Computer Analysis of Sequence Data, Part 1, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; Sequence Analysis in Molecular Biology, von Heinje, G., Academic Press, 1987; Sequence Analysis Primer, Gribskov, M. and Devereux, J., eds., M. Stockton Press, New York, 1991; and Carillo et al., SIAM J. Applied Math. 48, 1073 (1988). Preferred methods for determining identity are designed to give the largest match between the sequences tested. Methods of determining identity are described in publicly available computer programs. Preferred computer program methods for determining identity between two sequences include the GCG program package, including GAP (Devereux et al., Nucl. Acid. Res. \2, 387 (1984); Genetics Computer Group, University of Wisconsin, Madison, Wis.), BLASTP, BLASTN, and FASTA (Altschul et al., J. MoI. Biol. 215, 403-410 (1990)). The BLASTX program is publicly available from the National Center for Biotechnology Information (NCBI) and other sources (BLAST Manual, Altschul et al. NCB/NLM/NIH Bethesda, Md. 20894; Altschul et al., supra). The well-known Smith Waterman algorithm may also be used to determine identity.

In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

Certain embodiments provide a compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 or at least 8 contiguous nucleobases of a sequence having at least 70% identity with any of the nucleobase sequences of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2879 or a sequence having at least 70% identity with SEQ ID NO: 2879. In certain embodiments, the nucleobase sequence of the modified

oligonucleotide comprises or consists of SEQ ID NO: 3056 or a sequence having at least 70% identity with SEQ ID NO: 3056. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2123 or a sequence having at least 70% identity with SEQ ID NO: 2123. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2189 or a sequence having at least 70% identity with SEQ ID NO: 2189. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2453 or a sequence having at least 70% identity with SEQ ID NO: 2453. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2160 or a sequence having at least 70% identity with SEQ ID NO: 2160. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2232 or a sequence having at least 70% identity with SEQ ID NO: 2232. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide has a nucleobase sequence comprising at least 12 contiguous nucleobases of any of SEQ ID Numbers from 7 to 3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Certain embodiments provide a compound comprising a modified oligonucleotide 10 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

Certain embodiments provide a compound comprising a modified oligonucleotide 11 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the

compound is double-stranded. In certain embodiments, the modified oligonucleotide is 11 to 30 linked nucleosides in length.

Certain embodiments provide a compound comprising a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 12 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 12 to 30 linked nucleosides in length.

In certain embodiments, the compound comprises a modified oligonucleotide 16 linked nucleosides in length. In certain embodiments, the compound is an antisense compound or oligomeric compound.

Certain embodiments provide a compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded. In certain embodiments, the modified oligonucleotide is 16 to 30 linked nucleosides in length.

Certain embodiments provide a compound comprising a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134 or of any sequence having at least about 70% identity with any of the nucleobase sequences of SEQ ID NOs: 7-3134, such as, for example, at least about 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% identity or more with any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound is an antisense compound or oligomeric compound. In certain embodiments, the compound is single-stranded. In certain embodiments, the compound is double-stranded.

In certain embodiments, compounds comprise or consist of modified oligonucleotides complementary to an intron of a DNM2 nucleic acid transcript. In certain embodiments, modified oligonucleotides are complementary to intron 1, intron 2, intron 3, intron 4, intron 5, intron 6, intron 7, intron 8, intron 9, intron 9-10a, intron 10, intron 10a-11, intron 11, intron 12, intron 13, intron 14, intron 15, intron 16, intron 17, intron 18, intron 19, or intron 19-20a of a DNM2 nucleic acid transcript. In certain such embodiments, modified oligonucleotides are complementary to a sequence within nucleotides 3404-44,737; 44,812-57,478; 57,629-60,702; 60,907-62,117; 62,217-67,959; 68,121-71,563; 71,707-78,719; 78,856-80,371; 80,440-81,060;

80,440-82,379; 81,200-83,485; 82,519-83,485; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 105,090-108,787; 108,990-110,056; 110,222-114,035; 114,269-115,126; 115,379-115,977; or 115,379-115,980 of SEQ ID NO: 1. In certain embodiments, compounds comprise or consist of oligonucleotides having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion of intron 1, intron 2, intron 3, intron 4, intron 5, intron 6, intron 7, intron 8, intron 9, intron 9-10a, intron 10, intron 10a-11, intron 11, intron 12, intron 13, intron 14, intron 15, intron 16, intron 17, intron 18, intron 19, or intron 19-20a of a DNM2 nucleic acid transcript. In certain embodiments, such oligonucleotides have at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 3404-44,737; 44,812-57,478; 57,629-60,702; 60,907-62,117; 62,217-67,959; 68,121-71,563; 71,707-78,719; 78,856-80,371; 80,440-81,060; 80,440-82,379; 81,200-83,485; 82,519-83,485; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 105,090-108,787; 108,990-110,056; 110,222-114,035; 114,269-115,126; 115,379-115,977; or 115,379-115,980 of SEQ ID NO: 1. In certain embodiments, these compounds are antisense compounds or oligomeric compounds. Compounds comprising a modified oligonucleotide complementary to certain introns of a DNM2 nucleic acid transcript, *e.g.*, intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 pre-mRNA, are generally especially potent and tolerable. Thus, such certain introns can be considered hot spot regions for targeting a DNM2 nucleic acid transcript.

In certain embodiments, compounds comprise or consist of modified oligonucleotides complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, modified oligonucleotides are complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, compounds comprise or consist of oligonucleotides having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion of intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, such oligonucleotides have at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, these compounds are antisense compounds or oligomeric compounds.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

In certain embodiments, compounds comprise or consist of modified oligonucleotides complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain

embodiments, modified oligonucleotides are complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, compounds comprise or consist of oligonucleotides having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion of intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, such oligonucleotides have at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, these compounds are antisense compounds or oligomeric compounds.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion complementary to an equal length portion within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979; of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and complementary within nucleotides 89,722-89,737; 83,880-83,895; 90,081-90,096; 94,450-94,465; 11,960-11,975; 93,322-93,337; or 97,855-97,870 of SEQ ID NO: 1. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, or 16 contiguous nucleobase portion of the nucleobase sequence of any one of compound numbers 951799, 949935, 950023, 950089, 951372, 950060, or 950132 (SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232). In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2879 or of a sequence having at least 70% identity with SEQ ID NO: 2879. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 3056 or of a sequence having at least 70% identity with SEQ ID NO: 3056. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2123 or of a sequence having at least 70% identity with SEQ ID NO: 2123. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2189 or of a sequence having at least 70% identity with SEQ ID NO: 2189. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2453 or of a sequence having at least 70% identity with SEQ ID NO: 2453. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2160 or of a sequence having at least 70% identity with SEQ ID NO: 2160. In certain embodiments, the nucleobase sequence of the modified oligonucleotide comprises or consists of SEQ ID NO: 2232 or of a sequence having at least 70% identity with SEQ ID NO: 2232.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of compound numbers 951799, 949935, 950023, 950089, 951372, 950060, or 950132 (SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232). In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide having a nucleobase sequence consisting of the nucleobase sequence of any one of compound numbers 951799, 949935, 950023, 950089, 951372, 950060, or 950132 (SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232).

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of the compound number 951799 (SEQ ID NO: 2879). In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length.

In certain embodiments, a compound comprising or consisting of a modified oligonucleotide complementary to DNM2 is compound number 951799. Out of the over 3,000 compounds that were screened as described in the Examples section below, compound numbers 951799, 949935, 950023, 950089, 951372, 950060, and 950132 emerged as the top lead compounds. In particular, compound number 951799 exhibited the best combination of properties in terms of potency and tolerability out of over 3,000 compounds.

In certain embodiments, any of the foregoing oligonucleotides is a modified oligonucleotide comprising at least one modified internucleoside linkage, at least one modified sugar, and/or at least one modified nucleobase.

In certain embodiments, any of the foregoing modified oligonucleotides comprises at least one modified sugar. In certain embodiments, at least one modified sugar is a bicyclic sugar, such as a cEt bicyclic sugar, an LNA bicyclic sugar, or an ENA bicyclic sugar.

In certain embodiments, the modified oligonucleotide comprises at least one modified internucleoside linkage, such as a phosphorothioate internucleoside linkage.

In certain embodiments, any of the foregoing modified oligonucleotides comprises at least one modified nucleobase, such as 5-methylcytosine.

In certain embodiments, any of the foregoing modified oligonucleotides comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar. In certain embodiments, the modified oligonucleotide is 16 to 50 linked nucleosides in length having a nucleobase sequence comprising the

sequence recited in any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 or a sequence having at least 70% identity with any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the modified oligonucleotide is 16 to 50 linked nucleosides in length having a nucleobase sequence comprising the sequence recited in SEQ ID NO: 2879 or a sequence having at least 70% identity with SEQ ID NO: 2879. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 or a sequence having at least 70% identity with any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the modified oligonucleotide is 10 to 30 linked nucleosides in length having a nucleobase sequence comprising the sequence recited in SEQ ID NO: 2879 or a sequence having at least 70% identity with SEQ ID NO: 2879. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length having a nucleobase sequence consisting of the sequence recited in any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 or a sequence having at least 70% identity with any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 2879 or a sequence having at least 70% identity with SEQ ID NO: 2879.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide 20-50 linked nucleobases in length having a nucleobase sequence comprising the sequence recited in any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 or a sequence having at least 70% identity with any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises

a gap segment consisting of ten linked 2'-deoxynucleosides;

a 5' wing segment consisting of three linked nucleosides; and

a 3' wing segment consisting of three linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein the nucleosides of the 5' wing segment each comprise a cEt bicyclic sugar; wherein the nucleosides of the 3' wing segment each comprises a cEt bicyclic sugar; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide is 16-80 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16-30 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is 16 linked nucleosides in length.

In certain embodiments, a compound comprises or consists of a modified oligonucleotide according to one of the following formulas:

Gks Tks Tks Tds Ads Tds Tds Ads Tds Ads Gds Gds Gds mCks Tks Tk (SEQ ID NO: 2879);

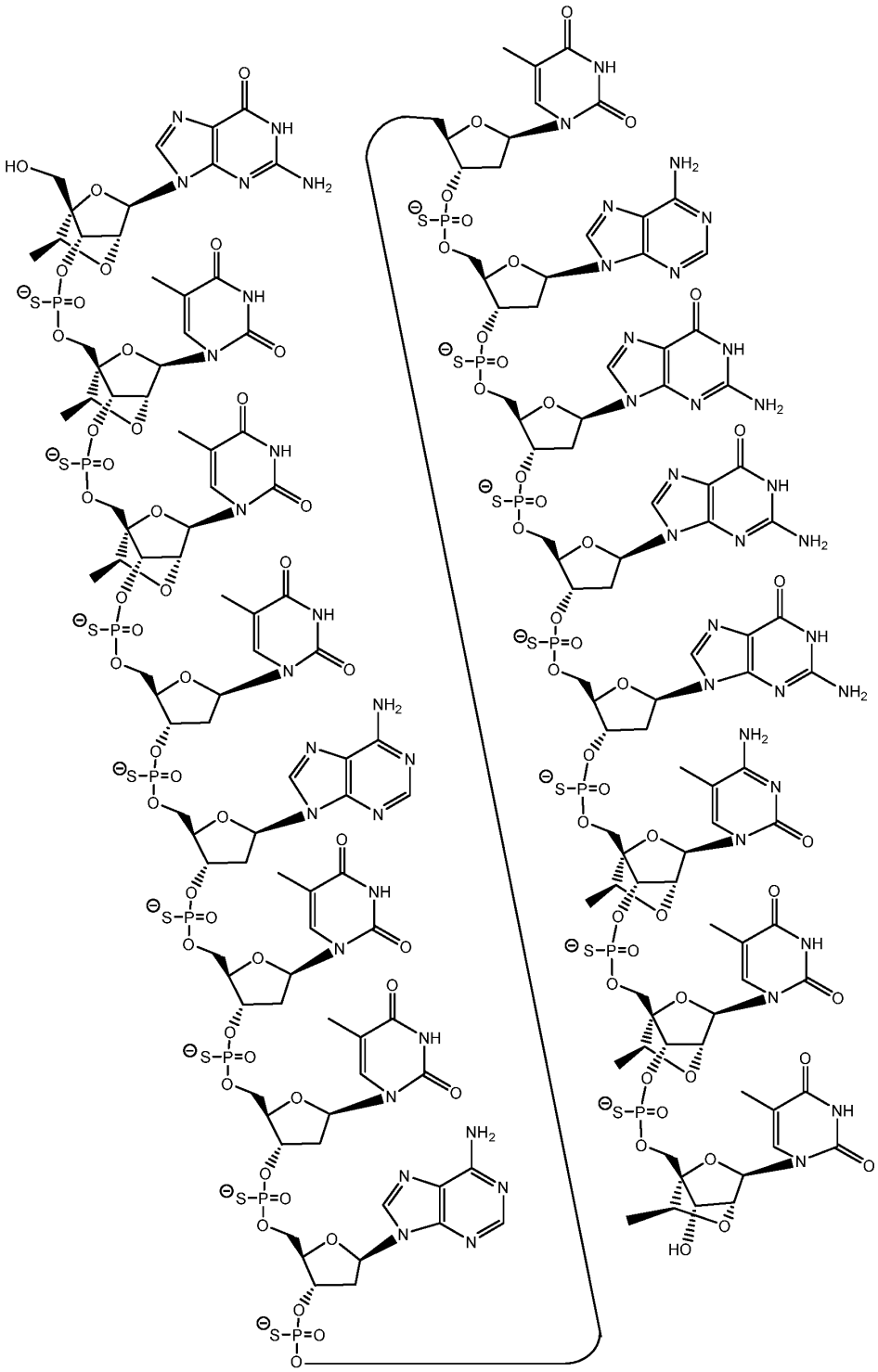
Gks Gks Aks Tds Tds Tds Tds Ads Gds Gds Ads Gds Gds Tks Gks Ak (SEQ ID NO: 3056);

Gks mCks Aks Tds Ads Gds Ads mCds Ads Ads Ads Tds mCds mCks mCks Ak (SEQ ID NO: 2123);

Gks mCks Aks Ads Ads Tds Ads Tds Gds Ads Tds Tds mCds Aks Tks mCk (SEQ ID NO: 2189);
Gks Gks Tks mCds Ads Tds Tds Ads Ads Ads Gds Ads Tds Tks mCks Tk (SEQ ID NO: 2453);
Aks Tks Gks Tds Ads Tds Tds Ads mCds mCds Tds Ads mCds Gks Gks mCk (SEQ ID NO: 2160); or
Gks Tks Aks mCds Ads Ads Tds Gds Tds Ads Ads Gds mCds mCks Tks Tk (SEQ ID NO: 2232)

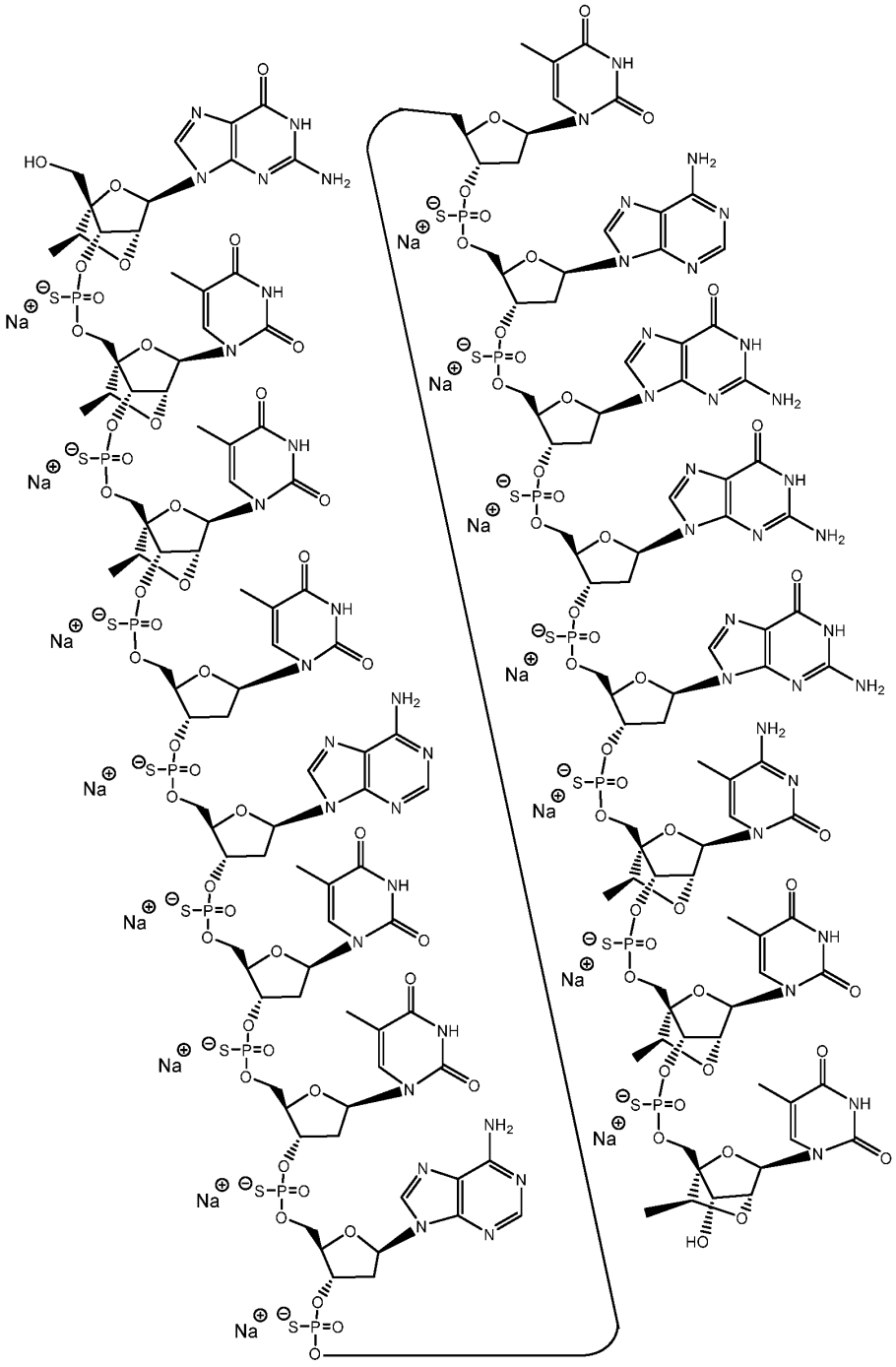
wherein A = an adenine, mC = a 5-methylcytosine, G = a guanine, T = a thymine, k = a cEt sugar moiety, d = a 2'-deoxyribosyl sugar moiety, and s = a phosphorothioate internucleoside linkage.

In certain embodiments, a compound comprises or consists of compound 951799, or salt thereof, a modified oligonucleotide having the following chemical structure:



[SEQ ID NO: 2879]

In certain embodiments, a compound comprises or consists of the sodium salt of compound 951799 having the following chemical structure:



[SEQ ID NO: 2879]

In any of the foregoing embodiments, the compound or oligonucleotide can be at least 85%, at least 90%, at least 95%, at least 98%, at least 99%, or 100% complementary to a nucleic acid encoding DNM2.

In any of the foregoing embodiments, the compound can be single-stranded. In certain embodiments, the compound comprises 2'-deoxyribonucleosides. In certain embodiments, the compound is double-stranded. In certain embodiments, the compound is double-stranded and comprises ribonucleosides. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

In any of the foregoing embodiments, the compound can be 8 to 80, 10 to 30, 12 to 50, 13 to 30, 13 to 50, 14 to 30, 14 to 50, 15 to 30, 15 to 50, 16 to 30, 16 to 50, 17 to 30, 17 to 50, 18 to 22, 18 to 24, 18 to 30, 18 to 50, 19 to 22, 19 to 30, 19 to 50, or 20 to 30 linked nucleosides in length. In certain embodiments, the compound comprises or consists of an oligonucleotide.

The present invention thus relates to a modified oligonucleotide or compounds comprising modified oligonucleotides complementary to a DNM2 nucleic acid as described hereinabove.

In certain embodiments, a compound comprises a modified oligonucleotide described herein and a conjugate group. In certain embodiments, the conjugate group is linked to the modified oligonucleotide at the 5' end of the modified oligonucleotide. In certain embodiments, the conjugate group is linked to the modified oligonucleotide at the 3' end of the modified oligonucleotide.

In certain embodiments, compounds or compositions provided herein comprise a salt of the modified oligonucleotide. In certain embodiments, the salt is a sodium salt. In certain embodiments, the salt is a potassium salt.

In certain embodiments, the compounds or compositions as described herein are active by virtue of having at least one of an *in vitro* IC_{50} of less than 300 nM, 200 nM, 100 nM, 80 nM, 50 nM, or 30 nM in a standard cell assay. Standard cell assays are described in the Examples.

In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having at least one of an increase an alanine transaminase (ALT) or aspartate transaminase (AST) value of no more than 4 fold, 3 fold, 2 fold, or 1.5 fold over saline treated animals or an increase in liver, spleen, or kidney weight of no more than 30%, 20%, 15%, 12%, 10%, 5%, or 2% compared to control treated animals. In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having no increase of ALT or AST over control treated animals. In certain embodiments, the compounds or compositions as described herein are highly tolerable as demonstrated by having no increase in liver, spleen, or kidney weight over control animals.

Certain embodiments provide a composition comprising or consisting essentially of the compound of any of the aforementioned embodiments or salt thereof.

Certain embodiments provide a composition comprising or consisting essentially of the compound of any of the aforementioned embodiments or salt thereof and at least one of a pharmaceutically acceptable carrier or diluent. Therefore, in one embodiment, the composition of the invention is a pharmaceutical composition.

Certain embodiments provide a medicament comprising or consisting essentially of the compound of any of the aforementioned embodiments or salt thereof. Therefore, in one embodiment, the composition of the invention is a medicament.

As used herein, the term "consists essentially of", with reference to a composition, pharmaceutical composition or medicament, means that the compound of the invention is the only active ingredient, therapeutic agent or agent with a biologic activity within said pharmaceutical composition or medicament.

In certain embodiments, the composition has a viscosity less than about 40 centipoise (cP), less than about 30 cP, less than about 20 cP, less than about 15 cP, less than about 10 cP, less than about 5 cP, or less than about 3 cP, or less than about 1.5 cP. In certain embodiments, the composition having any of the aforementioned viscosities comprises a compound provided herein at a concentration of about 15 mg/mL, 20 mg/mL, 25 mg/mL, 50 mg/mL, 100 mg/mL, 150 mg/mL, or about 200 mg/mL. In certain embodiments, the composition having any of the aforementioned viscosities and/or compound concentrations has a temperature of room temperature or about 20°C, about 21°C, about 22°C, about 23°C, about 24°C, about 25°C, about 26°C, about 27°C, about 28°C, about 29°C, or about 30°C.

Embodiment 1. A compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Embodiment 2. A compound comprising a modified oligonucleotide 9 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 9 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Embodiment 3. A compound comprising a modified oligonucleotide 10 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 10 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Embodiment 4. A compound comprising a modified oligonucleotide 11 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 11 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Embodiment 5. A compound comprising a modified oligonucleotide 12 to 50 linked nucleosides in length having a nucleobase sequence comprising at least 12, at least 13, at least 14, or at least 15 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134.

Embodiment 6. A compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 7-3134.

Embodiment 7. A compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 7-3134.

Embodiment 8. A compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length complementary within nucleobases 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1, wherein said modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1.

Embodiment 9. A compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length having a nucleobase sequence comprising a portion of at least 8 contiguous nucleobases 100% complementary to an equal length portion of nucleobases 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1.

Embodiment 10. A compound comprising a modified oligonucleotide 8 to 50 linked nucleosides in length complementary within nucleobases 83,573-87,287 or 87,359-90,915 of SEQ ID NO: 1, wherein said modified oligonucleotide is at least 85%, 90%, 95%, or 100% complementary to SEQ ID NO: 1.

Embodiment 11. A compound comprising a modified oligonucleotide complementary to intron 1 of a human DNM2 pre-mRNA.

Embodiment 12. A compound comprising a modified oligonucleotide complementary to intron 11 of a human DNM2 pre-mRNA.

Embodiment 13. A compound comprising a modified oligonucleotide complementary to intron 12 of a human DNM2 pre-mRNA.

Embodiment 14. A compound comprising a modified oligonucleotide complementary to intron 13 of a human DNM2 pre-mRNA.

Embodiment 15. A compound comprising a modified oligonucleotide complementary to intron 14 of a human DNM2 pre-mRNA.

Embodiment 16. A compound comprising a modified oligonucleotide complementary to exon 10 of a human DNM2 pre-mRNA or human DNM2 mRNA.

Embodiment 17. A compound comprising a modified oligonucleotide complementary to the 3'-UTR of a human DNM2 pre-mRNA or human DNM2 mRNA.

Embodiment 18. A compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232.

Embodiment 19. A compound comprising a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232.

Embodiment 20. A compound comprising a modified oligonucleotide having a nucleobase sequence comprising SEQ ID NO: 2879.

Embodiment 21. A compound comprising a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises:

a gap segment consisting of 8-12 linked 2'-deoxynucleosides;

a 5' wing segment consisting of 1-7 linked nucleosides; and

a 3' wing segment consisting of 1-7 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each terminal wing nucleoside comprises a modified sugar.

Embodiment 22. A compound comprising a modified oligonucleotide 16 linked nucleosides in length having a nucleobase sequence consisting of the sequence recited in SEQ ID NO: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises

a gap segment consisting of 10 linked 2'-deoxynucleosides;

a 5' wing segment consisting of 3 linked nucleosides; and

a 3' wing segment consisting of 3 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment; wherein each nucleoside of each wing segment comprises a cEt sugar moiety; wherein each internucleoside linkage is a phosphorothioate linkage; and wherein each cytosine is a 5-methylcytosine.

Embodiment 23. The compound of any one of embodiments 1-22, wherein the oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to any of SEQ ID NO: 1, 2, 3, or 3135.

Embodiment 24. The compound of any one of embodiments 1-23, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

Embodiment 25. The compound of embodiments 24, wherein the at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 26. The compound of any one of embodiments 1-21 or 23-25, wherein the modified oligonucleotide comprises at least one bicyclic sugar.

Embodiment 27. The compound of Embodiments 26, wherein the at least one bicyclic sugar is selected from the group consisting of LNA, ENA, and cEt.

Embodiment 28. The compound of embodiment 27, wherein the at least one bicyclic sugar moiety is a cEt sugar moiety.

Embodiment 29. The compound of any one of embodiments 1-28, wherein the modified oligonucleotide comprises at least one 5-methylcytosine.

Embodiment 30. The compound of any one of embodiments 1-29, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar moiety.

Embodiment 31. The compound of any one of embodiments 1-30, wherein the compound is single-stranded.

Embodiment 32. The compound of any one of embodiments 1-30, wherein the compound is double-stranded.

Embodiment 33. The compound of any one of embodiments 1-32, wherein the compound comprises at least one unmodified ribosyl sugar moiety.

Embodiment 34. The compound of any one of embodiments 1-33, wherein the compound comprises at least one unmodified 2'-deoxyribosyl sugar moiety.

Embodiment 35. The compound of any one of embodiments 1-34, wherein the modified oligonucleotide consists of 10 to 30 linked nucleosides.

Embodiment 36. The compound of any one of embodiments 1-34, wherein the modified oligonucleotide consists of 12 to 30 linked nucleosides.

Embodiment 37. The compound of any one of embodiments 1-34, wherein the modified oligonucleotide consists of 15 to 30 linked nucleosides.

Embodiment 38. The compound of any one of embodiments 1-34, wherein the modified oligonucleotide consists of 16 to 20 linked nucleosides.

Embodiment 39. A compound comprising a modified oligonucleotide according to the following formula: Gks Tks Tks Tds Ads Tds Tds Ads Tds Ads Gds Gds Gds mCks Tks Tk; wherein,

A = an adenine,

mC = a 5-methylcytosine

G = a guanine,

T = a thymine,

k = a cEt sugar moiety,

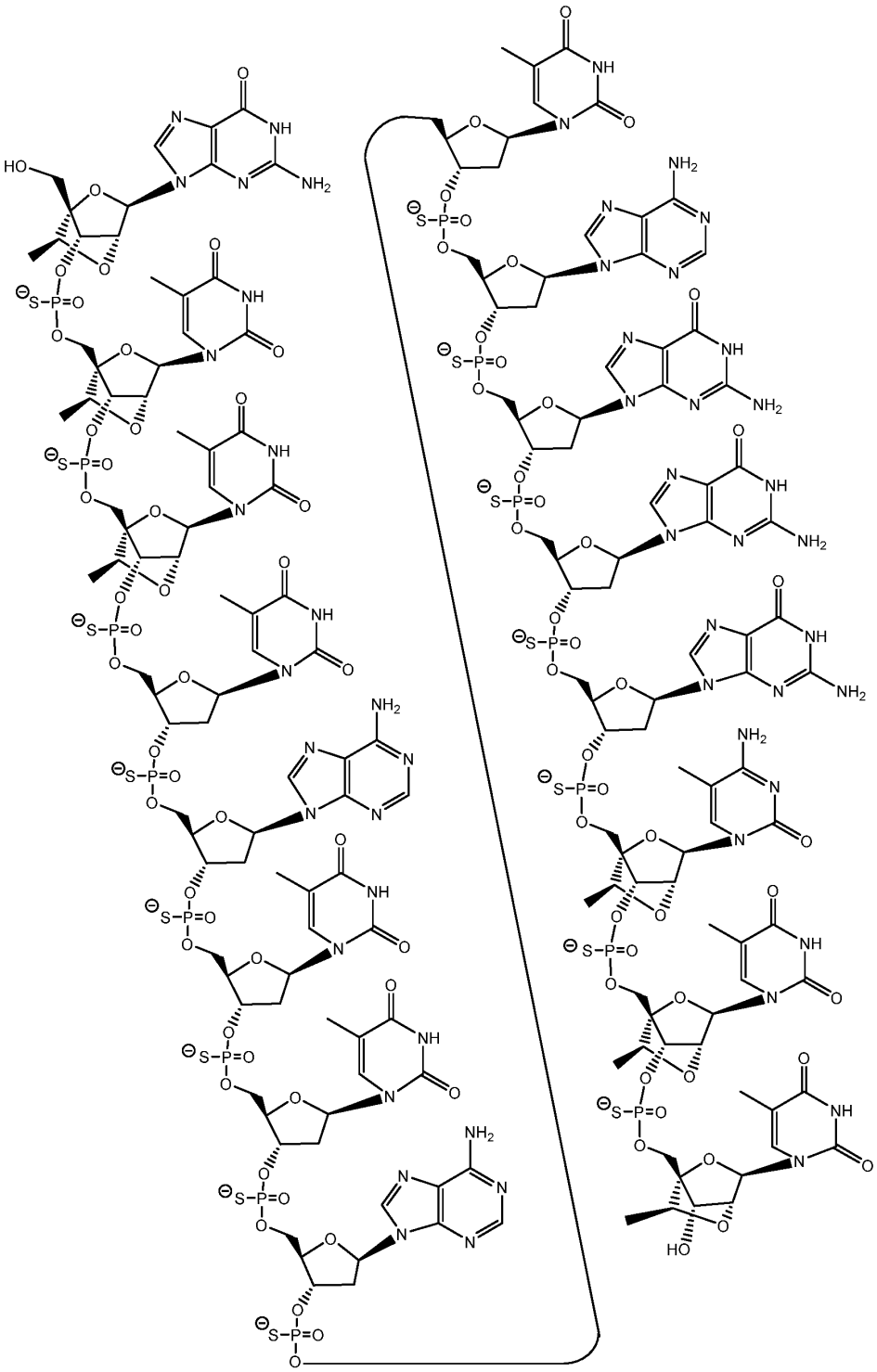
d = a 2'-deoxyribosyl sugar moiety, and

s = a phosphorothioate internucleoside linkage.

Embodiment 40. The compound of any one of embodiments 1-39 comprising a conjugate group.

Embodiment 41. The compound of embodiment 40, wherein the compound consists of the modified oligonucleotide and the conjugate group.

Embodiment 42. A compound according to the following formula:



[SEQ ID NO: 2879] or a salt thereof.

Embodiment 43. The compound of any one of embodiments 1-39 or 42, wherein the compound consists of the

modified oligonucleotide.

Embodiment 44. A compound consisting of a pharmaceutically acceptable salt form of any one of the compounds of embodiments 1-43.

Embodiment 45. The compound of embodiment 44, wherein the pharmaceutically acceptable salt is a sodium salt.

Embodiment 46. The compound of embodiment 44, wherein the pharmaceutically acceptable salt is a potassium salt.

Embodiment 47. A pharmaceutical composition comprising the compound of any one of embodiments 1-44 and at least one pharmaceutically acceptable carrier or diluent.

Embodiment 48. A chirally enriched population of the compounds of any one of embodiments 1-46, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

Embodiment 49. The chirally enriched population of embodiment 48, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*S*p) configuration.

Embodiment 50. The chirally enriched population of embodiment 48, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*R*p) configuration.

Embodiment 51. The chirally enriched population of embodiment 48, wherein the population is enriched for modified oligonucleotides having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage

Embodiment 52. The chirally enriched population of embodiment 51, wherein the population is enriched for modified oligonucleotides having the (*S*p) configuration at each phosphorothioate internucleoside linkage.

Embodiment 53. The chirally enriched population of embodiment 51, wherein the population is enriched for modified oligonucleotides having the (*R*p) configuration at each phosphorothioate internucleoside linkage.

Embodiment 54. The chirally enriched population of embodiment 51, wherein the population is enriched for modified oligonucleotides having the (*R*p) configuration at one particular phosphorothioate internucleoside linkage and the (*S*p) configuration at each of the remaining phosphorothioate internucleoside linkages.

Embodiment 55. The chirally enriched population of embodiment 48 or embodiment 51, wherein the population is enriched for modified oligonucleotides having at least 3 contiguous phosphorothioate internucleoside linkages in the *S*p, *S*p, and *R*p configurations, in the 5' to 3' direction.

Embodiment 56. A chirally enriched population of the compounds of any one of embodiments 1-46, wherein all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

Embodiment 57. A pharmaceutical composition comprising the population of compounds of any one of embodiments 48-56 and at least one pharmaceutically acceptable diluent or carrier.

Embodiment 58. The compound of any one of embodiments 1-46, a pharmaceutical composition comprising the compound of any one of embodiments 1-46 and at least one pharmaceutically acceptable carrier or diluent, or a pharmaceutical composition comprising the population of compounds of any one of embodiments 48-56 and at least one pharmaceutically acceptable carrier or diluent, for use in therapy.

Embodiment 59. The compound or composition of embodiment 58, for use in treating, preventing, or ameliorating centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 60. A method of treating, preventing, or ameliorating a disease associated with DNM2 in an individual comprising administering to the individual any of the compounds or compositions of embodiment 1-59, thereby treating, preventing, or ameliorating the disease.

Embodiment 61. A method of treating, preventing, or ameliorating a disease associated with DNM2 in an individual comprising administering to the individual a compound comprising a modified oligonucleotide 100% complementary to an exon 10, an intron, or the 3'-UTR of a DNM2 nucleic acid transcript, thereby treating, preventing, or ameliorating the disease.

Embodiment 62. The method of embodiment 60 or 61, wherein the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 63. The method of any one of embodiments 60-62, wherein the compound is single-stranded.

Embodiment 64. The method of any one of embodiments 60-63, wherein the DNM2 nucleic acid transcript is a pre-mRNA.

Embodiment 65. The method of any one of embodiments 60-64, wherein the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy.

Embodiment 66. The method of embodiment 65, wherein the individual has at least one mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

Embodiment 67. The method of any one of embodiments 60-66, wherein the administering increases body weight or muscle strength.

Embodiment 68. A method of inhibiting expression of DNM2 in a cell comprising contacting the cell with a single-stranded compound comprising a modified oligonucleotide 100% complementary to exon 10, an intron, or the 3'-UTR of a DNM2 nucleic acid transcript, thereby inhibiting expression of DNM2 in the cell.

Embodiment 69. The method of embodiment 68, wherein the cell is in the muscle of an individual.

Embodiment 70. The method of embodiment 69, wherein the individual has, or is at risk of having, a centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 71. A method of increasing body weight or muscle strength in an individual having, or at risk of having, a disease associated with DNM2 comprising administering a single-stranded compound comprising a modified oligonucleotide 100% complementary to a DNM2 nucleic acid transcript to the individual, thereby increasing body weight or muscle strength in the individual.

Embodiment 72. The method of embodiment 71, wherein the individual has, or is at risk of having, centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 73. The method of any one of embodiments 60-72, wherein the compound is the compound of any one of embodiments 1-46.

Embodiment 74. The method of any one of embodiments 60-72, wherein the compound is a member of the chirally enriched population of any one of embodiments 48-56.

Embodiment 75. The method of any one of embodiments 60-72, wherein the compound is a component of the pharmaceutical composition of embodiment 57.

Embodiment 76. The method any one of embodiments 60-67 or 69-75, wherein the compound is administered to the individual via subcutaneous injection.

Embodiment 77. The method any one of embodiments 60-67 or 69-75, wherein the compound is administered to the individual via intramuscular injection.

Embodiment 78. The method of any one of embodiments 60-67 or 69-77, wherein the compound is administered to the individual via intravenous injection.

Embodiment 79. Use of a single-stranded compound comprising a modified oligonucleotide 100% complementary to exon 10, intron 1, intron 11, intron, 12, intron 13, intron 14, or the 3'-UTR of a DNM2 nucleic acid transcript for treating, preventing, or ameliorating a disease associated with DNM2.

Embodiment 80. The use of embodiment 79, wherein the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 81. Use of the compound of any one of embodiments 1-46 or the composition of embodiment 57 for treating, preventing, or ameliorating a disease associated with DNM2.

Embodiment 82. Use of the compound of any one of embodiments 1-46 or the composition of embodiment 57 in the manufacture of a medicament for treating, preventing, or ameliorating a disease associated with DNM2.

Embodiment 83. The use of embodiment 81 or 82, wherein the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 84. The use of embodiment 80 or 83, wherein the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy.

Embodiment 85. The use of embodiment 84, wherein the disease is associated with a mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

Embodiment 86. Use of the compound of any one of embodiments 1-46 or the composition of embodiment 57 in the preparation of a medicament for treating, preventing, or ameliorating a disease associated with DNM2.

Embodiment 87. The use of embodiment 86, wherein the disease is centronuclear myopathy, Duchenne Muscular Dystrophy, or Charcot-Marie Tooth disease.

Embodiment 88. The use of embodiment 87, wherein the disease is X-linked myotubular myopathy, autosomal recessive centronuclear myopathy, or autosomal dominant centronuclear myopathy.

Embodiment 89. The use of embodiment 88, wherein the disease is associated with a mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

Certain Indications

Certain embodiments provided herein relate to methods of inhibiting DNM2 expression, which can be useful for treating, preventing, or ameliorating a disease associated with DNM2 in an individual, by administration of a compound that targets DNM2, such as the compound described herein. In certain diseases associated with DNM2, modest or partial inhibition of DNM2 expression is sufficient to treat, prevent, or ameliorate the disease (See, *e.g.*, Cowling et al. *J. Clin. Invest*. 124, 1350-1363 (2014) and Tasfaout et al. *Nat. Commun*. Jun 7; 8:15661 (2017).) In certain embodiments, the compound can be an antisense compound, oligomeric compound, or oligonucleotide complementary to DNM2, such as the ones described herein.

Examples of diseases associated with DNM2 that are treatable, preventable, and/or ameliorable with the methods provided herein include centronuclear myopathy (CNM), Charcot-Marie-Tooth disease (CMT), and Duchenne's Muscular Dystrophy (DMD). Centronuclear myopathy includes X-linked CNM (XLCNM), autosomal dominant CNM (ADCNM) and autosomal recessive CNM (ARCNM). Mutations in several genes are associated with CNM, including mutations in MTM1, BIN1, and DNM2. Other genes have been linked to a CNM-like myopathy: RYR1 encoding for the ryanodine receptor, TTN encoding Titin, CCDC78 (OMIM 614807) and the phosphoinositides phosphatase MTMR14 (called hJUMPY; OMIM 160150).

In certain embodiments, a method of treating, preventing, or ameliorating a disease associated with DNM2 in an individual comprises administering to the individual a compound comprising an antisense

compound targeted to DNM2, thereby treating, preventing, or ameliorating the disease. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual subcutaneously, intradermally, intranodally, intramedullary, intramuscularly, intrasternally, by intravenous (i.v.) injection, by infusion techniques or intraperitoneally. In certain embodiments, the compound is administered to the individual via subcutaneous injection. In certain embodiments, administering the compound increases or preserves body weight or muscle strength.

In certain embodiments, a method of treating, preventing, or ameliorating CNM, DMD, or CMT comprises administering to the individual a compound comprising a modified oligonucleotide complementary to a DNM2 nucleic acid, thereby treating, preventing, or ameliorating CNM, DMD, or CMT. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound is an antisense compound targeted to DNM2. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the

3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, intrasternally, by intravenous (i.v.) injection, by infusion techniques or intraperitoneally. In certain embodiments, the compound is administered to the individual systemically, *e.g.*, via subcutaneous or intramuscular injection. In certain embodiments, administering the compound increases or preserves body weight or muscle strength. In certain such embodiments, time taken to rise from the floor, nine-meter walking time, or time taken to climb four stairs is decreased. In certain embodiments, ability to lift weight, distance of a 6 minute walk, or leg function grade is increased. In certain embodiments, pulmonary function or cardiac function is improved. In certain embodiments, the individual is identified as having or at risk of having a disease associated with DNM2. Examples of factors of risk of having a disease associated with DNM2 include, but are not limited to, genetic predisposition, such as, for example, a mutation in at least one gene selected from among MTM1, BIN1, and DNM2.

In certain embodiments, a method of inhibiting expression of DNM2 in an individual having, or at risk of having, a disease associated with DNM2 comprises administering to the individual a compound comprising a modified oligonucleotide complementary to a DNM2 nucleic acid, thereby inhibiting expression of DNM2

in the individual. In certain embodiments, administering the compound inhibits expression of DNM2 in skeletal muscle. In certain embodiments, the individual has, or is at risk of having CNM, DMD, or CMT. In certain embodiments, the compound comprises an antisense compound targeted to DNM2. In certain embodiments, the antisense compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual subcutaneously, intradermally, intranodally, intramedullary, intramuscularly, intrasternally, by intravenous (i.v.) injection, by infusion techniques or intraperitoneally. In certain embodiments, the compound is administered to the individual systemically, *e.g.*, via subcutaneous or intramuscular injection. In certain embodiments, administering the compound increases or preserves body weight or muscle strength. In certain embodiments, the individual is identified as having or at risk of having a disease associated with DNM2.

In certain embodiments, a method of inhibiting expression of DNM2 in a cell comprises contacting the cell with a compound comprising an antisense compound targeted to DNM2, thereby inhibiting expression of DNM2 in the cell. In one embodiment, the expression of DNM2 is inhibited by at least about 40%, at least

about 50%, at least about 60%, at least about 70%, at least about 80%, or at least about 90%.In one embodiment, the expression of DNM2 is inhibited by at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% as compared to an untreated or control sample. In one embodiment, the method is an in vitro method. In certain embodiments, the cell is a muscle cell. In certain embodiments, the cell is a skeletal muscle cell. In certain embodiments, the muscle cell is in an individual who has, or is at risk of having CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

In certain embodiments, a method of increasing or preserving body weight or muscle strength of an individual having, or at risk of having, a disease associated with DNM2 comprises administering to the individual a compound comprising an antisense compound targeted to DNM2, increasing or preserving body weight or muscle strength of the individual. In certain such embodiments, time taken to rise from the floor, nine-meter walking time, or time taken to climb four stairs is decreased. In certain embodiments, ability to lift weight, distance of a 6 minute walk, or leg function grade is increased. In certain embodiments, pulmonary

function or cardiac function is improved. In certain embodiments, the individual has, or is at risk of having, CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual subcutaneously, intradermally, intranodally, intramedullary, intramuscularly, intrasternally, by intravenous (i.v.) injection, by infusion techniques or intraperitoneally. In certain embodiments, the compound is administered to the individual systemically, *e.g.*, via subcutaneous or intramuscular injection. In certain embodiments, the individual is identified as having or at risk of having a disease associated with DNM2.

Certain embodiments are drawn to a compound comprising an antisense compound targeted to DNM2 for use in treating a disease associated with DNM2. In certain embodiments, the disease is CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1,

intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound. In certain embodiments, the compound is administered to the individual subcutaneously, intradermally, intranodally, intramedullary, intramuscularly, intrasternally, by intravenous (i.v.) injection, by infusion techniques or intraperitoneally. In certain embodiments, the compound is to be administered to the individual systemically, *e.g.*, via subcutaneous or intramuscular injection.

Certain embodiments are drawn to a compound comprising an antisense compound targeted to DNM2 for use in increasing or preserving body weight or muscle strength of an individual having or at risk of having CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid

transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

Certain embodiments are drawn to use of the compound comprising an antisense compound targeted to DNM2 for the manufacture or preparation of a medicament for treating a disease associated with DNM2. Certain embodiments are drawn to use of the compound comprising an antisense compound targeted to DNM2 for the preparation of a medicament for treating a disease associated with DNM2. In certain embodiments, the disease is CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a

modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

Certain embodiments are drawn to use of a compound comprising an antisense compound targeted to DNM2 for the manufacture or preparation of a medicament for increasing or preserving body weight or muscle strength of an individual having or at risk of having CNM, DMD, or CMT. In certain embodiments, the compound comprises an oligonucleotide complementary to a DNM2 nucleic acid transcript. In certain embodiments, the compound is a compound as described herein. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, intron 14, exon 10, or the 3'-UTR of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; 97,378-104,979; 81,061-81,199; or 116,048-116,903 of SEQ ID NO: 1. In certain embodiments, the compound comprises or consists of a modified oligonucleotide complementary to intron 1, intron 11, intron 12, intron 13, or intron 14 of a DNM2 nucleic acid transcript. In certain embodiments, the modified oligonucleotide is complementary to a sequence within nucleotides 3,404-44,737; 83,573-87,287; 87,359-90,915; 90,968-97,263; or 97,378-104,979 of SEQ ID NO: 1. In certain embodiments, the compound comprises a modified oligonucleotide 8 to 50 linked nucleosides in length and having a nucleobase sequence comprising at least 8 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 12 to 50 linked nucleosides in length and having a nucleobase sequence comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide consisting of the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a modified oligonucleotide 16 to 50 linked nucleosides in length having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises a modified oligonucleotide having a nucleobase sequence consisting of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In any of the foregoing embodiments, the modified oligonucleotide can be 10 to 30 linked nucleosides in length. In certain embodiments, the compound is compound number 951799, 949935, 950023, 950089, 951372, 950060, or 950132. In any of the foregoing embodiments, the compound

can be single-stranded or double-stranded. In any of the foregoing embodiments, the compound can be an antisense compound or oligomeric compound.

In any of the foregoing methods or uses, the compound can be targeted to a DNM2 nucleic acid transcript. In certain embodiments, the compound comprises or consists of a modified oligonucleotide, for example a modified oligonucleotide 8 to 50 linked nucleosides in length, 10 to 30 linked nucleosides in length, 12 to 30 linked nucleosides in length, or 20 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to any of the nucleobase sequences recited in SEQ ID NOs: 1, 2, 3, or 3135. In certain embodiments, the modified oligonucleotide comprises at least one modified internucleoside linkage, at least one modified sugar, and at least one modified nucleobase. In certain such embodiments, the at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage, the at least one modified sugar is a bicyclic sugar, and the at least one modified nucleobase is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide comprises a gap segment consisting of linked 2'-deoxynucleosides; a 5' wing segment consisting of linked nucleosides; and a 3' wing segment consisting of linked nucleosides, wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each terminal wing nucleoside comprises a modified sugar.

In any of the foregoing embodiments, the modified oligonucleotide may be 12 to 30, 15 to 30, 15 to 25, 15 to 24, 16 to 24, 17 to 24, 18 to 24, 19 to 24, 20 to 24, 19 to 22, 20 to 22, 16 to 20, or 17 or 20 linked nucleosides in length. In certain embodiments, the modified oligonucleotide is at least 80%, 85%, 90%, 95% or 100% complementary to any of the nucleobase sequences recited in SEQ ID NOs: 1, 2, 3, or 3135. In certain embodiments, the modified oligonucleotide comprises at least one modified internucleoside linkage, at least one modified sugar, and at least one modified nucleobase. In certain embodiments, the at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage, the at least one modified sugar is a bicyclic sugar, and the at least one modified nucleobase is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide comprises a gap segment consisting of linked 2'-deoxynucleosides; a 5' wing segment consisting of linked nucleosides; and a 3' wing segment consisting of linked nucleosides, wherein the gap segment is positioned immediately adjacent to and between the 5' wing segment and the 3' wing segment and wherein each terminal wing nucleoside comprises a modified sugar.

In any of the foregoing methods or uses, the compound may comprise or consist of a modified oligonucleotide 16 to 30 linked nucleosides in length and having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment and wherein each nucleoside of each wing segment comprises a modified sugar.

In any of the foregoing methods or uses, the compound may comprise or consist of a modified oligonucleotide 16 to 30 linked nucleosides in length and having a nucleobase sequence comprising any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises:

a gap segment consisting of linked 2'-deoxynucleosides;

a 5' wing segment consisting of linked nucleosides; and

a 3' wing segment consisting of linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, wherein each terminal wing nucleoside comprises a modified sugar.

In any of the foregoing methods or uses, the compound may comprise or consist of a modified oligonucleotide 16 to 50 linked nucleobases in length having a nucleobase sequence comprising or consisting of the sequence recited in any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232, wherein the modified oligonucleotide comprises:

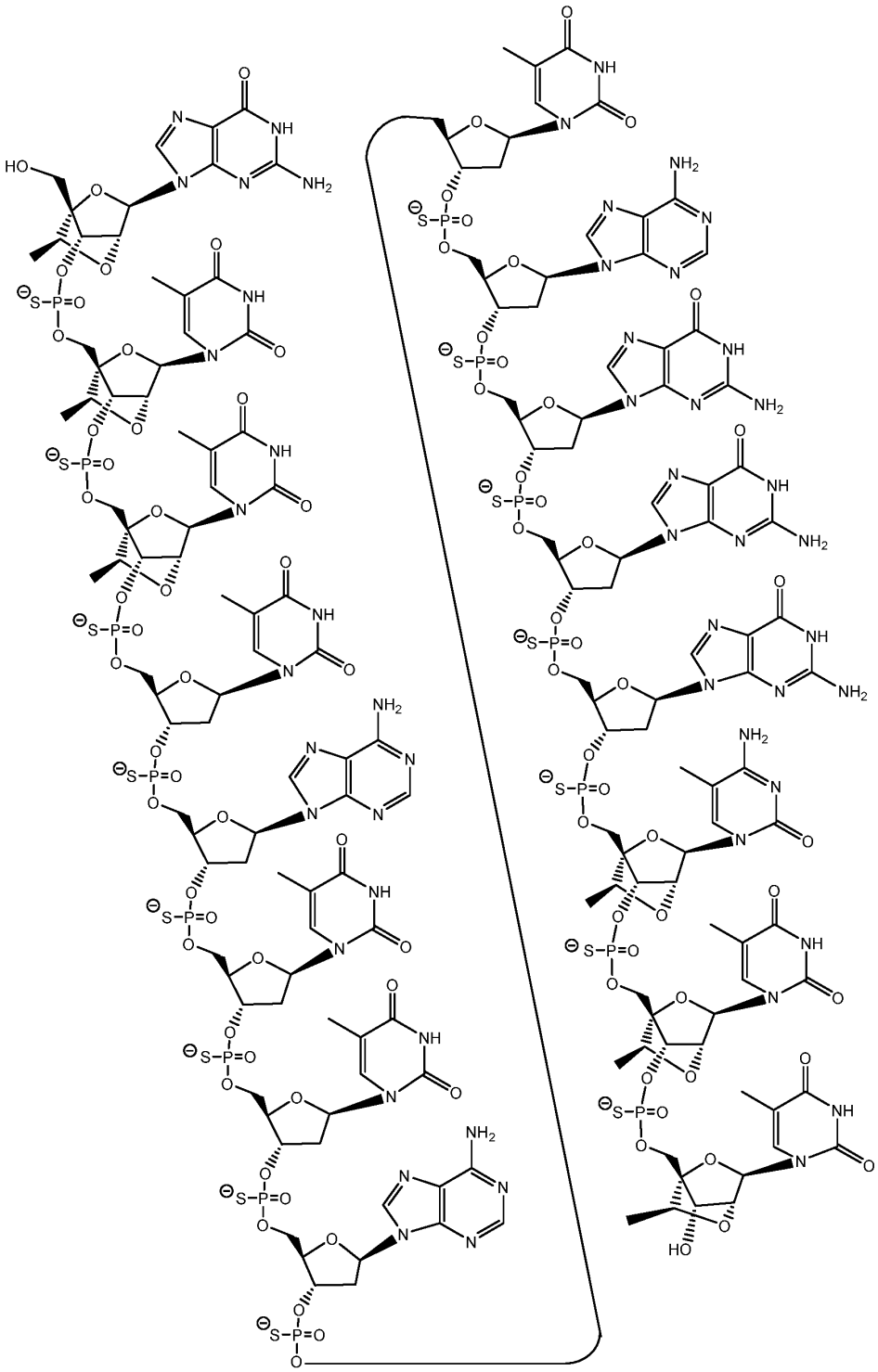
a gap segment consisting of 10 linked 2'-deoxynucleosides;

a 5' wing segment consisting of 3 linked nucleosides; and

a 3' wing segment consisting of 3 linked nucleosides;

wherein the gap segment is positioned between the 5' wing segment and the 3' wing segment, wherein each nucleoside of each wing segment comprises a cEt sugar; wherein each internucleoside linkage is a phosphorothioate linkage and wherein each cytosine is a 5-methylcytosine. In certain embodiments, the modified oligonucleotide consists of 16-30 linked nucleosides. In certain embodiments, the modified oligonucleotide consists of 16 linked nucleosides.

In one embodiment, in any of the foregoing methods or uses, the compound has the following chemical structure:



[SEQ ID NO: 2879]

In one embodiment, in any of the foregoing methods or uses, the compound can be administered systemically. In certain embodiments, the compound of any of the foregoing methods or uses can be administered through injection or infusion. In certain embodiments, the compound of any of the foregoing methods or uses can be administered via subcutaneous administration, intravenous administration, intramuscular administration, intraarterial administration, intraperitoneal administration, or intracranial administration, *e.g.* intrathecal or intracerebroventricular administration. In certain embodiments, the compound is administered to the individual intradermally, intranodally, intramedullary or intrasternally. In certain embodiments, the compound of any of the foregoing methods or uses can be administered orally.

Certain Combinations and Combination Therapies

In certain embodiments, a first agent comprising the compound described herein is co-administered with one or more secondary agents. In certain embodiments, such second agents are designed to treat the same disease, disorder, or condition as the first agent described herein. In certain embodiments, such second agents are designed to treat a different disease, disorder, or condition as the first agent described herein. In certain embodiments, a first agent is designed to treat an undesired side effect of a second agent. In certain embodiments, second agents are co-administered with the first agent to treat an undesired effect of the first agent. In certain embodiments, such second agents are designed to treat an undesired side effect of one or more pharmaceutical compositions as described herein. In certain embodiments, second agents are co-administered with the first agent to produce a combinational effect. In certain embodiments, second agents are co-administered with the first agent to produce a synergistic effect. In certain embodiments, the co-administration of the first and second agents permits use of lower dosages than would be required to achieve a therapeutic or prophylactic effect if the agents were administered as independent therapy.

In certain embodiments, one or more compounds or compositions provided herein are co-administered with one or more secondary agents. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are administered at different times. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are prepared together in a single formulation. In certain embodiments, one or more compounds or compositions provided herein and one or more secondary agents, are prepared separately.

Certain embodiments are directed to the use of a compound comprising a modified oligonucleotide complementary to a DNM2 nucleic acid transcript as described herein in combination with a secondary agent. In particular embodiments such use is in a method of treating a patient suffering from CNM, DMD, or CMT, or in the preparation or manufacture of a medicament for treating CNM, DMD, or CMT.

In certain embodiments the compound comprising a modified oligonucleotide complementary to a DNM2 nucleic acid transcript as described herein and the secondary agent are used in combination treatment by administering the two agents simultaneously, separately or sequentially. In certain embodiments the two

agents are formulated as a fixed dose combination product. In other embodiments the two agents are provided to the patient as separate units which can then either be taken simultaneously or serially (sequentially).

Certain Compounds

In certain embodiments, compounds described herein can be antisense compounds. In certain embodiments, the antisense compound comprises or consists of an oligomeric compound. In certain embodiments, the oligomeric compound comprises or consists of a modified oligonucleotide. In certain embodiments, the modified oligonucleotide has a nucleobase sequence complementary to that of a target nucleic acid.

In certain embodiments, a compound described herein comprises or consists of a modified oligonucleotide. In certain embodiments, the modified oligonucleotide has a nucleobase sequence complementary to that of a target nucleic acid.

In certain embodiments, a compound or antisense compound is single-stranded. Such a single-stranded compound or antisense compound comprises or consists of an oligomeric compound. In certain embodiments, such an oligomeric compound comprises or consists of an oligonucleotide and optionally a conjugate group. In certain embodiments, the oligonucleotide is an antisense oligonucleotide. In certain embodiments, the oligonucleotide is modified. In certain embodiments, the oligonucleotide of a single-stranded antisense compound or oligomeric compound comprises a self-complementary nucleobase sequence.

In certain embodiments, a compound or antisense compound is double-stranded. Such double-stranded compounds comprise a first oligomeric compound comprising or consisting of a first modified oligonucleotide having a region complementary to a target nucleic acid and a second oligomeric compound comprising or consisting of a second oligonucleotide having a region complementary to the first modified oligonucleotide. In certain embodiments, the first oligonucleotide is 100% complementary to the second oligonucleotide. In certain embodiments, the first and second oligonucleotides include non-complementary, overhanging nucleosides. In certain embodiments, the first modified oligonucleotide comprises unmodified ribosyl sugar moieties as those found in RNA. In such embodiments, thymine nucleobases in the first and/or second oligonucleotide are replaced by uracil nucleobases. In certain embodiments, the first and/or second oligomeric compound comprises a conjugate group. In certain embodiments, the first modified oligonucleotide is 12-30 linked nucleosides in length and the second oligonucleotide is 12-30 linked nucleosides in length. In certain embodiments, the second oligonucleotide is modified. In certain embodiments, the first modified oligonucleotide has a nucleobase sequence comprising at least 8 contiguous nucleobases of any of SEQ ID NOs: 7-3134.

Examples of single-stranded and double-stranded compounds include but are not limited to oligonucleotides, siRNAs, microRNA targeting oligonucleotides, and single-stranded RNAi compounds, such as small hairpin RNAs (shRNAs), single-stranded siRNAs (ssRNAs), and microRNA mimics.

In certain embodiments, a compound described herein has a nucleobase sequence that, when written in the 5' to 3' direction, comprises the reverse complement of the target segment of a target nucleic acid to which it is targeted.

In certain embodiments, a compound described herein comprises an oligonucleotide 10 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 12 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 12 to 22 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 14 to 30 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 14 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 15 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 15 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 16 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 16 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 30 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 21 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 18 to 20 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 20 to 30 linked subunits in length. In other words, such oligonucleotides are 12 to 30 linked subunits, 14 to 30 linked subunits, 14 to 20 subunits, 15 to 30 subunits, 15 to 20 subunits, 16 to 30 subunits, 16 to 20 subunits, 17 to 30 subunits, 17 to 20 subunits, 18 to 30 subunits, 18 to 20 subunits, 18 to 21 subunits, 20 to 30 subunits, or 12 to 22 linked subunits in length, respectively. In certain embodiments, a compound described herein comprises an oligonucleotide 14 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 16 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 17 linked subunits in length. In certain embodiments, compound described herein comprises an oligonucleotide 18 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 19 linked subunits in length. In certain embodiments, a compound described herein comprises an oligonucleotide 20 linked subunits in length. In other embodiments, a compound described herein comprises an oligonucleotide 8 to 80, 12 to 50, 13 to 30, 13 to 50, 14 to 30, 14 to 50, 15 to 30, 15 to 50, 16 to 30, 16 to 50, 17 to 30, 17 to 50, 18 to 22, 18 to 24, 18 to 30, 18 to 50, 19 to 22, 19 to 30, 19 to 50, or 20 to 30 linked subunits. In certain such embodiments, the compound described herein comprises an oligonucleotide 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46,

47, 48, 49, or 50 linked subunits in length, or a range defined by any two of the above values. In some embodiments the linked subunits are nucleotides, nucleosides, or nucleobases.

In certain embodiments, the compound may further comprise additional features or elements, such as a conjugate group, that are attached to the oligonucleotide. In certain embodiments, such compounds are antisense compounds. In certain embodiments, such compounds are oligomeric compounds. In embodiments where a conjugate group comprises a nucleoside (*i.e.* a nucleoside that links the conjugate group to the oligonucleotide), the nucleoside of the conjugate group is not counted in the length of the oligonucleotide.

In certain embodiments, compounds may be shortened or truncated. For example, a single subunit may be deleted from the 5' end (5' truncation), or alternatively from the 3' end (3' truncation). A shortened or truncated compound targeted to a DNM2 nucleic acid may have two subunits deleted from the 5' end, or alternatively may have two subunits deleted from the 3' end, of the compound. Alternatively, the deleted nucleosides may be dispersed throughout the compound.

When a single additional subunit is present in a lengthened compound, the additional subunit may be located at the 5' or 3' end of the compound. When two or more additional subunits are present, the added subunits may be adjacent to each other, for example, in a compound having two subunits added to the 5' end (5' addition), or alternatively to the 3' end (3' addition), of the compound. Alternatively, the added subunits may be dispersed throughout the compound.

It is possible to increase or decrease the length of a compound, such as an oligonucleotide, and/or introduce mismatch bases without eliminating activity (Woolf et al. *Proc. Natl. Acad. Sci. USA* 1992, 89:7305-7309; Gautschi *et al. J. Natl. Cancer Inst*. March 2001, 93:463-471; Maher and Dolnick *Nuc. Acid. Res*. 1998, 16:3341-3358). However, seemingly small changes in oligonucleotide sequence, chemistry and motif can make large differences in one or more of the many properties required for clinical development (Seth et al. *J. Med. Chem.* 2009, 52, 10; Egli et al. *J. Am. Chem. Soc.* 2011, 133, 16642).

In certain embodiments, compounds described herein are interfering RNA compounds (RNAi), which include double-stranded RNA compounds (also referred to as short-interfering RNA or siRNA) and single-stranded RNAi compounds (or ssRNA). Such compounds work at least in part through the RISC pathway to degrade and/or sequester a target nucleic acid (thus, include microRNA/microRNA-mimic compounds). As used herein, the term siRNA is meant to be equivalent to other terms used to describe nucleic acid molecules that are capable of mediating sequence specific RNAi, for example short interfering RNA (siRNA), double-stranded RNA (dsRNA), micro-RNA (miRNA), short hairpin RNA (shRNA), short interfering oligonucleotide, short interfering nucleic acid, short interfering modified oligonucleotide, chemically modified siRNA, post-transcriptional gene silencing RNA (ptgsRNA), and others. In addition, as used herein, the term "RNAi" is meant to be equivalent to other terms used to describe sequence specific RNA interference, such as post transcriptional gene silencing, translational inhibition, or epigenetics.

In certain embodiments, a compound described herein can comprise any of the oligonucleotide sequences targeted to a DNM2 nucleic acid transcript described herein. In certain embodiments, the compound can be double-stranded. In certain embodiments, the compound comprises a first strand comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of any one of SEQ ID NOs: 7-3134 and a second strand. In certain embodiments, the compound can be double-stranded. In certain embodiments, the compound comprises a first strand comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 and a second strand. In certain embodiments, the compound can be double-stranded. In certain embodiments, the compound comprises a first strand comprising at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of SEQ ID NO: 2879 and a second strand. In certain embodiments, the compound comprises a first strand comprising the nucleobase sequence of any one of SEQ ID NOs: 7-3134 and a second strand. In certain embodiments, the compound comprises a first strand comprising the nucleobase sequence of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232 and a second strand. In certain embodiments, the compound comprises a first strand comprising the nucleobase sequence of SEQ ID NO: 2879 and a second strand. In certain embodiments, the compound comprises ribonucleotides in which the first strand has uracil (U) in place of thymine (T) in any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises (i) a first strand comprising a nucleobase sequence complementary to the site on a DNM2 nucleic acid to which any of SEQ ID NOs: 7-3134 is complementary, and (ii) a second strand. In certain embodiments, the compound comprises one or more modified nucleotides in which the 2' position in the sugar contains a halogen (such as fluorine group; 2'-F) or contains an alkoxy group (such as a methoxy group; 2'-OMe). In certain embodiments, the compound comprises at least one 2'-F sugar modification and at least one 2'-OMe sugar modification. In certain embodiments, the at least one 2'-F sugar modification and at least one 2'-OMe sugar modification are arranged in an alternating pattern for at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases along a strand of the dsRNA compound. In certain embodiments, the compound comprises one or more linkages between adjacent nucleotides other than a naturally-occurring phosphodiester linkage. Examples of such linkages include phosphoramide, phosphorothioate, and phosphorodithioate linkages. The compounds may also be chemically modified nucleic acid molecules as taught in U.S. Pat. No. 6,673,661. In other embodiments, the compound contains one or two capped strands, as disclosed, for example, by WO 00/63364, filed Apr. 19, 2000.

In certain embodiments, the first strand of the compound is an siRNA guide strand and the second strand of the compound is an siRNA passenger strand. In certain embodiments, the second strand of the compound is complementary to the first strand. In certain embodiments, each strand of the compound is 16, 17, 18, 19, 20, 21, 22, or 23 linked nucleosides in length. In certain embodiments, the first or second strand of the compound can comprise a conjugate group.

In certain embodiments, a compound described herein can comprise any of the oligonucleotide sequences targeted to a DNM2 nucleic acid described herein. In certain embodiments, the compound is single-stranded. In certain embodiments, such a compound is a single-stranded RNAi (ssRNAi) compound. In certain embodiments, the compound comprises at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises at least an 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobase portion of SEQ ID NO: 2879. In certain embodiments, the compound comprises the nucleobase sequence of any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises the nucleobase sequence of any one of SEQ ID NOs: 2879, 3056, 2123, 2189, 2453, 2160, or 2232. In certain embodiments, the compound comprises the nucleobase sequence of SEQ ID NO: 2879. In certain embodiments, the compound comprises ribonucleotides in which uracil (U) is in place of thymine (T) in any one of SEQ ID NOs: 7-3134. In certain embodiments, the compound comprises a nucleobase sequence complementary to the site on DNM2 to which any of SEQ ID NOs: 7-3134 is targeted. In certain embodiments, the compound comprises one or more modified nucleotides in which the 2' position in the sugar contains a halogen (such as fluorine group; 2'-F) or contains an alkoxy group (such as a methoxy group; 2'-OMe). In certain embodiments, the compound comprises at least one 2'-F sugar modification and at least one 2'-OMe sugar modification. In certain embodiments, the at least one 2'-F sugar modification and at least one 2'-OMe sugar modification are arranged in an alternating pattern for at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 contiguous nucleobases along a strand of the compound. In certain embodiments, the compound comprises one or more linkages between adjacent nucleotides other than a naturally-occurring phosphodiester linkage. Examples of such linkages include phosphoramide, phosphorothioate, and phosphorodithioate linkages. The compounds may also be chemically modified nucleic acid molecules as taught in U.S. Pat. No. 6,673,661. In other embodiments, the compound contains a capped strand, as disclosed, for example, by WO 00/63364, filed Apr. 19, 2000. In certain embodiments, the compound consists of 16, 17, 18, 19, 20, 21, 22, or 23 linked nucleosides. In certain embodiments, the compound can comprise a conjugate group.

Certain compounds described herein (*e.g.*, modified oligonucleotides) have one or more asymmetric center and thus give rise to enantiomers, diastereomers, and other stereoisomeric configurations that may be defined, in terms of absolute stereochemistry, as (*R*) or (*S*), as α or β, such as for sugar anomers, or as (D) or (L), such as for amino acids, etc. Compounds provided herein that are drawn or described as having certain stereoisomeric configurations include only the indicated compounds. Compounds provided herein that are drawn or described with undefined stereochemistry include all such possible isomers, including their stereorandom and optically pure forms. All tautomeric forms of the compounds provided herein are included unless otherwise indicated.

The compounds described herein include variations in which one or more atoms are replaced with a non-radioactive isotope or radioactive isotope of the indicated element. For example, compounds herein that comprise hydrogen atoms encompass all possible deuterium substitutions for each of the ^{1}H hydrogen atoms. Isotopic substitutions encompassed by the compounds herein include but are not limited to: ^{2}H or ^{3}H in place of ^{1}H, ^{13}C or ^{14}C in place of ^{12}C, ^{15}N in place of ^{14}N, ^{17}O or ^{18}O in place of ^{16}O, and ^{33}S, ^{34}S, ^{35}S, or ^{36}S in place of ^{32}S. In certain embodiments, non-radioactive isotopic substitutions may impart new properties on the oligomeric compound that are beneficial for use as a therapeutic or research tool. In certain embodiments, radioactive isotopic substitutions may make the compound suitable for research or diagnostic purposes such as imaging.

Certain Mechanisms

In certain embodiments, compounds described herein comprise or consist of modified oligonucleotides. In certain embodiments, compounds described herein are antisense compounds. In certain embodiments, compounds comprise oligomeric compounds. In certain embodiments, compounds described herein are capable of hybridizing to a DNM2 target nucleic acid, resulting in at least one antisense activity. In certain embodiments, compounds described herein selectively affect one or more target nucleic acid. Such compounds comprise a nucleobase sequence that hybridizes to one or more target nucleic acid, resulting in one or more desired antisense activity and does not hybridize to one or more non-target nucleic acid or does not hybridize to one or more non-target nucleic acid in such a way that results in a significant undesired antisense activity.

In certain antisense activities, hybridization of a compound described herein to a target nucleic acid results in recruitment of a protein that cleaves the target nucleic acid. For example, certain compounds described herein result in RNase H mediated cleavage of the target nucleic acid. RNase H is a cellular endonuclease that cleaves the RNA strand of an RNA:DNA duplex. The DNA in such an RNA:DNA duplex need not be unmodified DNA. In certain embodiments, compounds described herein are sufficiently "DNA-like" to elicit RNase H activity. Further, in certain embodiments, one or more non-DNA-like nucleoside in the gap of a gapmer is tolerated.

In certain antisense activities, compounds described herein or a portion of the compound is loaded into an RNA-induced silencing complex (RISC), ultimately resulting in cleavage of the target nucleic acid. For example, certain compounds described herein result in cleavage of the target nucleic acid by Argonaute. Compounds that are loaded into RISC are RNAi compounds. RNAi compounds may be double-stranded (siRNA) or single-stranded (ssRNA).

Antisense activities may be observed directly or indirectly. In certain embodiments, observation or detection of an antisense activity involves observation or detection of a change in an amount of a target nucleic acid or protein encoded by such target nucleic acid, a change in the ratio of splice variants of a nucleic acid or protein, and/or a phenotypic change in a cell or animal.

Target Nucleic Acids, Target Regions and Nucleotide Sequences

In certain embodiments, compounds described herein comprise or consist of an oligonucleotide comprising a region that is complementary to a target nucleic acid. In certain embodiments, the target nucleic acid is an endogenous RNA molecule. In certain embodiments, the target nucleic acid encodes a protein. In certain such embodiments, the target nucleic acid is selected from: an mRNA and a pre-mRNA, including intronic, exonic and untranslated regions. In certain embodiments, the target RNA is an mRNA. In certain embodiments, the target nucleic acid is a pre-mRNA. In certain embodiments, a pre-mRNA and corresponding mRNA are both target nucleic acids of a single compound. In certain such embodiments, the target region is entirely within an intron of a target pre-mRNA. In certain embodiments, the target region spans an intron/exon junction. In certain embodiments, the target region is at least 50% within an intron. Target nucleic acid sequences that encode DNM2 include, without limitation, the following: RefSeq or GenBank Accession No. NC_000019.10 truncated from nucleosides 10715001 to 10835000, NM_004945.3, NM_001005361.2, or NM_001005360.2 (SEQ ID Nos: 1, 2, 3, and 3135, respectively).

Hybridization

In some embodiments, hybridization occurs between a compound disclosed herein and a DNM2 nucleic acid. The most common mechanism of hybridization involves hydrogen bonding (e.g., Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding) between complementary nucleobases of the nucleic acid molecules.

Hybridization can occur under varying conditions. Hybridization conditions are sequence-dependent and are determined by the nature and composition of the nucleic acid molecules to be hybridized.

Methods of determining whether a sequence is specifically hybridizable to a target nucleic acid are well known in the art. In certain embodiments, the compounds provided herein are specifically hybridizable with a DNM2 nucleic acid.

Complementarity

In certain embodiments, compounds described herein comprise or consist of modified oligonucleotides. In certain embodiments, compounds described herein are antisense compounds. In certain embodiments, compounds comprise oligomeric compounds. In certain embodiments, oligonucleotides complementary to a DNM2 nucleic acid comprise nucleobase that are non-complementary with the DNM2 nucleic acid, yet may be tolerated provided that the compound remains able to specifically hybridize to a target nucleic acid. Moreover, a compound may hybridize over one or more segments of a DNM2 nucleic acid such that intervening or adjacent segments are not involved in the hybridization event (*e.g.*, a loop structure, mismatch or hairpin structure).

In certain embodiments, the compounds provided herein, or a specified portion thereof, are, are at least, or are up to 70%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% complementary to a DNM2 nucleic acid, a target region, target segment, or specified portion thereof. In certain embodiments, the compounds provided herein, or a specified portion thereof, are 70% to 75%, 75% to 80%, 80% to 85%, 85% to 90%, 90% to 95%, 95% to 100%, or any number in between these ranges, complementary to a DNM2 nucleic acid, a target region, target segment, or specified portion thereof. Percent complementarity of a compound with a target nucleic acid can be determined using routine methods.

For example, a compound in which 18 of 20 nucleobases of the compound are complementary to a target region, and would therefore specifically hybridize, would represent 90 percent complementarity. In this example, the remaining non-complementary nucleobases may be clustered or interspersed with complementary nucleobases and need not be contiguous to each other or to complementary nucleobases. As such, a compound which is 18 nucleobases in length having four non-complementary nucleobases which are flanked by two regions of complete complementarity with the target nucleic acid would have 77.8% overall complementarity with the target nucleic acid. Percent complementarity of a compound with a region of a target nucleic acid can be determined routinely using BLAST programs (basic local alignment search tools) and PowerBLAST programs known in the art (Altschul *et al*., *J. Mol. Biol*., 1990, 215, 403 410; Zhang and Madden, Genome Res., 1997, 7, 649 656). Percent homology, sequence identity or complementarity, can be determined by, for example, the Gap program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, Madison Wis.), using default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2, 482 489).

In certain embodiments, compounds described herein, or specified portions thereof, are fully complementary (*i.e*. 100% complementary) to a target nucleic acid, or specified portion thereof. For example, a compound may be 100% complementary to a DNM2 nucleic acid, or a target region, or a target segment or target sequence thereof. As used herein, "fully complementary" means each nucleobase of a compound is complementary to the corresponding nucleobase of a target nucleic acid. For example, a 20 nucleobase compound is fully complementary to a target sequence that is 400 nucleobases long, so long as there is a corresponding 20 nucleobase portion of the target nucleic acid that is fully complementary to the compound. Fully complementary can also be used in reference to a specified portion of the first and /or the second nucleic acid. For example, a 20 nucleobase portion of a 30 nucleobase compound can be "fully complementary" to a target sequence that is 400 nucleobases long. The 20 nucleobase portion of the 30 nucleobase compound is fully complementary to the target sequence if the target sequence has a corresponding 20 nucleobase portion wherein each nucleobase is complementary to the 20 nucleobase portion of the compound. At the same time, the entire 30 nucleobase compound may or may not be fully complementary to the target sequence, depending on whether the remaining 10 nucleobases of the compound are also complementary to the target sequence.

In certain embodiments, compounds described herein comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain such embodiments, antisense activity against the target is reduced by such mismatch, but activity against a non-target is reduced by a greater amount. Thus, in certain such embodiments selectivity of the compound is improved. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide having a gapmer motif. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, or 8 from the 5'-end of the gap segment. In certain such embodiments, the mismatch is at position 9, 8, 7, 6, 5, 4, 3, 2, 1 from the 3'-end of the gap segment. In certain such embodiments, the mismatch is at position 1, 2, 3, or 4 from the 5'-end of the wing segment. In certain such embodiments, the mismatch is at position 4, 3, 2, or 1 from the 3'-end of the wing segment. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide not having a gapmer motif. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 5'-end of the oligonucleotide. In certain such embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 from the 3'-end of the oligonucleotide.

The location of a non-complementary nucleobase may be at the 5' end or 3' end of the compound. Alternatively, the non-complementary nucleobase or nucleobases may be at an internal position of the compound. When two or more non-complementary nucleobases are present, they may be contiguous (i.e., linked) or non-contiguous. In one embodiment, a non-complementary nucleobase is located in the wing segment of a gapmer oligonucleotide.

In certain embodiments, compounds described herein that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 nucleobases in length comprise no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a DNM2 nucleic acid, or specified portion thereof.

In certain embodiments, compounds described herein that are, or are up to 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleobases in length comprise no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 non-complementary nucleobase(s) relative to a target nucleic acid, such as a DNM2 nucleic acid, or specified portion thereof.

In certain embodiments, compounds described herein also include those which are complementary to a portion (a defined number of contiguous nucleobases within a region or segment) of a target nucleic acid. In certain embodiments, the compounds, are complementary to at least an 8 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 9 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 10 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least an 11 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 12 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 13 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at

least a 14 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 15 nucleobase portion of a target segment. In certain embodiments, the compounds are complementary to at least a 16 nucleobase portion of a target segment. Also contemplated are compounds that are complementary to at least a 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more nucleobase portion of a target segment, or a range defined by any two of these values.

Certain Compounds

In certain embodiments, compounds described herein comprise or consist of oligonucleotides consisting of linked nucleosides. Oligonucleotides may be unmodified oligonucleotides (RNA or DNA) or may be modified oligonucleotides. Modified oligonucleotides comprise at least one modification relative to unmodified RNA or DNA (i.e., comprise at least one modified nucleoside (comprising a modified sugar moiety and/or a modified nucleobase) and/or at least one modified internucleoside linkage).

I. Modifications

A. Modified Nucleosides

Modified nucleosides comprise a modified sugar moiety or a modified nucleobase or both a modifed sugar moiety and a modified nucleobase.

1. Modified Sugar Moieties

In certain embodiments, sugar moieties are non-bicyclic modified sugar moieties. In certain embodiments, modified sugar moieties are bicyclic or tricyclic sugar moieties. In certain embodiments, modified sugar moieties are sugar surrogates. Such sugar surrogates may comprise one or more substitutions corresponding to those of other types of modified sugar moieties.

In certain embodiments, modified sugar moieties are non-bicyclic modified furanosyl sugar moieties comprising one or more acyclic substituent, including but not limited to substituents at the 2', 4', and/or 5' positions. In certain embodiments, the furanosyl sugar moiety is a ribosyl sugar moiety. In certain embodiments one or more acyclic substituent of non-bicyclic modified sugar moieties is branched. Examples of 2'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 2'-F, 2'-OCH_3 ("OMe" or "O-methyl"), and 2'-$O(CH_2)_2OCH_3$ ("MOE"). In certain embodiments, 2'-substituent groups are selected from among: halo, allyl, amino, azido, SH, CN, OCN, CF_3, OCF_3, O-C_1-C_{10} alkoxy, O-C_1-C_{10} substituted alkoxy, O-C_1-C_{10} alkyl, O-C_1-C_{10} substituted alkyl, S-alkyl, N(R_m)-alkyl, O-alkenyl, S-alkenyl, N(R_m)-alkenyl, O-alkynyl, S-alkynyl, N(R_m)-alkynyl, O-alkylenyl-O-alkyl, alkynyl, alkaryl, aralkyl, O-alkaryl, O-aralkyl, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(R_m)(R_n)$ or $OCH_2C(=O)$-$N(R_m)(R_n)$, where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C_1-C_{10} alkyl, and the 2'-substituent groups described in Cook et al., U.S. 6,531,584; Cook et al., U.S. 5,859,221; and Cook et al., U.S. 6,005,087. Certain embodiments of these 2'-substituent groups can be further substituted with one or more substituent groups independently selected from among: hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro (NO_2), thiol, thioalkoxy,

thioalkyl, halogen, alkyl, aryl, alkenyl and alkynyl. Examples of 4'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to alkoxy (*e.g.*, methoxy), alkyl, and those described in Manoharan et al., WO 2015/106128. Examples of 5'-substituent groups suitable for non-bicyclic modified sugar moieties include but are not limited to: 5'-methyl (R or S), 5'-vinyl, and 5'-methoxy. In certain embodiments, non-bicyclic modified sugars comprise more than one non-bridging sugar substituent, for example, 2'-F-5'-methyl sugar moieties and the modified sugar moieties and modified nucleosides described in Migawa et al., WO 2008/101157 and Rajeev et al., US2013/0203836.).

In certain embodiments, a 2'-substituted nucleoside or 2'- non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, NH_2, N_3, OCF_3, OCH_3, $O(CH_2)_3NH_2$, $CH_2CH{=}CH_2$, $OCH_2CH{=}CH_2$, $OCH_2CH_2OCH_3$, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(R_m)(R_n)$, $O(CH_2)_2O(CH_2)_2N(CH_3)_2$, and N-substituted acetamide ($OCH_2C(=O)$-$N(R_m)(R_n)$), where each R_m and R_n is, independently, H, an amino protecting group, or substituted or unsubstituted C_1-C_{10} alkyl.

In certain embodiments, a 2'-substituted nucleoside or 2'- non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCF_3, OCH_3, $OCH_2CH_2OCH_3$, $O(CH_2)_2SCH_3$, $O(CH_2)_2ON(CH_3)_2$, $O(CH_2)_2O(CH_2)_2N(CH_3)_2$, and $OCH_2C(=O)$-$N(H)CH_3$ ("NMA").

In certain embodiments, a 2'-substituted nucleoside or 2'- non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCH_3, and $OCH_2CH_2OCH_3$.

Nucleosides comprising modified sugar moieties, such as non-bicyclic modified sugar moieties, may be referred to by the position(s) of the substitution(s) on the sugar moiety of the nucleoside. For example, nucleosides comprising 2'-substituted or 2-modified sugar moieties are referred to as 2'-substituted nucleosides or 2-modified nucleosides.

Certain modifed sugar moieties comprise a bridging sugar substituent that forms a second ring resulting in a bicyclic sugar moiety. In certain such embodiments, the bicyclic sugar moiety comprises a bridge between the 4' and the 2' furanose ring atoms. In certain such embodiments, the furanose ring is a ribose ring. Examples of such 4' to 2' bridging sugar substituents include but are not limited to: 4'-CH_2-2', 4'-$(CH_2)_2$-2', 4'-$(CH_2)_3$-2', 4'-CH_2-O-2' ("LNA"), 4'-CH_2-S-2', 4'-$(CH_2)_2$-O-2' ("ENA"), 4'-$CH(CH_3)$-O-2' (referred to as "constrained ethyl" or "cEt" when in the *S* configuration), 4'-CH_2-O-CH_2-2', 4'-CH_2-N(R)-2', 4'-$CH(CH_2OCH_3)$-O-2' ("constrained MOE" or "cMOE") and analogs thereof (*see, e.g.,* Seth et al., U.S. 7,399,845, Bhat et al., U.S. 7,569,686, Swayze et al., U.S. 7,741,457, and Swayze et al., U.S. 8,022,193), 4'-$C(CH_3)(CH_3)$-O-2' and analogs thereof (*see, e.g.,*Seth et al., U.S. 8,278,283), 4'-CH_2-$N(OCH_3)$-2' and analogs thereof (*see, e.g.,* Prakash et al., U.S. 8,278,425), 4'-CH_2-O-$N(CH_3)$-2' (*see, e.g.,* Allerson et al., U.S. 7,696,345 and Allerson et al., U.S. 8,124,745), 4'-CH_2-$C(H)(CH_3)$-2' (*see, e.g.,* Zhou, *et al., J. Org. Chem.,*2009, *74*, 118-134), 4'-CH_2-$C(=CH_2)$-2' and analogs thereof (*see e.g.*, Seth et al., U.S. 8,278,426), 4'-$C(R_aR_b)$-N(R)-O-2', 4'-$C(R_aR_b)$-O-

N(R)-2', 4'-CH_2-O-N(R)-2', and 4'-CH_2-N(R)-O-2', wherein each R, R_a, and R_b is, independently, H, a protecting group, or C_1-C_{12} alkyl (*see, e.g.* Imanishi et al., U.S. 7,427,672).

In certain embodiments, such 4' to 2' bridges independently comprise from 1 to 4 linked groups independently selected from: -$[C(R_a)(R_b)]_n$-, -$[C(R_a)(R_b)]_n$-O-, -$C(R_a)$=$C(R_b)$-, -$C(R_a)$=N-, -$C(=NR_a)$-, -C(=O)-, -C(=S)-, -O-, -$Si(R_a)_2$-, -$S(=O)_x$-, and -$N(R_a)$-;

wherein:

x is 0, 1, or 2;

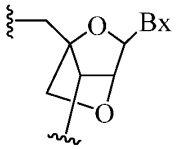
n is 1, 2, 3, or 4;

each R_a and R_b is, independently, H, a protecting group, hydroxyl, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C_5-C_7 alicyclic radical, substituted C_5-C_7 alicyclic radical, halogen, OJ_1, NJ_1J_2, SJ_1, N_3, $COOJ_1$, acyl (C(=O)-H), substituted acyl, CN, sulfonyl ($S(=O)_2$-J_1), or sulfoxyl (S(=O)-J_1); and

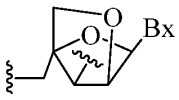
each J_1 and J_2 is, independently, H, C_1-C_{12} alkyl, substituted C_1-C_{12} alkyl, C_2-C_{12} alkenyl, substituted C_2-C_{12} alkenyl, C_2-C_{12} alkynyl, substituted C_2-C_{12} alkynyl, C_5-C_{20} aryl, substituted C_5-C_{20} aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C_1-C_{12} aminoalkyl, substituted C_1-C_{12} aminoalkyl, or a protecting group.

Additional bicyclic sugar moieties are known in the art, see, for example: Freier *et al., Nucleic Acids Research*, 1997, *25*(*22*), 4429-4443, Albaek *et al., J. Org. Chem.*, 2006, *71*, 7731-7740, Singh et al., *Chem. Commun.*, 1998, *4*, 455-456; Koshkin et al., *Tetrahedron*, 1998, *54*, 3607-3630; Kumar et al., *Bioorg. Med. Chem. Lett.*, 1998, *8*, 2219-2222; Singh et al., *J. Org. Chem.*, 1998, *63*, 10035-10039; Srivastava et al., *J. Am. Chem. Soc.*, 20017, *129,* 8362-8379; Elayadi *et al.,*; Wengel et a., U.S. 7,053,207; Imanishi et al., U.S. 6,268,490; Imanishi et al. U.S. 6,770,748; Imanishi et al., U.S. RE44,779; Wengel et al., U.S. 6,794,499; Wengel et al., U.S. 6,670,461; Wengel et al., U.S. 7,034,133; Wengel et al., U.S. 8,080,644; Wengel et al., U.S. 8,034,909; Wengel et al., U.S. 8,153,365; Wengel et al., U.S. 7,572,582; and Ramasamy et al., U.S. 6,525,191;; Torsten et al., WO 2004/106356;Wengel et al., WO 1999/014226; Seth et al., WO 2007/134181; Seth et al., U.S. 7,547,684; Seth et al., U.S. 7,666,854; Seth et al., U.S. 8,088,746; Seth et al., U.S. 7,750,131; Seth et al., U.S. 8,030,467; Seth et al., U.S. 8,268,980; Seth et al., U.S. 8,546,556; Seth et al., U.S. 8,530,640; Migawa et al., U.S. 9,012,421; Seth et al., U.S. 8,501,805; and U.S. Patent Publication Nos. Allerson et al., US2008/0039618 and Migawa et al., US2015/0191727..

In certain embodiments, bicyclic sugar moieties and nucleosides incorporating such bicyclic sugar moieties are further defined by isomeric configuration. For example, an LNA nucleoside (described herein) may be in the α-L configuration or in the β-D configuration.



LNA (β-D-configuration)
bridge = 4'-CH_2-O-2'



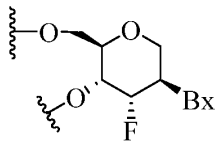
α-*L*-LNA (α-*L*-configuration)
bridge = 4'-CH_2-O-2'

α-L-methyleneoxy (4'-CH_2-O-2') or α-L-LNA bicyclic nucleosides have been incorporated into antisense oligonucleotides that showed antisense activity (Frieden et al., *Nucleic Acids Research,* 2003, *21*, 6365-6372). Herein, general descriptions of bicyclic nucleosides include both isomeric configurations. When the positions of specific bicyclic nucleosides (*e.g.*, LNA) are identified in exemplified embodiments herein, they are in the β-D configuration, unless otherwise specified.

In certain embodiments, modified sugar moieties comprise one or more non-bridging sugar substituent and one or more bridging sugar substituent (e.g., 5'-substituted and 4'-2' bridged sugars).

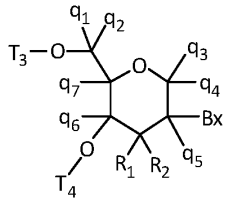
In certain embodiments, modified sugar moieties are sugar surrogates. In certain such embodiments, the oxygen atom of the sugar moiety is replaced, *e.g.,* with a sulfur, carbon or nitrogen atom. In certain such embodiments, such modified sugar moieties also comprise bridging and/or non-bridging substituents as described herein. For example, certain sugar surrogates comprise a 4'-sulfur atom and a substitution at the 2'-position (*see*, *e.g.,* Bhat et al., U.S. 7,875,733 and Bhat et al., U.S. 7,939,677) and/or the 5' position.

In certain embodiments, sugar surrogates comprise rings having other than 5 atoms. For example, in certain embodiments, a sugar surrogate comprises a six-membered tetrahydropyran ("THP"). Such tetrahydropyrans may be further modified or substituted. Nucleosides comprising such modified tetrahydropyrans include but are not limited to hexitol nucleic acid ("HNA"), anitol nucleic acid ("ANA"), manitol nucleic acid ("MNA") (*see, e.g.,* Leumann, CJ. *Bioorg. & Med. Chem.* 2002, *10*, 841-854), fluoro HNA:



F-HNA

("F-HNA", *see e.g.* Swayze et al., U.S. 8,088,904; Swayze et al., U.S. 8,440,803; Swayze et al., U.S. 8,796,437; and Swayze et al., U.S. 9,005,906; F-HNA can also be referred to as a F-THP or 3'-fluoro tetrahydropyran), and nucleosides comprising additional modified THP compounds having the formula:



wherein, independently, for each of said modified THP nucleoside:

Bx is a nucleobase moiety;

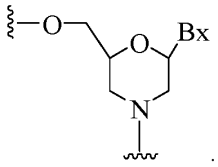
T_3 and T_4 are each, independently, an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide or one of T_3 and T_4 is an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide and the other of T_3 and T_4 is H, a hydroxyl protecting group, a linked conjugate group, or a 5' or 3'-terminal group;

q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each, independently, H, C_1-C_6 alkyl, substituted C_1-C_6 alkyl, C_2-C_6 alkenyl, substituted C_2-C_6 alkenyl, C_2-C_6 alkynyl, or substituted C_2-C_6 alkynyl; and

each of R_1 and R_2 is independently selected from among: hydrogen, halogen, substituted or unsubstituted alkoxy, NJ_1J_2, SJ_1, N_3, $OC(=X)J_1$, $OC(=X)NJ_1J_2$, $NJ_3C(=X)NJ_1J_2$, and CN, wherein X is O, S or NJ_1, and each J_1, J_2, and J_3 is, independently, H or C_1-C_6 alkyl.

In certain embodiments, modified THP nucleosides are provided wherein q_1, q_2, q_3, q_4, q_5, q_6 and q_7 are each H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is other than H. In certain embodiments, at least one of q_1, q_2, q_3, q_4, q_5, q_6 and q_7 is methyl. In certain embodiments, modified THP nucleosides are provided wherein one of R_1 and R_2 is F. In certain embodiments, R_1 is F and R_2 is H, in certain embodiments, R_1 is methoxy and R_2 is H, and in certain embodiments, R_1 is methoxyethoxy and R_2 is H.

In certain embodiments, sugar surrogates comprise rings having more than 5 atoms and more than one heteroatom. For example, nucleosides comprising morpholino sugar moieties and their use in oligonucleotides have been reported (*see, e.g.,* Braasch et al., Biochemistry, 2002, *41*, 4503-4510 and Summerton et al., U.S. 5,698,685; Summerton et al., U.S. 5,166,315; Summerton et al., U.S. 5,185,444; and Summerton et al., U.S. 5,034,506). As used here, the term "morpholino" means a sugar surrogate having the following structure:



In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are refered to herein as "modifed morpholinos."

In certain embodiments, sugar surrogates comprise acyclic moieites. Examples of nucleosides and oligonucleotides comprising such acyclic sugar surrogates include but are not limited to: peptide nucleic acid ("PNA"), acyclic butyl nucleic acid (*see, e.g.,* Kumar et al., *Org. Biomol. Chem.*, 2013, *11*, 5853-5865), and nucleosides and oligonucleotides described in Manoharan et al., WO2011/133876.

Many other bicyclic and tricyclic sugar and sugar surrogate ring systems are known in the art that can be used in modified nucleosides).

2. Modified Nucleobases

In certain embodiments, modified nucleobases are selected from: 5-substituted pyrimidines, 6-azapyrimidines, alkyl or alkynyl substituted pyrimidines, alkyl substituted purines, and N-2, N-6 and O-6 substituted purines. In certain embodiments, modified nucleobases are selected from: 2-aminopropyladenine, 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-N-methylguanine, 6-N-methyladenine, 2-propyladenine , 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-propynyl (-C≡C-CH_3) uracil, 5-propynylcytosine, 6-azouracil, 6-azocytosine, 6-azothymine, 5-ribosyluracil (pseudouracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8-thioalkyl, 8-hydroxyl, 8-aza and other 8-substituted purines, 5-halo, particularly 5-bromo, 5-trifluoromethyl, 5-halouracil, and 5-halocytosine, 7-methylguanine, 7-methyladenine, 2-F-adenine, 2-aminoadenine, 7-deazaguanine, 7-deazaadenine, 3-deazaguanine, 3-deazaadenine, 6-N-benzoyladenine, 2-N-isobutyrylguanine, 4-N-benzoylcytosine, 4-N-benzoyluracil, 5-methyl 4-N-benzoylcytosine, 5-methyl 4-N-benzoyluracil, universal bases, hydrophobic bases, promiscuous bases, size-expanded bases, and fluorinated bases. Further modified nucleobases include tricyclic pyrimidines, such as 1,3-diazaphenoxazine-2-one, 1,3-diazaphenothiazine-2-one and 9-(2-aminoethoxy)-1,3-diazaphenoxazine-2-one (G-clamp). Modified nucleobases may also include those in which the purine or pyrimidine base is replaced with other heterocycles, for example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in Merigan et al., U.S. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, Kroschwitz, J.I., Ed., John Wiley & Sons, 1990, 858-859; Englisch *et al.*, *Angewandte Chemie*, International Edition, 1991, *30*, 613; Sanghvi, Y.S., Chapter 15, *Antisense Research and Applications*, Crooke, S.T. and Lebleu, B., Eds., CRC Press, 1993, 273-288; and those disclosed in Chapters 6 and 15, *Antisense Drug Technology*, Crooke S.T., Ed., CRC Press, 2008, 163-166 and 442-443.

Publications that teach the preparation of certain of the above noted modified nucleobases as well as other modified nucleobases include without limitation, Manohara et al., US2003/0158403; Manoharan et al., US2003/0175906;; Dinh et al., U.S. 4,845,205; Spielvogel et al., U.S. 5,130,302; Rogers et al., U.S. 5,134,066; Bischofberger et al., U.S. 5,175,273; Urdea et al., U.S. 5,367,066; Benner et al., U.S. 5,432,272; Matteucci et al., U.S. 5,434,257; Gmeiner et al., U.S. 5,457,187; Cook et al., U.S. 5,459,255; Froehler et al., U.S. 5,484,908; Matteucci et al., U.S. 5,502,177; Hawkins et al., U.S. 5,525,711; Haralambidis et al., U.S. 5,552,540; Cook et al., U.S. 5,587,469; Froehler et al., U.S. 5,594,121; Switzer et al., U.S. 5,596,091; Cook et al., U.S. 5,614,617;

Froehler et al., U.S. 5,645,985; Cook et al., U.S. 5,681,941; Cook et al., U.S. 5,811,534; Cook et al., U.S. 5,750,692; Cook et al., U.S. 5,948,903; Cook et al., U.S. 5,587,470; Cook et al., U.S. 5,457,191; Matteucci et al., U.S. 5,763,588; Froehler et al., U.S. 5,830,653; Cook et al., U.S. 5,808,027; Cook et al., 6,166,199; and Matteucci et al., U.S. 6,005,096.

In certain embodiments, compounds comprise or consist of a modified oligonucleotide complementary to an α-DNM2 nucleic acid comprising one or more modified nucleobases. In certain embodiments, the modified nucleobase is 5-methylcytosine. In certain embodiments, each cytosine is a 5-methylcytosine.

B. Modified Internucleoside Linkages

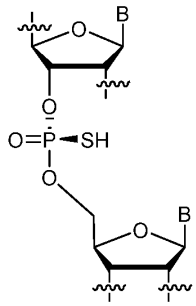
In certain embodiments, compounds described herein having one or more modified internucleoside linkages are selected over compounds having only phosphodiester internucleoside linkages because of desirable properties such as, for example, enhanced cellular uptake, enhanced affinity for target nucleic acids, and increased stability in the presence of nucleases.

In certain embodiments, compounds comprise or consist of a modified oligonucleotide complementary to a DNM2 nucleic acid comprising one or more modified internucleoside linkages. In certain embodiments, the modified internucleoside linkages are phosphorothioate linkages. In certain embodiments, each internucleoside linkage of an antisense compound is a phosphorothioate internucleoside linkage.

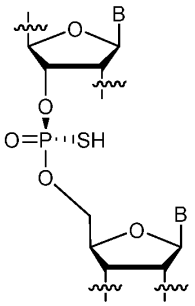
In certain embodiments, nucleosides of modified oligonucleotides may be linked together using any internucleoside linkage. The two main classes of internucleoside linking groups are defined by the presence or absence of a phosphorus atom. Representative phosphorus-containing internucleoside linkages include but are not limited to phosphates, which contain a phosphodiester bond ("P=O") (also referred to as unmodified or naturally occurring linkages), phosphotriesters, methylphosphonates, phosphoramidates, and phosphorothioates ("P=S"), and phosphorodithioates ("HS-P=S"). Representative non-phosphorus containing internucleoside linking groups include but are not limited to methylenemethylimino (-CH_2-N(CH_3)-O-CH_2-), thiodiester , thionocarbamate (-O-C(=O)(NH)-S-); siloxane (-O-SiH_2-O-); and N,N'-dimethylhydrazine (-CH_2-N(CH_3)-N(CH_3)-). Modified internucleoside linkages, compared to naturally occurring phosphate linkages, can be used to alter, typically increase, nuclease resistance of the oligonucleotide. Methods of preparation of phosphorous-containing and non-phosphorous-containing internucleoside linkages are well known to those skilled in the art.

Representative internucleoside linkages having a chiral center include but are not limited to alkylphosphonates and phosphorothioates. Modified oligonucleotides comprising internucleoside linkages having a chiral center can be prepared as populations of modified oligonucleotides comprising stereorandom internucleoside linkages, or as populations of modified oligonucleotides comprising phosphorothioate linkages in particular stereochemical configurations. In certain embodiments, populations of modified oligonucleotides

comprise phosphorothioate internucleoside linkages wherein all of the phosphorothioate internucleoside linkages are stereorandom. Such modified oligonucleotides can be generated using synthetic methods that result in random selection of the stereochemical configuration of each phosphorothioate linkage. Nonetheless, as is well understood by those of skill in the art, each individual phosphorothioate of each individual oligonucleotide molecule has a defined stereoconfiguration. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising one or more particular phosphorothioate internucleoside linkages in a particular, independently selected stereochemical configuration. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 65% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 70% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 80% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 90% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate linkage is present in at least 99% of the molecules in the population. Such chirally enriched populations of modified oligonucleotides can be generated using synthetic methods known in the art, *e.g.*, methods described in Oka et al., *JACS* 125, 8307 (2003), Wan et al. *Nuc. Acid. Res*. 42, 13456 (2014), and WO 2017/015555. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one indicated phosphorothioate in the (*S*p) configuration. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one phosphorothioate in the (*R*p) configuration. In certain embodiments, modified oligonucleotides comprising (*R*p) and/or (*S*p) phosphorothioates comprise one or more of the following formulas, respectively, wherein "B" indicates a nucleobase:



(R_p)



(S_p)

Unless otherwise indicated, chiral internucleoside linkages of modified oligonucleotides described herein can be stereorandom or in a particular stereochemical configuration.

Neutral internucleoside linkages include, without limitation, phosphotriesters, methylphosphonates, MMI (3'-CH_2-N(CH_3)-O-5'), amide-3 (3'-CH_2-C(=O)-N(H)-5'), amide-4 (3'-CH_2-N(H)-C(=O)-5'), formacetal (3'-O-CH_2-O-5'), methoxypropyl, and thioformacetal (3'-S-CH_2-O-5'). Further neutral internucleoside linkages

include nonionic linkages comprising siloxane (dialkylsiloxane), carboxylate ester, carboxamide, sulfide, sulfonate ester and amides (See for example: Carbohydrate Modifications in Antisense Research; Y.S. Sanghvi and P.D. Cook, Eds., ACS Symposium Series 580; Chapters 3 and 4, 40-65). Further neutral internucleoside linkages include nonionic linkages comprising mixed N, O, S and CH2 component parts.

II. Certain Motifs

In certain embodiments, compounds described herein comprise or consist of oligonucleotides. Oligonucleotides can have a motif, *e.g.* a pattern of unmodified and/or modified sugar moieties, nucleobases, and/or internucleoside linkages. In certain embodiments, modified oligonucleotides comprise one or more modified nucleoside comprising a modified sugar. In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more modified internucleoside linkage. In such embodiments, the modified, unmodified, and differently modified sugar moieties, nucleobases, and/or internucleoside linkages of a modified oligonucleotide define a pattern or motif. In certain embodiments, the patterns or motifs of sugar moieties, nucleobases, and internucleoside linkages are each independent of one another. Thus, a modified oligonucleotide may be described by its sugar motif, nucleobase motif and/or internucleoside linkage motif (as used herein, nucleobase motif describes the modifications to the nucleobases independent of the sequence of nucleobases).

A. Certain Sugar Motifs

In certain embodiments, compounds described herein comprise or consist of oligonucleotides. In certain embodiments, oligonucleotides comprise one or more type of modified sugar and/or unmodified sugar moiety arranged along the oligonucleotide or region thereof in a defined pattern or sugar motif. In certain instances, such sugar motifs include but are not limited to any of the sugar modifications discussed herein.

In certain embodiments, modified oligonucleotides comprise or consist of a region having a gapmer motif, which comprises two external segments or "wings" and a central or internal segment or "gap." The three segments of a gapmer motif (the 5'-wing, the gap, and the 3'-wing) form a contiguous sequence of nucleosides wherein at least some of the sugar moieties of the nucleosides of each of the wings differ from at least some of the sugar moieties of the nucleosides of the gap. Specifically, at least the sugar moieties of the nucleosides of each wing that are immediately adjacent to the gap (the 3'-terminal wing nucleoside of the 5'-wing and the 5'-terminal wing nucleoside of the 3'-wing) differ from the sugar moiety of the adjacent gap nucleosides. In certain embodiments, the sugar moieties within the gap are the same as one another. In certain embodiments, the gap includes one or more nucleoside having a sugar moiety that differs from the sugar moiety of one or more other nucleosides of the gap.

In certain embodiments, the wings of a gapmer each comprise 1-5 nucleosides. In certain embodiments, the wings of a gapmer each comprise 2-5 nucleosides. In certain embodiments, the wings of a gapmer each comprise 3-5 nucleosides. In certain embodiments, the nucleosides of the wings of a gapmer are

all modified nucleosides. In certain such embodiments, the sugar moieties of the wings of a gapmer are all modified sugar moieties.

In certain embodiments, the gap of a gapmer comprises 7-12 nucleosides. In certain embodiments, the gap of a gapmer comprises 7-10 nucleosides. In certain embodiments, the gap of a gapmer comprises 8-10 nucleosides. In certain embodiments, the gap of a gapmer comprises 10 nucleosides. In certain embodiments, each nucleoside of the gap of a gapmer is a 2'-deoxynucleoside.

In certain embodiments, the gapmer is a deoxy gapmer. In such embodiments, the nucleosides on the gap side of each wing/gap junction are 2'-deoxynucleosides and the terminal wing nucleosides immediately adjacent to the gap comprise modified sugar moieties. In certain such embodiments, each nucleoside of the gap is a 2'-deoxynucleoside. In certain such embodiments, each nucleoside of each wing comprises a modified sugar moiety.

In certain embodiments, a modified oligonucleotide has a fully modified sugar motif wherein each nucleoside of the modified oligonucleotide comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a region having a fully modified sugar motif wherein each nucleoside of the region comprises a modified sugar moiety. In certain embodiments, modified oligonucleotides comprise or consist of a region having a fully modified sugar motif, wherein each nucleoside within the fully modified region comprises the same modified sugar moiety, referred to herein as a uniformly modified sugar motif. In certain embodiments, a fully modified oligonucleotide is a uniformly modified oligonucleotide. In certain embodiments, each nucleoside of a uniformly modified oligonucleotide comprises the same 2'-modification.

B. Certain Nucleobase Motifs

In certain embodiments, compounds described herein comprise or consist of oligonucleotides. In certain embodiments, oligonucleotides comprise modified and/or unmodified nucleobases arranged along the oligonucleotide or region thereof in a defined pattern or motif. In certain embodiments, each nucleobase is modified. In certain embodiments, none of the nucleobases are modified. In certain embodiments, each purine or each pyrimidine is modified. In certain embodiments, each adenine is modified. In certain embodiments, each guanine is modified. In certain embodiments, each thymine is modified. In certain embodiments, each uracil is modified. In certain embodiments, each cytosine is modified. In certain embodiments, some or all of the cytosine nucleobases in a modified oligonucleotide are 5-methylcytosines.

In certain embodiments, modified oligonucleotides comprise a block of modified nucleobases. In certain such embodiments, the block is at the 3'-end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 3'-end of the oligonucleotide. In certain embodiments, the block is at the 5'-end of the oligonucleotide. In certain embodiments the block is within 3 nucleosides of the 5'-end of the oligonucleotide.

In certain embodiments, oligonucleotides having a gapmer motif comprise a nucleoside comprising a

modified nucleobase. In certain such embodiments, one nucleoside comprising a modified nucleobase is in the gap of an oligonucleotide having a gapmer motif. In certain such embodiments, the sugar moiety of said nucleoside is a 2'-deoxyribosyl moiety. In certain embodiments, the modified nucleobase is selected from: a 2-thiopyrimidine and a 5-propynepyrimidine.

C. Certain Internucleoside Linkage Motifs

In certain embodiments, compounds described herein comprise or consist of oligonucleotides. In certain embodiments, oligonucleotides comprise modified and/or unmodified internucleoside linkages arranged along the oligonucleotide or region thereof in a defined pattern or motif. In certain embodiments, each internucleoside linking group is a phosphodiester internucleoside linkage (P=O). In certain embodiments, each internucleoside linking group of a modified oligonucleotide is a phosphorothioate internucleoside linkage (P=S). In certain embodiments, each internucleoside linkage of a modified oligonucleotide is independently selected from a phosphorothioate internucleoside linkage and phosphodiester internucleoside linkage. In certain embodiments, each phosphorothioate internucleoside linkage is independently selected from a stereorandom phosphorothioate, a (*S*p) phosphorothioate, and a (*R*p) phosphorothioate. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer and the internucleoside linkages within the gap are all modified. In certain such embodiments, some or all of the internucleoside linkages in the wings are unmodified phosphate linkages. In certain embodiments, the terminal internucleoside linkages are modified. In certain embodiments, the sugar motif of a modified oligonucleotide is a gapmer, and the internucleoside linkage motif comprises at least one phosphodiester internucleoside linkage in at least one wing, wherein the at least one phosphodiester linkage is not a terminal internucleoside linkage, and the remaining internucleoside linkages are phosphorothioate internucleoside linkages. In certain such embodiments, all of the phosphorothioate linkages are stereorandom. In certain embodiments, all of the phosphorothioate linkages in the wings are (*S*p) phosphorothioates, and the gap comprises at least one *S*p, *S*p, *R*p motif. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising such internucleoside linkage motifs.

In certain embodiments, oligonucleotides comprise a region having an alternating internucleoside linkage motif. In certain embodiments, oligonucleotides comprise a region of uniformly modified internucleoside linkages. In certain such embodiments, the internucleoside linkages are phosphorothioate internucleoside linkages. In certain embodiments, all of the internucleoside linkages of the oligonucleotide are phosphorothioate internucleoside linkages. In certain embodiments, each internucleoside linkage of the oligonucleotide is selected from phosphodiester or phophate and phosphorothioate. In certain embodiments, each internucleoside linkage of the oligonucleotide is selected from phosphodiester or phosphate and phosphorothioate and at least one internucleoside linkage is phosphorothioate.

In certain embodiments, the oligonucleotide comprises at least 6 phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least 8 phosphorothioate internucleoside

linkages. In certain embodiments, the oligonucleotide comprises at least 10 phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 6 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 8 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least one block of at least 10 consecutive phosphorothioate internucleoside linkages. In certain embodiments, the oligonucleotide comprises at least block of at least one 12 consecutive phosphorothioate internucleoside linkages. In certain such embodiments, at least one such block is located at the 3' end of the oligonucleotide. In certain such embodiments, at least one such block is located within 3 nucleosides of the 3' end of the oligonucleotide.

In certain embodiments, oligonucleotides comprise one or more methylphosponate linkages. In certain embodiments, oligonucleotides having a gapmer nucleoside motif comprise a linkage motif comprising all phosphorothioate linkages except for one or two methylphosponate linkages. In certain embodiments, one methylphosponate linkage is in the gap of an oligonucleotide having a gapmer sugar motif.

In certain embodiments, it is desirable to arrange the number of phosphorothioate internucleoside linkages and phosphodiester internucleoside linkages to maintain nuclease resistance. In certain embodiments, it is desirable to arrange the number and position of phosphorothioate internucleoside linkages and the number and position of phosphodiester internucleoside linkages to maintain nuclease resistance. In certain embodiments, the number of phosphorothioate internucleoside linkages may be decreased and the number of phosphodiester internucleoside linkages may be increased. In certain embodiments, the number of phosphorothioate internucleoside linkages may be decreased and the number of phosphodiester internucleoside linkages may be increased while still maintaining nuclease resistance. In certain embodiments it is desirable to decrease the number of phosphorothioate internucleoside linkages while retaining nuclease resistance. In certain embodiments it is desirable to increase the number of phosphodiester internucleoside linkages while retaining nuclease resistance.

III. Certain Modified Oligonucleotides

In certain embodiments, compounds described herein comprise or consist of modified oligonucleotides. In certain embodiments, the above modifications (sugar, nucleobase, internucleoside linkage) are incorporated into a modified oligonucleotide. In certain embodiments, modified oligonucleotides are characterized by their modifications, motifs, and overall lengths. In certain embodiments, such parameters are each independent of one another. Thus, unless otherwise indicated, each internucleoside linkage of an oligonucleotide having a gapmer sugar motif may be modified or unmodified and may or may not follow the gapmer modification pattern of the sugar modifications. Likewise, such gapmer oligonucleotides may comprise one or more modified nucleobase independent of the gapmer pattern of the sugar modifications. Furthermore, in certain instances, an oligonucleotide is described by an overall length or range and by lengths or length ranges of two or more regions (*e.g.*, a region of nucleosides having specified sugar modifications), in such

circumstances it may be possible to select numbers for each range that result in an oligonucleotide having an overall length falling outside the specified range. In such circumstances, both elements must be satisfied. For example, in certain embodiments, a modified oligonucleotide consists of 15-20 linked nucleosides and has a sugar motif consisting of three regions or segments, A, B, and C, wherein region or segment A consists of 2-6 linked nucleosides having a specified sugar motif, region or segment B consists of 6-10 linked nucleosides having a specified sugar motif, and region or segment C consists of 2-6 linked nucleosides having a specified sugar motif. Such embodiments do not include modified oligonucleotides where A and C each consist of 6 linked nucleosides and B consists of 10 linked nucleosides (even though those numbers of nucleosides are permitted within the requirements for A, B, and C) because the overall length of such oligonucleotide is 22, which exceeds the upper limit of 20 for the overall length of the modified oligonucleotide. Unless otherwise indicated, all modifications are independent of nucleobase sequence except that the modified nucleobase 5-methylcytosine is necessarily a "C" in an oligonucleotide sequence.

In certain embodiments, oligonucleotides consist of X to Y linked nucleosides, where X represents the fewest number of nucleosides in the range and Y represents the largest number nucleosides in the range. In certain such embodiments, X and Y are each independently selected from 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, and 50; provided that $X \leq Y$. For example, in certain embodiments, oligonucleotides consist of 12 to 13, 12 to 14, 12 to 15, 12 to 16, 12 to 17, 12 to 18, 12 to 19, 12 to 20, 12 to 21, 12 to 22, 12 to 23, 12 to 24, 12 to 25, 12 to 26, 12 to 27, 12 to 28, 12 to 29, 12 to 30, 13 to 14, 13 to 15, 13 to 16, 13 to 17, 13 to 18, 13 to 19, 13 to 20, 13 to 21, 13 to 22, 13 to 23, 13 to 24, 13 to 25, 13 to 26, 13 to 27, 13 to 28, 13 to 29, 13 to 30, 14 to 15, 14 to 16, 14 to 17, 14 to 18, 14 to 19, 14 to 20, 14 to 21, 14 to 22, 14 to 23, 14 to 24, 14 to 25, 14 to 26, 14 to 27, 14 to 28, 14 to 29, 14 to 30, 15 to 16, 15 to 17, 15 to 18, 15 to 19, 15 to 20, 15 to 21, 15 to 22, 15 to 23, 15 to 24, 15 to 25, 15 to 26, 15 to 27, 15 to 28, 15 to 29, 15 to 30, 16 to 17, 16 to 18, 16 to 19, 16 to 20, 16 to 21, 16 to 22, 16 to 23, 16 to 24, 16 to 25, 16 to 26, 16 to 27, 16 to 28, 16 to 29, 16 to 30, 17 to 18, 17 to 19, 17 to 20, 17 to 21, 17 to 22, 17 to 23, 17 to 24, 17 to 25, 17 to 26, 17 to 27, 17 to 28, 17 to 29, 17 to 30, 18 to 19, 18 to 20, 18 to 21, 18 to 22, 18 to 23, 18 to 24, 18 to 25, 18 to 26, 18 to 27, 18 to 28, 18 to 29, 18 to 30, 19 to 20, 19 to 21, 19 to 22, 19 to 23, 19 to 24, 19 to 25, 19 to 26, 19 to 29, 19 to 28, 19 to 29, 19 to 30, 20 to 21, 20 to 22, 20 to 23, 20 to 24, 20 to 25, 20 to 26, 20 to 27, 20 to 28, 20 to 29, 20 to 30, 21 to 22, 21 to 23, 21 to 24, 21 to 25, 21 to 26, 21 to 27, 21 to 28, 21 to 29, 21 to 30, 22 to 23, 22 to 24, 22 to 25, 22 to 26, 22 to 27, 22 to 28, 22 to 29, 22 to 30, 23 to 24, 23 to 25, 23 to 26, 23 to 27, 23 to 28, 23 to 29, 23 to 30, 24 to 25, 24 to 26, 24 to 27, 24 to 28, 24 to 29, 24 to 30, 25 to 26, 25 to 27, 25 to 28, 25 to 29, 25 to 30, 26 to 27, 26 to 28, 26 to 29, 26 to 30, 27 to 28, 27 to 29, 27 to 30, 28 to 29, 28 to 30, or 29 to 30 linked nucleosides.

In certain embodiments oligonucleotides have a nucleobase sequence that is complementary to a second oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain embodiments, a region of an oligonucleotide has a nucleobase sequence that is complementary to a second

oligonucleotide or an identified reference nucleic acid, such as a target nucleic acid. In certain embodiments, the nucleobase sequence of a region or entire length of an oligonucleotide is at least 70%, at least 80%, at least 90%, at least 95%, or 100% complementary to the second oligonucleotide or nucleic acid, such as a target nucleic acid.

IV. Certain Conjugated Compounds

In certain embodiments, the compounds described herein comprise or consist of an oligonucleotide (modified or unmodified) and optionally one or more conjugate groups and/or terminal groups. Conjugate groups consist of one or more conjugate moiety and a conjugate linker that links the conjugate moiety to the oligonucleotide. Conjugate groups may be attached to either or both ends of an oligonucleotide and/or at any internal position. In certain embodiments, conjugate groups are attached to the 2'-position of a nucleoside of a modified oligonucleotide. In certain embodiments, conjugate groups that are attached to either or both ends of an oligonucleotide are terminal groups. In certain such embodiments, conjugate groups or terminal groups are attached at the 3' and/or 5'-end of oligonucleotides. In certain such embodiments, conjugate groups (or terminal groups) are attached at the 3'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 3'-end of oligonucleotides. In certain embodiments, conjugate groups (or terminal groups) are attached at the 5'-end of oligonucleotides. In certain embodiments, conjugate groups are attached near the 5'-end of oligonucleotides.

Examples of terminal groups include but are not limited to conjugate groups, capping groups, phosphate moieties, protecting groups, modified or unmodified nucleosides, and two or more nucleosides that are independently modified or unmodified.

A. Certain Conjugate Groups

In certain embodiments, oligonucleotides are covalently attached to one or more conjugate groups. In certain embodiments, conjugate groups modify one or more properties of the attached oligonucleotide, including but not limited to pharmacodynamics, pharmacokinetics, stability, binding, absorption, tissue distribution, cellular distribution, cellular uptake, charge and clearance. In certain embodiments, conjugate groups impart a new property on the attached oligonucleotide, *e.g.*, fluorophores or reporter groups that enable detection of the oligonucleotide.

Certain conjugate groups and conjugate moieties have been described previously, for example: cholesterol moiety (Letsinger et al., Proc. Natl. Acad. Sci. USA, 1989, 86, 6553-6556), cholic acid (Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1994, *4*, 1053-1060), a thioether, *e.g.*, hexyl-S-tritylthiol (Manoharan et al., *Ann. N.Y. Acad. Sci.*, 1992, *660*, 306-309; Manoharan et al., *Bioorg. Med. Chem. Lett.*, 1993, *3*, 2765-2770), a thiocholesterol (Oberhauser et al., *Nucl. Acids Res.*, 1992, *20*, 533-538), an aliphatic chain, *e.g.*, do-decan-diol or undecyl residues (Saison-Behmoaras et al., *EMBO J.*, 1991, 10, 1111-1118; Kabanov et al., *FEBS Lett.*, 1990, 259, 327-330; Svinarchuk et al., *Biochimie*, 1993, *75*, 49-54), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethyl-ammonium 1,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate (Manoharan et al.,

Tetrahedron Lett., 1995, *36*, 3651-3654; Shea et al., *Nucl. Acids Res.*, 1990, 18, 3777-3783), a polyamine or a polyethylene glycol chain (Manoharan et al., *Nucleosides & Nucleotides*, 1995, 14, 969-973), or adamantane acetic, a palmityl moiety (Mishra et al., *Biochim. Biophys. Acta*, 1995, 1264, 229-237), an octadecylamine or hexylamino-carbonyl-oxycholesterol moiety (Crooke et al., *J. Pharmacol. Exp. Ther.*, 1996, *i*, 923-937), a tocopherol group (Nishina et al., *Molecular Therapy Nucleic Acids*, 2015, *4*, e220; doi:10.1038/mtna.2014.72 and Nishina et al., *Molecular Therapy*, 2008, 16, 734-740), or a GalNAc cluster (*e.g.*, WO2014/179620).

1. Conjugate Moieties

Conjugate moieties include, without limitation, intercalators, reporter molecules, polyamines, polyamides, peptides, carbohydrates (e.g., GalNAc), vitamin moieties, polyethylene glycols, thioethers, polyethers, cholesterols, thiocholesterols, cholic acid moieties, folate, lipids, phospholipids, biotin, phenazine, phenanthridine, anthraquinone, adamantane, acridine, fluoresceins, rhodamines, coumarins, fluorophores, and dyes.

In certain embodiments, a conjugate moiety comprises an active drug substance, for example, aspirin, warfarin, phenylbutazone, ibuprofen, suprofen, fen-bufen, ketoprofen, (*S*)-(+)-pranoprofen, carprofen, dansylsarcosine, 2,3,5-triiodobenzoic acid, fingolimod, flufenamic acid, folinic acid, a benzothiadiazide, chlorothiazide, a diazepine, indo-methicin, a barbiturate, a cephalosporin, a sulfa drug, an antidiabetic, an antibacterial or an antibiotic.

2. Conjugate linkers

Conjugate moieties are attached to oligonucleotides through conjugate linkers. In certain compounds, a conjugate group is a single chemical bond (i.e. conjugate moiety is attached to an oligonucleotide via a conjugate linker through a single bond). In certain embodiments, the conjugate linker comprises a chain structure, such as a hydrocarbyl chain, or an oligomer of repeating units such as ethylene glycol, nucleosides, or amino acid units.

In certain embodiments, a conjugate linker comprises one or more groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether, and hydroxylamino. In certain such embodiments, the conjugate linker comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and amide groups. In certain embodiments, the conjugate linker comprises groups selected from alkyl and ether groups. In certain embodiments, the conjugate linker comprises at least one phosphorus moiety. In certain embodiments, the conjugate linker comprises at least one phosphate group. In certain embodiments, the conjugate linker includes at least one neutral linking group.

In certain embodiments, conjugate linkers, including the conjugate linkers described above, are bifunctional linking moieties, *e.g.*, those known in the art to be useful for attaching conjugate groups to parent compounds, such as the oligonucleotides provided herein. In general, a bifunctional linking moiety comprises at least two functional groups. One of the functional groups is selected to bind to a particular site on a compound

and the other is selected to bind to a conjugate group. Examples of functional groups used in a bifunctional linking moiety include but are not limited to electrophiles for reacting with nucleophilic groups and nucleophiles for reacting with electrophilic groups. In certain embodiments, bifunctional linking moieties comprise one or more groups selected from amino, hydroxyl, carboxylic acid, thiol, alkyl, alkenyl, and alkynyl.

Examples of conjugate linkers include but are not limited to pyrrolidine, 8-amino-3,6-dioxaoctanoic acid (ADO), succinimidyl 4-(N-maleimidomethyl) cyclohexane-1-carboxylate (SMCC) and 6-aminohexanoic acid (AHEX or AHA). Other conjugate linkers include but are not limited to substituted or unsubstituted C_1-C_{10} alkyl, substituted or unsubstituted C_2-C_{10} alkenyl or substituted or unsubstituted C_2-C_{10} alkynyl, wherein a nonlimiting list of preferred substituent groups includes hydroxyl, amino, alkoxy, carboxy, benzyl, phenyl, nitro, thiol, thioalkoxy, halogen, alkyl, aryl, alkenyl and alkynyl.

In certain embodiments, conjugate linkers comprise 1-10 linker-nucleosides. In certain embodiments, such linker-nucleosides are modified nucleosides. In certain embodiments such linker-nucleosides comprise a modified sugar moiety. In certain embodiments, linker-nucleosides are unmodified. In certain embodiments, linker-nucleosides comprise an optionally protected heterocyclic base selected from a purine, substituted purine, pyrimidine or substituted pyrimidine. In certain embodiments, a cleavable moiety is a nucleoside selected from uracil, thymine, cytosine, 4-N-benzoylcytosine, 5-methylcytosine, 4-N-benzoyl-5-methylcytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the compound after it reaches a target tissue. Accordingly, linker-nucleosides are typically linked to one another and to the remainder of the compound through cleavable bonds. In certain embodiments, such cleavable bonds are phosphodiester bonds.

Herein, linker-nucleosides are not considered to be part of the oligonucleotide. Accordingly, in embodiments in which a compound comprises an oligonucleotide consisting of a specified number or range of linked nucleosides and/or a specified percent complementarity to a reference nucleic acid and the compound also comprises a conjugate group comprising a conjugate linker comprising linker-nucleosides, those linker-nucleosides are not counted toward the length of the oligonucleotide and are not used in determining the percent complementarity of the oligonucleotide for the reference nucleic acid. For example, a compound may comprise (1) a modified oligonucleotide consisting of 8-30 nucleosides and (2) a conjugate group comprising 1-10 linker-nucleosides that are contiguous with the nucleosides of the modified oligonucleotide. The total number of contiguous linked nucleosides in such a compound is more than 30. Alternatively, an compound may comprise a modified oligonucleotide consisting of 8-30 nucleosides and no conjugate group. The total number of contiguous linked nucleosides in such a compound is no more than 30. Unless otherwise indicated conjugate linkers comprise no more than 10 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 5 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 2 linker-nucleosides. In certain embodiments, conjugate linkers comprise no more than 1 linker-nucleoside.

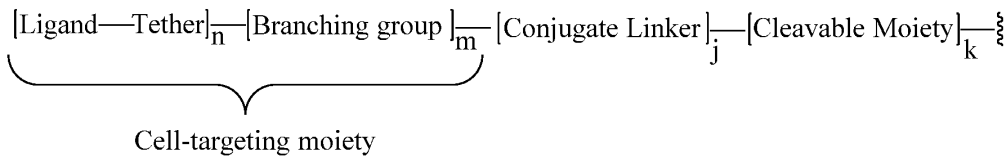
In certain embodiments, it is desirable for a conjugate group to be cleaved from the oligonucleotide. For example, in certain circumstances compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the compound has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate may comprise one or more cleavable moieties, typically within the conjugate linker. In certain embodiments, a cleavable moiety is a cleavable bond. In certain embodiments, a cleavable moiety is a group of atoms comprising at least one cleavable bond. In certain embodiments, a cleavable moiety comprises a group of atoms having one, two, three, four, or more than four cleavable bonds. In certain embodiments, a cleavable moiety is selectively cleaved inside a cell or subcellular compartment, such as a lysosome. In certain embodiments, a cleavable moiety is selectively cleaved by endogenous enzymes, such as nucleases.

In certain embodiments, a cleavable bond is selected from among: an amide, an ester, an ether, one or both esters of a phosphodiester, a phosphate ester, a carbamate, or a disulfide. In certain embodiments, a cleavable bond is one or both of the esters of a phosphodiester. In certain embodiments, a cleavable moiety comprises a phosphate or phosphodiester. In certain embodiments, the cleavable moiety is a phosphate linkage between an oligonucleotide and a conjugate moiety or conjugate group.

In certain embodiments, a cleavable moiety comprises or consists of one or more linker-nucleosides. In certain such embodiments, one or more linker-nucleosides are linked to one another and/or to the remainder of the compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxy nucleoside that is attached to either the 3' or 5'-terminal nucleoside of an oligonucleotide by a phosphate internucleoside linkage and covalently attached to the remainder of the conjugate linker or conjugate moiety by a phosphate or phosphorothioate linkage. In certain such embodiments, the cleavable moiety is 2'-deoxyadenosine.

3. Certain Cell-Targeting Conjugate Moieties

In certain embodiments, a conjugate group comprises a cell-targeting conjugate moiety. In certain embodiments, a conjugate group has the general formula:



wherein n is from 1 to about 3, m is 0 when n is 1, m is 1 when n is 2 or greater, j is 1 or 0, and k is 1 or 0.

In certain embodiments, n is 1, j is 1 and k is 0. In certain embodiments, n is 1, j is 0 and k is 1. In certain embodiments, n is 1, j is 1 and k is 1. In certain embodiments, n is 2, j is 1 and k is 0. In certain embodiments, n is 2, j is 0 and k is 1. In certain embodiments, n is 2, j is 1 and k is 1. In certain embodiments, n is 3, j is 1 and k is 0. In certain embodiments, n is 3, j is 0 and k is 1. In certain embodiments, n is 3, j is 1 and k is 1.

In certain embodiments, conjugate groups comprise cell-targeting moieties that have at least one tethered ligand. In certain embodiments, cell-targeting moieties comprise two tethered ligands covalently attached to a branching group. In certain embodiments, cell-targeting moieties comprise three tethered ligands covalently attached to a branching group.

In certain embodiments, the cell-targeting moiety comprises a branching group comprising one or more groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether and hydroxylamino groups. In certain embodiments, the branching group comprises a branched aliphatic group comprising groups selected from alkyl, amino, oxo, amide, disulfide, polyethylene glycol, ether, thioether and hydroxylamino groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl, amino, oxo, amide and ether groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl, amino and ether groups. In certain such embodiments, the branched aliphatic group comprises groups selected from alkyl and ether groups. In certain embodiments, the branching group comprises a mono or polycyclic ring system.

In certain embodiments, each tether of a cell-targeting moiety comprises one or more groups selected from alkyl, substituted alkyl, ether, thioether, disulfide, amino, oxo, amide, phosphodiester, and polyethylene glycol, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, ether, thioether, disulfide, amino, oxo, amide, and polyethylene glycol, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, phosphodiester, ether, amino, oxo, and amide, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, ether, amino, oxo, and amid, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl, amino, and oxo, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl and oxo, in any combination. In certain embodiments, each tether is a linear aliphatic group comprising one or more groups selected from alkyl and phosphodiester, in any combination. In certain embodiments, each tether comprises at least one phosphorus linking group or neutral linking group. In certain embodiments, each tether comprises a chain from about 6 to about 20 atoms in length. In certain embodiments, each tether comprises a chain from about 10 to about 18 atoms in length. In certain embodiments, each tether comprises about 10 atoms in chain length.

In certain embodiments, each ligand of a cell-targeting moiety has an affinity for at least one type of receptor on a target cell. In certain embodiments, each ligand has an affinity for at least one type of receptor on the surface of a mammalian lung cell.

In certain embodiments, each ligand of a cell-targeting moiety is a carbohydrate, carbohydrate derivative, modified carbohydrate, polysaccharide, modified polysaccharide, or polysaccharide derivative. In certain such embodiments, the conjugate group comprises a carbohydrate cluster (*see*, e.g., Maier et al., "Synthesis of Antisense Oligonucleotides Conjugated to a Multivalent Carbohydrate Cluster for Cellular Targeting," *Bioconjugate Chemistry*, 2003, 14, 18-29, or Rensen et al., "Design and Synthesis of Novel *N*-Acetylgalactosamine-Terminated Glycolipids for Targeting of Lipoproteins to the Hepatic Asiaglycoprotein Receptor," *J. Med. Chem.* 2004, 47, 5798-5808, which are incorporated herein by reference in their entirety). In certain such embodiments, each ligand is an amino sugar or a thio sugar. For example, amino sugars may be selected from any number of compounds known in the art, such as sialic acid, α-D-galactosamine, β-muramic acid, 2-deoxy-2-methylamino-L-glucopyranose, 4,6-dideoxy-4-formamido-2,3-di-*O*-methyl-D-mannopyranose, 2-deoxy-2-sulfoamino-D-glucopyranose and *N*-sulfo-D-glucosamine, and *N*-glycoloyl-α-neuraminic acid. For example, thio sugars may be selected from 5-Thio-β-D-glucopyranose, methyl 2,3,4-tri-*O*-acetyl-1-thio-6-*O*-trityl-α-D-glucopyranoside, 4-thio-β-D-galactopyranose, and ethyl 3,4,6,7-tetra-*O*-acetyl-2-deoxy-1,5-dithio-α-D-*gluco*-heptopyranoside.

In certain embodiments compounds described herein comprise a conjugate group found in any of the following references: Lee, *Carbohydr Res*, 1978, 67, 509-514; Connolly et al., *J Biol Chem*, 1982, 257, 939-945; Pavia et al., *Int J Pep Protein Res*, 1983, 22, 539-548; Lee et al., *Biochem*, 1984, 23, 4255-4261; Lee et al., *Glycoconjugate J*, 1987, 4, 317-328; Toyokuni et al., *Tetrahedron Lett*, 1990, 31, 2673-2676; Biessen et al., *J Med Chem*, 1995, 38, 1538-1546; Valentijn et al., *Tetrahedron*, 1997, 53, 759-770; Kim et al., *Tetrahedron Lett*, 1997, 38, 3487-3490; Lee et al., *Bioconjug Chem*, 1997, 8, 762-765; Kato et al., *Glycobiol*, 2001, 11, 821-829; Rensen et al., *J Biol Chem*, 2001, 276, 37577-37584; Lee et al., *Methods Enzymol*, 2003, 362, 38-43; Westerlind et al., *Glycoconj J*, 2004, 21, 227-241; Lee et al., *Bioorg Med Chem Lett*, 2006, 16(19), 5132-5135; Maierhofer et al., *Bioorg Med Chem*, 2007, 15, 7661-7676; Khorev et al., *Bioorg Med Chem*, 2008, 16, 5216-5231; Lee et al., *Bioorg Med Chem*, 2011, 19, 2494-2500; Kornilova et al., Analyt Biochem, 2012, 425, 43-46; Pujol et al., *Angew Chemie Int Ed Engl*, 2012, 51, 7445-7448; Biessen et al., *J Med Chem*, 1995, 38, 1846-1852; Sliedregt et al., *J Med Chem*, 1999, 42, 609-618; Rensen et al., *J Med Chem*, 2004, 47, 5798-5808; Rensen et al., *Arterioscler Thromb Vasc Biol*, 2006, 26, 169-175; van Rossenberg et al., *Gene Ther*, 2004, 11, 457-464; Sato et al., *J Am Chem Soc*, 2004, 126, 14013-14022; Lee et al., *J Org Chem*, 2012, 77, 7564-7571; Biessen et al., *FASEB J*, 2000, 14, 1784-1792; Rajur et al., *Bioconjug Chem*, 1997, 8, 935-940; Duff et al., *Methods Enzymol*, 2000, 313, 297-321; Maier et al., *Bioconjug Chem*, 2003, 14, 18-29; Jayaprakash et al., *Org Lett*, 2010, 12, 5410-5413; Manoharan, *Antisense Nucleic Acid Drug Dev*, 2002, 12, 103-128; Merwin et al., *Bioconjug Chem*, 1994, 5, 612-620; Tomiya et al., Bioorg Med Chem, 2013, 21, 5275-5281;

International applications WO1998/013381; WO2011/038356; WO1997/046098; WO2008/098788; WO2004/101619; WO2012/037254; WO2011/120053; WO2011/100131; WO2011/163121; WO2012/177947; WO2013/033230; WO2013/075035; WO2012/083185; WO2012/083046; WO2009/082607; WO2009/134487; WO2010/144740; WO2010/148013; WO1997/020563; WO2010/088537; WO2002/043771; WO2010/129709; WO2012/068187; WO2009/126933; WO2004/024757; WO2010/054406; WO2012/089352; WO2012/089602; WO2013/166121; WO2013/165816; U.S. Patents 4,751,219; 8,552,163; 6,908,903; 7,262,177; 5,994,517; 6,300,319; 8,106,022; 7,491,805; 7,491,805; 7,582,744; 8,137,695; 6,383,812; 6,525,031; 6,660,720; 7,723,509; 8,541,548; 8,344,125; 8,313,772; 8,349,308; 8,450,467; 8,501,930; 8,158,601; 7,262,177; 6,906,182; 6,620,916; 8,435,491; 8,404,862; 7,851,615; Published U.S. Patent Application Publications US2011/0097264; US2011/0097265; US2013/0004427; US2005/0164235; US2006/0148740; US2008/0281044; US2010/0240730; US2003/0119724; US2006/0183886; US2008/0206869; US2011/0269814; US2009/0286973; US2011/0207799; US2012/0136042; US2012/0165393; US2008/0281041; US2009/0203135; US2012/0035115; US2012/0095075; US2012/0101148; US2012/0128760; US2012/0157509; US2012/0230938; US2013/0109817; US2013/0121954; US2013/0178512; US2013/0236968; US2011/0123520; US2003/0077829; US2008/0108801; and US2009/0203132.

Compositions and Methods for Formulating Pharmaceutical Compositions

Compounds described herein may be admixed with pharmaceutically acceptable active or inert substances for the preparation of pharmaceutical compositions. Compositions and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

Certain embodiments provide pharmaceutical compositions comprising one or more compounds or a salt thereof. Certain embodiments provide pharmaceutical compositions comprising one or more compounds described herein or a salt thereof. In certain embodiments, the compounds are antisense compounds or oligomeric compounds. In certain embodiments, the compounds comprise or consist of a modified oligonucleotide. In certain such embodiments, the pharmaceutical composition comprises a suitable pharmaceutically acceptable diluent or carrier. In certain embodiments, a pharmaceutical composition comprises a sterile saline solution and one or more compound. In certain embodiments, such pharmaceutical composition consists of a sterile saline solution and one or more compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises one or more compound and sterile water. In certain embodiments, a pharmaceutical composition consists of one compound and sterile water. In certain embodiments, the sterile water is pharmaceutical grade water. In certain embodiments, a pharmaceutical composition comprises or consists of one or more compound and phosphate-buffered saline (PBS). In certain embodiments, a pharmaceutical composition consists of one or more compound and sterile PBS. In certain embodiments, the sterile PBS is pharmaceutical grade PBS. Compositions

and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

A compound described herein complementary to a DNM2 nucleic acid can be utilized in pharmaceutical compositions by combining the compound with a suitable pharmaceutically acceptable diluent or carrier and/or additional components such that the pharmaceutical composition is suitable for injection. In certain embodiments, a pharmaceutically acceptable diluent is phosphate buffered saline. Accordingly, in one embodiment, employed in the methods described herein is a pharmaceutical composition comprising a compound complementary to a DNM2 nucleic acid and a pharmaceutically acceptable diluent. In certain embodiments, the pharmaceutically acceptable diluent is phosphate buffered saline. In certain embodiments, the compound comprises or consists of a modified oligonucleotide provided herein.

Pharmaceutical compositions comprising compounds provided herein encompass any pharmaceutically acceptable salts, esters, or salts of such esters, or any other oligonucleotide which, upon administration to an animal, including a human, is capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. In certain embodiments, the compounds are antisense compounds or oligomeric compounds. In certain embodiments, the compound comprises or consists of a modified oligonucleotide. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of compounds, prodrugs, pharmaceutically acceptable salts of such prodrugs, and other bioequivalents. Suitable pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts.

A prodrug can include the incorporation of additional nucleosides at one or both ends of a compound which are cleaved by endogenous nucleases within the body, to form the active compound.

In certain embodiments, the compounds or compositions further comprise a pharmaceutically acceptable carrier or diluent.

EXAMPLES

The Examples below describe the screening process used to identify lead compounds targeted to DNM2. Out of over 3,000 oligonucleotides that were screened, many potent and tolerable oligonucleotides were identified, and compounds 951799, 949935, 950023, 950089, 951372, 950060, and 950132 emerged as the top lead compounds. In particular, compound 951799 exhibited the best combination of properties in terms of potency and tolerability.

Non-limiting disclosure and incorporation by reference

Although the sequence listing accompanying this filing identifies each sequence as either "RNA" or "DNA" as required, in reality, those sequences may be modified with any combination of chemical modifications. One of skill in the art will readily appreciate that such designation as "RNA" or "DNA" to describe modified oligonucleotides is, in certain instances, arbitrary. For example, an oligonucleotide comprising a nucleoside comprising a 2'-OH sugar moiety and a thymine nucleobase could be described as a

DNA having an RNA sugar, or as an RNA having a DNA nucleobase.

Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic acids containing any combination of unmodified or modified RNA and/or DNA, including, but not limited to such nucleic acids having modified nucleobases. By way of further example and without limitation, an oligonucleotide having the nucleobase sequence "ATCGATCG" encompasses any oligonucleotides having such nucleobase sequence, whether modified or unmodified, including, but not limited to, such compounds comprising RNA bases, such as those having sequence "AUCGAUCG" and those having some DNA bases and some RNA bases such as "AUCGATCG" and compounds having other modified nucleobases, such as "AT^{m}CGAUCG," wherein ^{m}C indicates a cytosine base comprising a methyl group at the 5-position.

While certain compounds, compositions and methods described herein have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the compounds described herein and are not intended to limit the same. Each of the references recited in the present application is incorporated herein by reference in its entirety.

Example 1: Effect of modified oligonucleotides complementary to dynamin 2 *in vitro*

Modified oligonucleotides complementary to one or more dynamin 2 (DNM2) nucleic acids were designed and tested for their effect on dynamin 2 mRNA expression *in vitro*. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions.

A431 cells were cultured at a density of 10,000 cells per well and treated with 4,000 nM modified oligonucleotide via free uptake or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and DNM2 mRNA levels were measured by quantitative real-time PCR. Human primer probe set RTS36027 (forward sequence GACCTCATGCCAAAGACCAT, designated herein as SEQ ID NO: 4; reverse sequence GTCTGCCGAGGAGTATAGGTA, designated herein as SEQ ID NO: 5; probe sequence CCTTCATCCACCACGAGCTGCT, designated herein as SEQ ID: 6) was used to measure mRNA levels. DNM2 mRNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Results are presented in the tables below as normalized DNM2 mRNA level, relative to untreated control cells.

The modified oligonucleotides in the tables below each have a 3-10-3 cEt gapmer motif, wherein the central gap segment contains ten 2'-deoxynucleosides and is flanked by wing segments on the 3' and 5' ends, each containing three cEt nucleosides. All cytosine residues throughout each modified oligonucleotide are 5-methyl cytosines. All internucleoside linkages are phosphorothioate internucleoside linkages.

Each modified oligonucleotide listed in the table below is 100% complementary to human DNM2 nucleic acid sequence GENBANK Number NC_000019.10, truncated from 10715001 to 1083500 (designated herein as SEQ ID NO: 1) and/or GENBANK Number NM_004945.3 (designated herein as SEQ ID NO: 2).

"Start Site" indicates the 5'-most nucleoside of the DNM2 nucleic acid to which the oligonucleotide is complementary. "Stop Site" indicates the 3'-most nucleoside of the DNM2 nucleic acid to which the oligonucleotide is complementary. 'N/A' indicates that the modified oligonucleotide is not 100% complementary to the particular nucleic acid. Several oligonucleotides match two or more sites on a nucleic acid, as shown in the table below. As shown below, modified oligonucleotides complementary to human DNM2 inhibited human DNM2 mRNA expression.

Table 1: DNM2 mRNA Expression

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	Sequence	DNM2 (%Control)	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	SEQ ID NO
694793	3066	3081	CTCAGGCGACACCCGA	96	14	29	7
694833	60707	60722	GATGAGGGTCAAGTTC	20	580	595	8
694838	60773	60788	CTTGATCTGGTACTCG	5	646	661	9
694852	N/A	N/A	GTCCGTAGGCCTTGGG	46	774	789	10
694853	62119	62134	ACCGATGGTCCGTAGG	76	781	796	11
695014	115999	116014	AATGGTGGGCCGGCTG	99	N/A	N/A	12
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	5	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
907925	3055	3070	CCCGACCCGAGCGACC	96	3	18	14
907926	3057	3072	CACCCGACCCGAGCGA	77	5	20	15
907927	3059	3074	GACACCCGACCCGAGC	115	7	22	16
907928	3062	3077	GGCGACACCCGACCCG	96	10	25	17
907929	3069	3084	GTTCTCAGGCGACACC	101	17	32	18
907930	3072	3087	CCGGTTCTCAGGCGAC	95	20	35	19
907931	3075	3090	CATCCGGTTCTCAGGC	58	23	38	20
907932	3078	3093	CCTCATCCGGTTCTCA	47	26	41	21
907933	3083	3098	CGCCGCCTCATCCGGT	69	31	46	22
907934	3086	3101	GGTCGCCGCCTCATCC	65	34	49	23
907935	3089	3104	CACGGTCGCCGCCTCA	29	37	52	24
907936	3091	3106	CTCACGGTCGCCGCCT	42	39	54	25
907937	3093	3108	GCCTCACGGTCGCCGC	65	41	56	26
907938	3095	3110	CGGCCTCACGGTCGCC	106	43	58	27

907939	3098	3113	GCTCGGCCTCACGGTC	44	46	61	28
907940	3101	3116	CCGGCTCGGCCTCACG	87	49	64	29
907941	3111	3126	ACGCCCGCTCCCGGCT	100	59	74	30
907942	3123	3138	GGCCTCGGCAAGACGC	96	71	86	31
907943	3126	3141	CCGGGCCTCGGCAAGA	97	74	89	32
907944	3129	3144	CGCCCGGGCCTCGGCA	84	77	92	33
907945	3144	3159	CCGTTGCTCCCCGCCC	5	92	107	34
907946	3146	3161	AGCCGTTGCTCCCCGC	12	94	109	35
907947	3149	3164	TGTAGCCGTTGCTCCC	10	97	112	36
907948	3153	3168	CGTCTGTAGCCGTTGC	8	101	116	37
907949	3171	3186	AACGACCTGGCCCCGC	12	119	134	38
907950	3177	3192	ACCCTCAACGACCTGG	41	125	140	39
907951	3180	3195	CCGACCCTCAACGACC	26	128	143	40
907952	3182	3197	CGCCGACCCTCAACGA	54	130	145	41
907953	3186	3201	CCGCCGCCGACCCTCA	35	134	149	42
907954	3190	3205	TCGCCCGCCGCCGACC	61	138	153	43
907955	3196	3211	CGCTCCTCGCCCGCCG	52	144	159	44
907956	3198	3213	TGCGCTCCTCGCCCGC	120	146	161	45
907957	3201	3216	CCCTGCGCTCCTCGCC	32	149	164	46
907958	3204	3219	GCGCCCTGCGCTCCTC	105	152	167	47
907959	3220	3235	GCGGCCCCCGGCCCGA	90	168	183	48
907960	3302	3317	CTGGCCGATGGAGCTG	129	250	265	49
907961	3304	3319	CTCTGGCCGATGGAGC	70	252	267	50
907962	3308	3323	GCAGCTCTGGCCGATG	46	256	271	51
907963	N/A	N/A	GGGAAGGAAGTCCCGG	97	349	364	52
907964	44749	44764	ATTCCTGAACCGCGGG	89	363	378	53
907965	44751	44766	CGATTCCTGAACCGCG	47	365	380	54
907966	44753	44768	GACGATTCCTGAACCG	11	367	382	55
907967	57491	57506	GACTTGCAGTGCAAAA	6	438	453	56
907968	57493	57508	TGGACTTGCAGTGCAA	15	440	455	57
907969	57495	57510	TTTGGACTTGCAGTGC	2	442	457	58
907970	57499	57514	ACTTTTTGGACTTGCA	5	446	461	59
907971	57526	57541	CCTGCCGGACTTCATC	17	473	488	60
907972	57529	57544	TCTCCTGCCGGACTTC	13	476	491	61
907973	57532	57547	CAATCTCCTGCCGGAC	20	479	494	62
907974	57534	57549	TTCAATCTCCTGCCGG	25	481	496	63
907975	60711	60726	GGTCGATGAGGGTCAA	8	584	599	64
907976	60716	60731	CGGGAGGTCGATGAGG	66	589	604	65
907977	60718	60733	CCCGGGAGGTCGATGA	117	591	606	66
907978	60722	60737	GATACCCGGGAGGTCG	55	595	610	67
907979	60724	60739	GTGATACCCGGGAGGT	11	597	612	68

907980	60728	60743	CTTGGTGATACCCGGG	57	601	616	69
907981	60734	60749	AGGCACCTTGGTGATA	40	607	622	70
907982	60776	60791	GTCCTTGATCTGGTAC	28	649	664	71
907983	60778	60793	ATGTCCTTGATCTGGT	8	651	666	72
907984	60784	60799	AGGATCATGTCCTTGA	58	657	672	73
907985	60788	60803	CTGCAGGATCATGTCC	35	661	676	74
907986	60798	60813	GGCTGATGAACTGCAG	56	671	686	75
907987	60806	60821	GCTCTCCCGGCTGATG	40	679	694	76
907988	60809	60824	GCTGCTCTCCCGGCTG	68	682	697	77
907989	60826	60841	GTGACAGCCAGAATGA	26	699	714	78
907990	60842	60857	GTCCATGTTGGCGGGC	66	715	730	79
907991	60882	60897	CGACTTCCTTGGCCAG	68	755	770	80
907992	60884	60899	ATCGACTTCCTTGGCC	99	757	772	81
907993	N/A	N/A	TGGTCCGTAGGCCTTG	72	776	791	82
907994	62116	62131	GATGGTCCGTAGGCCT	68	778	793	83
907995	62195	62210	TCAACGGGAGCAACTT	18	857	872	84
907996	N/A	N/A	GCCTCTTCTCAACGGG	105	865	880	85
907997	N/A	N/A	TAGCCTCTTCTCAACG	17	867	882	86
907998	68005	68020	GCACGGATGTCCTTCT	8	924	939	87
907999	68008	68023	GCTGCACGGATGTCCT	25	927	942	88
908000	68013	68028	CCAGTGCTGCACGGAT	17	932	947	89
908001	68057	68072	GTGCCGGTAGGCCGGG	91	976	991	90
908002	68059	68074	ATGTGCCGGTAGGCCG	83	978	993	91
908003	68062	68077	GCCATGTGCCGGTAGG	77	981	996	92
908004	68064	68079	CGGCCATGTGCCGGTA	90	983	998	93
908005	68096	68111	CGTCTTCTGCAGATGT	26	1015	1030	94
908006	71583	71598	GCCGGCAGCGACTCCC	107	1059	1074	95
908007	71586	71601	AGGGCCGGCAGCGACT	64	1062	1077	96
908008	71589	71604	CGTAGGGCCGGCAGCG	67	1065	1080	97
908009	71603	71618	TCTGTAGTTTGCTACG	34	1079	1094	98
908010	71605	71620	GCTCTGTAGTTTGCTA	42	1081	1096	99
908011	71659	71674	GTCGGGCCGAAAGTTC	15	1135	1150	100
908012	71681	71696	CTTTGGTTTTGCGGGT	36	1157	1172	101
908013	78772	78787	GAGTGTCCACCTGATC	11	1235	1250	102
908014	78786	78801	CCCGGAGAGCTCCAGA	58	1249	1264	103
908015	78789	78804	GCCCCCGGAGAGCTCC	71	1252	1267	104
908016	78791	78806	GCGCCCCCGGAGAGCT	129	1254	1269	105
908017	78804	78819	GCGATTGATTCGGGCG	50	1267	1282	106
908018	78808	78823	AGATGCGATTGATTCG	14	1271	1286	107
908019	80422	80437	GACTCCATGGATGTTC	91	1369	1384	108
908020	N/A	N/A	GCCCGGTCCTGACTCC	54	1379	1394	109

908021	N/A	N/A	AAGCCCGGTCCTGACT	81	1381	1396	110
908022	81058	81073	GAAAAGCCCGGTCCTG	35	1384	1399	111
908023	81061	81076	GGTGAAAAGCCCGGTC	58	1387	1402	112
908024	81076	81091	GAATGCCAAGTCCGGG	43	1402	1417	113
908025	81079	81094	CTCGAATGCCAAGTCC	8	1405	1420	114
908026	81082	81097	GGCCTCGAATGCCAAG	169	1408	1423	115
908027	81103	81118	GACGACCTGCTTTTTC	4	1429	1444	116
908028	81106	81121	CTTGACGACCTGCTTT	13	1432	1447	117
908029	81107	81122	GCTTGACGACCTGCTT	14	1433	1448	118
908030	81109	81124	CAGCTTGACGACCTGC	33	1435	1450	119
908031	81111	81126	TTCAGCTTGACGACCT	5	1437	1452	120
908032	81113	81128	CTTTCAGCTTGACGAC	22	1439	1454	121
908033	81115	81130	CTCTTTCAGCTTGACG	7	1441	1456	122
908034	81137	81152	GGTCGACACATTTCAG	13	1463	1478	123
908035	81139	81154	CAGGTCGACACATTTC	2	1465	1480	124
908036	81147	81162	TGGATAACCAGGTCGA	14	1473	1488	125
908037	81160	81175	ATTGATTAGCTCCTGG	2	1486	1501	126
908038	81170	81185	GCCTAACTGTATTGAT	22	1496	1511	127
908039	81172	81187	CTGCCTAACTGTATTG	28	1498	1513	128
908040	81175	81190	ACACTGCCTAACTGTA	54	1501	1516	129
908041	81182	81197	TACTGGTACACTGCCT	4	1508	1523	130
908042	N/A	N/A	CTGAGCTTACTGGTAC	19	1515	1530	131
908043	N/A	N/A	GAACTGAGCTTACTGG	10	1518	1533	132
908044	N/A	N/A	GGTAGGAACTGAGCTT	8	1523	1538	133
908045	83499	83514	TCCTCTCGCAACCGGG	46	1539	1554	134
908046	83502	83517	GTCTCCTCTCGCAACC	34	1542	1557	135
908047	83505	83520	TCTGTCTCCTCTCGCA	11	1545	1560	136
908048	83517	83532	GTGACGATTCGCTCTG	48	1557	1572	137
908049	83522	83537	AAGTGGTGACGATTCG	5	1562	1577	138
908050	83524	83539	GTAAGTGGTGACGATT	17	1564	1579	139
908051	83536	83551	CCGTTCCCGGATGTAA	86	1576	1591	140
908052	83548	83563	CGTTCTCCCCTCCCGT	9	1588	1603	141
908053	N/A	N/A	CAGAAGAATCTGGTCC	33	1606	1621	142
908054	87290	87305	GTCGATCAGCAGAAGA	33	1615	1630	143
908055	87294	87309	CAATGTCGATCAGCAG	16	1619	1634	144
908056	87296	87311	CTCAATGTCGATCAGC	10	1621	1636	145
908057	87299	87314	CTGCTCAATGTCGATC	18	1624	1639	146
908058	87302	87317	GGACTGCTCAATGTCG	58	1627	1642	147
908059	87304	87319	TAGGACTGCTCAATGT	3	1629	1644	148
908060	87308	87323	GATGTAGGACTGCTCA	19	1633	1648	149
908061	87311	87326	GTTGATGTAGGACTGC	3	1636	1651	150

908062	97288	97303	GGCTGATGTTGTTGAT	31	1760	1775	151
908063	97290	97305	CAGGCTGATGTTGTTG	36	1762	1777	152
908064	97294	97309	TCATCAGGCTGATGTT	100	1766	1781	153
908065	97299	97314	GCCTTTCATCAGGCTG	89	1771	1786	154
908066	97338	97353	TGACTCGGCAGTCAGC	86	1810	1825	155
908067	97341	97356	CAGTGACTCGGCAGTC	24	1813	1828	156
908068	97345	97360	AGGACAGTGACTCGGC	17	1817	1832	157
908069	105015	105030	ATCACGGATCTTGAGG	40	1885	1900	158
908070	105019	105034	CCACATCACGGATCTT	12	1889	1904	159
908071	105020	105035	TCCACATCACGGATCT	31	1890	1905	160
908072	105022	105037	TCTCCACATCACGGAT	72	1892	1907	161
908073	105060	105075	GAAGATGGCGAAGACG	81	1930	1945	162
908074	108791	108806	CAGGTCCTTGTAGACG	60	1963	1978	163
908075	108804	108819	GCTCGATCTGCCGCAG	55	1976	1991	164
908076	108806	108821	CAGCTCGATCTGCCGC	54	1978	1993	165
908077	108857	108872	TCGGAGGAACGAGGCC	80	2029	2044	166
908078	108859	108874	GCTCGGAGGAACGAGG	67	2031	2046	167
908079	108861	108876	CAGCTCGGAGGAACGA	59	2033	2048	168
908080	108863	108878	GCCAGCTCGGAGGAAC	93	2035	2050	169
908081	N/A	N/A	GCCTGGTCCTTCTCGG	70	2058	2073	170
908082	110075	110090	AGGTGTTCTCCTGGGC	74	2090	2105	171
908083	110077	110092	GAAGGTGTTCTCCTGG	81	2092	2107	172
908084	110080	110095	GGAGAAGGTGTTCTCC	119	2095	2110	173
908085	110160	110175	ATGGACTTGTTGATGA	11	2175	2190	174
908086*	110166	110181	TCGCGGATGGACTTGT	36	2181	2196	175
908087*	110168	110183	GGTCGCGGATGGACTT	58	2183	2198	176
908088*	110171	110186	TGAGGTCGCGGATGGA	4	2186	2201	177
908089*	114042	114057	CGTGGTGGATGAAGGC	3	2243	2258	178
908090*	114069	114084	CCGAGGAGTATAGGTA	17	2270	2285	179
908091*	114072	114087	CTGCCGAGGAGTATAG	14	2273	2288	180
908092*	114074	114089	GTCTGCCGAGGAGTAT	11	2275	2290	181
908093*	114077	114092	CTGGTCTGCCGAGGAG	9	2278	2293	182
908094*	114080	114095	GCTCTGGTCTGCCGAG	39	2281	2296	183
908095	115141	115156	CTGGACACCGGTCGGC	39	2484	2499	184
908096	115144	115159	ATGCTGGACACCGGTC	47	2487	2502	185
908097	115146	115161	GTATGCTGGACACCGG	33	2489	2504	186
908098	115150	115165	GGGTGTATGCTGGACA	11	2493	2508	187
908099	115214	115229	CACGGGAACAGGAATC	25	2557	2572	188
908100	115221	115236	CTGCCCCCACGGGAAC	80	2564	2579	189
908101	115238	115253	CGCCGAGAAGGAGGCT	97	2581	2596	190
908102	115283	115298	GTTGGCAAACACGCTC	16	2626	2641	191

908103	115285	115300	CTGTTGGCAAACACGC	30	2628	2643	192
908104	115292	115307	GAGGTCACTGTTGGCA	9	2635	2650	193
908105	115324	115339	GGCCGAGATGGGATCT	73	2667	2682	194
908106	115326	115341	CTGGCCGAGATGGGAT	45	2669	2684	195
908107	115329	115344	GAACTGGCCGAGATGG	6	2672	2687	196
908108	115332	115347	TCCGAACTGGCCGAGA	33	2675	2690	197
908109	115336	115351	GGGATCCGAACTGGCC	82	2679	2694	198
908110	116010	116025	GCTGGGCGGATAATGG	45	2754	2769	199
908111	116015	116030	GCTCGGCTGGGCGGAT	101	2759	2774	200
908112	116017	116032	TGGCTCGGCTGGGCGG	89	2761	2776	201
908113	116022	116037	AGGGATGGCTCGGCTG	75	2766	2781	202
908114	116030	116045	AGTCGAGCAGGGATGG	53	2774	2789	203
908115	116035	116050	GGCCTAGTCGAGCAGG	104	2779	2794	204
908116	116038	116053	CGAGGCCTAGTCGAGC	79	2782	2797	205
908117	116042	116057	CCCTCGAGGCCTAGTC	87	2786	2801	206
908118	116045	116060	CCCCCCTCGAGGCCTA	69	2789	2804	207
908119	116047	116062	CGCCCCCCTCGAGGCC	89	2791	2806	208
908120	116057	116072	CCCGAGAGCACGCCCC	40	2801	2816	209
908121	116060	116075	CCCCCCGAGAGCACGC	38	2804	2819	210
908122	116063	116078	GGCCCCCCCGAGAGCA	95	2807	2822	211
908123	116068	116083	CGTGAGGCCCCCCCGA	67	2812	2827	212
908124	116088	116103	AAGCTCCTGCGCCGCG	55	2832	2847	213
908125	116096	116111	GACCACTGAAGCTCCT	32	2840	2855	214
908126	116098	116113	CAGACCACTGAAGCTC	38	2842	2857	215
908127	116108	116123	CGGAGGGCCCCAGACC	100	2852	2867	216
908128	116110	116125	GGCGGAGGGCCCCAGA	91	2854	2869	217
908129	116128	116143	TGGTCCCAGCATAGGG	88	2872	2887	218
908130	116130	116145	CCTGGTCCCAGCATAG	73	2874	2889	219
908131	116138	116153	ACTGGGAGCCTGGTCC	72	2882	2897	220
908132	116164	116179	CGTTAAGGAAGAGGCC	69	2908	2923	221
908133	116209	116224	GCGGTGTCCAGCCAGG	49	2953	2968	222
908134	116211	116226	GTGCGGTGTCCAGCCA	37	2955	2970	223
908135	116215	116230	CGCAGTGCGGTGTCCA	13	2959	2974	224
908136	116218	116233	TTGCGCAGTGCGGTGT	29	2962	2977	225
908137	116220	116235	CTTTGCGCAGTGCGGT	15	2964	2979	226
908138	116223	116238	CCCCTTTGCGCAGTGC	12	2967	2982	227
908139	116226	116241	GGGCCCCTTTGCGCAG	101	2970	2985	228
908140	116228	116243	CAGGGCCCCTTTGCGC	92	2972	2987	229
908141	116260	116275	TGCAACACCCCAGCGC	78	3004	3019	230
908142	116265	116280	CAAAGTGCAACACCCC	20	3009	3024	231
908143	116268	116283	CCCCAAAGTGCAACAC	47	3012	3027	232

908144	116300	116315	TGGTCCCCCCTCTGCC	64	3044	3059	233
908145	116309	116324	CAAGGGTTCTGGTCCC	45	3053	3068	234
908146	116312	116327	TGTCAAGGGTTCTGGT	15	3056	3071	235
908147	116314	116329	GGTGTCAAGGGTTCTG	8	3058	3073	236
908148	116318	116333	GGATGGTGTCAAGGGT	7	3062	3077	237
908149	116331	116346	GACCCCTCATTCAGGA	84	3075	3090	238
908150	116333	116348	TGGACCCCTCATTCAG	64	3077	3092	239
908151	116336	116351	GGCTGGACCCCTCATT	80	3080	3095	240
908152	116348	116363	GAGTCCCCCCCAGGCT	63	3092	3107	241
908153	116352	116367	GGTAGAGTCCCCCCCA	31	3096	3111	242
908154	116356	116371	CCTTGGTAGAGTCCCC	3	3100	3115	243
908155	116359	116374	AGACCTTGGTAGAGTC	73	3103	3118	244
908156	116385	116400	CCTACATGGGCTTTCC	37	3129	3144	245
908157	116389	116404	CTGCCCTACATGGGCT	115	3133	3148	246
908158	116398	116413	ATAGAAGGCCTGCCCT	71	3142	3157	247
908159	116400	116415	TTATAGAAGGCCTGCC	41	3144	3159	248
908160	116404	116419	GCACTTATAGAAGGCC	70	3148	3163	249
908161	116408	116423	GCCCGCACTTATAGAA	45	3152	3167	250
908162	116410	116425	GTGCCCGCACTTATAG	66	3154	3169	251
908163	116418	116433	CGCCCTTGGTGCCCGC	62	3162	3177	252
908164	116455	116470	TATACCCCTGCACCCC	11	3199	3214	253
908165	116464	116479	GGAAGTTGATATACCC	29	3208	3223	254
908166	116471	116486	GCTAATGGGAAGTTGA	13	3215	3230	255
908167	116474	116489	CCTGCTAATGGGAAGT	14	3218	3233	256
908168	116477	116492	GCTCCTGCTAATGGGA	139	3221	3236	257
908169	116481	116496	GGGAGCTCCTGCTAAT	102	3225	3240	258
908170	116497	116512	GCCAGGCTTGCCGCTG	80	3241	3256	259
908171	116499	116514	GGGCCAGGCTTGCCGC	87	3243	3258	260
908172	116511	116526	ACCGAGCCCACTGGGC	72	3255	3270	261
908173	116513	116528	CTACCGAGCCCACTGG	57	3257	3272	262
908174	116518	116533	GGGCACTACCGAGCCC	87	3262	3277	263
908175	116523	116538	CAGCTGGGCACTACCG	86	3267	3282	264
908176	116541	116556	TGTACACCTCAGGCCT	83	3285	3300	265
908177	116544	116559	CTATGTACACCTCAGG	10	3288	3303	266
908178	116547	116562	GGACTATGTACACCTC	7	3291	3306	267
908179	116550	116565	GAAGGACTATGTACAC	8	3294	3309	268
908180	116556	116571	GGCCGGGAAGGACTAT	51	3300	3315	269
908181	116558	116573	ATGGCCGGGAAGGACT	78	3302	3317	270
908182	116561	116576	AATATGGCCGGGAAGG	19	3305	3320	271
908183	116565	116580	GGTTAATATGGCCGGG	13	3309	3324	272
908184	116573	116588	GGCTGTGTGGTTAATA	8	3317	3332	273

908185	116603	116618	CCTCTGGCAGCCGAGG	100	3347	3362	274
908186	116606	116621	GCACCTCTGGCAGCCG	73	3350	3365	275
908187	116608	116623	AGGCACCTCTGGCAGC	61	3352	3367	276
908188	116614	116629	TAGCAAAGGCACCTCT	41	3358	3373	277
908189	116617	116632	GCCTAGCAAAGGCACC	146	3361	3376	278
908190	116621	116636	CCGGGCCTAGCAAAGG	60	3365	3380	279
908191	116624	116639	GCTCCGGGCCTAGCAA	123	3368	3383	280
908192	116626	116641	CGGCTCCGGGCCTAGC	97	3370	3385	281
908193	116630	116645	CCAACGGCTCCGGGCC	117	3374	3389	282
908194	116638	116653	GGCCCGGGCCAACGGC	109	3382	3397	283
908195	116640	116655	CCGGCCCGGGCCAACG	104	3384	3399	284
908196	116642	116657	GGCCGGCCCGGGCCAA	99	3386	3401	285
908197	116644	116659	AAGGCCGGCCCGGGCC	86	3388	3403	286
908198	116646	116661	GCAAGGCCGGCCCGGG	88	3390	3405	287
908199	116648	116663	GGGCAAGGCCGGCCCG	125	3392	3407	288
908200	116650	116665	TAGGGCAAGGCCGGCC	99	3394	3409	289
908201	116655	116670	AGGAATAGGGCAAGGC	6	3399	3414	290
908202	116712	116727	ACCACCCACATAGCCC	31	3456	3471	291
908203	116729	116744	CAAGACCCCCCGCCAC	64	3473	3488	292
908204	116732	116747	CCCCAAGACCCCCCGC	59	3476	3491	293
908205	116738	116753	AGAGGCCCCCAAGACC	86	3482	3497	294
908206	116772	116787	GGCCCACCCATCAGGG	110	3516	3531	295
908207	116774	116789	TGGGCCCACCCATCAG	127	3518	3533	296
908208	116789	116804	AGAGAGAGGCCGCCCT	37	3533	3548	297
908209	116791	116806	TCAGAGAGAGGCCGCC	70	3535	3550	298
908210	116808	116823	GAGTGGGTGAGGTCTC	77	3552	3567	299
908211	116815	116830	GAGCGAGGAGTGGGTG	59	3559	3574	300
908212	116819	116834	AACTGAGCGAGGAGTG	55	3563	3578	301
908213	116822	116837	TCAAACTGAGCGAGGA	5	3566	3581	302
908214	116826	116841	GTGGTCAAACTGAGCG	15	3570	3585	303
908215	116832	116847	CTTACAGTGGTCAAAC	10	3576	3591	304
908216	116843	116858	GAGTGCAGGCACTTAC	48	3587	3602	305
908217	116849	116864	AATACAGAGTGCAGGC	4	3593	3608	306
908221	82462	82477	CCACGAGATCAACACA	20	N/A	N/A	307
908222	82464	82479	GACCACGAGATCAACA	88	N/A	N/A	308
908223	82465	82480	AGACCACGAGATCAAC	82	N/A	N/A	309
908224	82468	82483	CTGAGACCACGAGATC	34	N/A	N/A	310
908225	82471	82486	GCTCTGAGACCACGAG	59	N/A	N/A	311
908226	82482	82497	GACCGTGGCCAGCTCT	52	N/A	N/A	312
908227	82484	82499	ATGACCGTGGCCAGCT	54	N/A	N/A	313
908228	82485	82500	TATGACCGTGGCCAGC	31	N/A	N/A	314

908229	82487	82502	TTTATGACCGTGGCCA	64	N/A	N/A	315
908230	82488	82503	TTTTATGACCGTGGCC	102	N/A	N/A	316
908231	82498	82513	CGGCACACTTTTTTAT	37	N/A	N/A	317
908232	82502	82517	TTCTCGGCACACTTTT	4	N/A	N/A	318
908236	N/A	N/A	CCCCGCCGCGGGCACG	103	3506	3521	319
908237	4387	4402	CCAAAGGAGGGCCCCC	88	N/A	N/A	320
908238	4857	4872	CGCCAGCCTAGTGGCC	142	N/A	N/A	321
908239	5585	5600	TGGGACTACCACCCTA	129	N/A	N/A	322
908240	6095	6110	CTCCATACTGGCCGGC	91	N/A	N/A	323
908241	6449	6464	CTTAACGAGGCCAGCC	56	N/A	N/A	324
908242	7057	7072	ACCCATCTAGGCCCCA	23	N/A	N/A	325
908243	7335	7350	TGGTGCACCGCAGACA	61	N/A	N/A	326
908244	8045	8060	TCAGGAGGCGAGATTG	93	N/A	N/A	327
908245	8318	8333	CGGGAAAACCCCGCCT	123	N/A	N/A	328
908246	8813	8828	AGCCACTAAGTGGCCC	130	N/A	N/A	329
908247	9601	9616	GCTAAACTGGCCTCCG	78	N/A	N/A	330
908248	9989	10004	GCCAACGGGCATCCGA	104	N/A	N/A	331
908249	10650	10665	GTCCACTCCCAGTAGG	77	N/A	N/A	332
908250	11631	11646	GGTGATCCGATGCTGG	34	N/A	N/A	333
908251	12300	12315	GGCCATCTTCCGCCCT	102	N/A	N/A	334
908252	12662	12677	CTAACCTAGGCCGGGT	70	N/A	N/A	335
908253	12991	13006	AGACGCAGGGCCACAT	66	N/A	N/A	336
908254	13381	13396	GGCTCTAGAGGGCCCA	110	N/A	N/A	337
908255	13954	13969	CCGCATACAGCCTTTT	12	N/A	N/A	338
908256	14620	14635	GCATTCCACGGGCAGC	34	N/A	N/A	339
908257	15396	15411	CACCGCTACCCTAGCT	63	N/A	N/A	340
908258	15792	15807	GGGCACCCCGCAGGTT	102	N/A	N/A	341
908259	16235	16250	TCTAGAAGGACCCTGT	64	N/A	N/A	342
908260	16810	16825	AGCCGGGCTTCCGTCT	84	N/A	N/A	343
908261	17238	17253	TTTAAGGGCGCGGTGG	99	N/A	N/A	344
908262	17624	17639	TGCACTTCCGGACAGG	82	N/A	N/A	345
908263	18173	18188	CACCAGCCCAGGCGCG	117	N/A	N/A	346
908264	18617	18632	AGCTAGGTTAATTTCT	64	N/A	N/A	347
908265	19070	19085	CAACATCCCGCCAGGC	80	N/A	N/A	348
908266	19407	19422	AGCAATCTAGCCTCCC	39	N/A	N/A	349
908267	19819	19834	TGCAATGTCCAGTCCT	11	N/A	N/A	350
908268	20435	20450	ACCTAGCAAGCCTACC	64	N/A	N/A	351
908269	21415	21430	GCTACAGCAATATAGA	67	N/A	N/A	352
908270	21839	21854	TCTTAACAGGCTCCCT	63	N/A	N/A	353
908271	22199	22214	CCTCAGGGACGACTTC	87	N/A	N/A	354
908272	22636	22651	TATACGGGCATGTTGA	55	N/A	N/A	355

908273	22916	22931	GTGCATCCCGAGAGGG	89	N/A	N/A	356
908274	23292	23307	ATGAAAGTCTCCACTT	61	N/A	N/A	357
908275	23543	23558	AACCGCTGGGATCCCC	71	N/A	N/A	358
908276	24229	24244	GTACAGGAGTTCCCCA	90	N/A	N/A	359
908277	25038	25053	AAATACACCCTAGATG	83	N/A	N/A	360
908278	25670	25685	GAAGATTTTGGCCGGG	85	N/A	N/A	361
908279	25997	26012	CTCCAGGACACACCGT	42	N/A	N/A	362
908280	27088	27103	GGGAGTAGGCTCGACC	51	N/A	N/A	363
908281	27400	27415	CCCTATTCCACAGGAC	85	N/A	N/A	364
908282	27746	27761	GCTAAGAGCAGCCCTC	80	N/A	N/A	365
908283	28198	28213	GGCATCACGGCCGGGC	76	N/A	N/A	366
908284	29125	29140	TGTCACCCCAGCCGAA	67	N/A	N/A	367
908285	29568	29583	AGCCGGGCACCACCCA	67	N/A	N/A	368
908286	30330	30345	GGCAAGGACAGCCGAC	94	N/A	N/A	369
908287	30334	30349	GTTTGGCAAGGACAGC	40	N/A	N/A	370
908288	30337	30352	GTGGTTTGGCAAGGAC	14	N/A	N/A	371
908289	30340	30355	GCAGTGGTTTGGCAAG	46	N/A	N/A	372
908290	30342	30357	ATGCAGTGGTTTGGCA	86	N/A	N/A	373
908291	30401	30416	TCAACACCTTGAGGGC	34	N/A	N/A	374
908292	30498	30513	TGCCTAGGCGATCCTC	88	N/A	N/A	375
908293	30928	30943	GACATTGCTGTCGCAG	78	N/A	N/A	376
908294	31347	31362	TCCCAAGTGCCCCCCA	90	N/A	N/A	377
908295	31703	31718	AGCCGGCACGGTTGCT	125	N/A	N/A	378
908296	32187	32202	GAGAACATTCGCCCCA	27	N/A	N/A	379
908297	32386	32401	TGACCTGTGGCAATTC	26	N/A	N/A	380
908298	32388	32403	GGTGACCTGTGGCAAT	44	N/A	N/A	381
908299	32689	32704	TCCCGTATCGGCCCCT	85	N/A	N/A	382
908300	33343	33358	GTCCAGCCGCGAGTCC	59	N/A	N/A	383
908301	33635	33650	GGCAGACCCGCAGTCA	73	N/A	N/A	384
908302	34108	34123	GGGCAAGCCACCCCTC	93	N/A	N/A	385
908303	34623	34638	AAGTCGAGCTCCGCCC	63	N/A	N/A	386
908304	35031	35046	TGGTCCTAGCCCGTCC	78	N/A	N/A	387
908305	35549	35564	GGGTACAGGCAAACCT	88	N/A	N/A	388
908306	36028	36043	CCATACCCCCATCTGA	102	N/A	N/A	389
908307	36712	36727	GCGCAGAGGGCCTCGC	123	N/A	N/A	390
908308	37097	37112	CACTACAGACATCCCT	64	N/A	N/A	391
908309	37538	37553	AGCCAGGGCCCGGCTT	93	N/A	N/A	392
908310	38044	38059	CTCCAACTGTAGGGCT	87	N/A	N/A	393
908311	39735	39750	GCGGATGGTGGCATTC	90	N/A	N/A	394
908312	40399	40414	CAGCAGCGGCGGTGAC	84	N/A	N/A	395
908313	41143	41158	CTCTTAGCATGGCCCC	73	N/A	N/A	396

908314	41620	41635	GGCCTGGGATGCTACC	129	N/A	N/A	397
908315	41957	41972	TTAAACCCCCCTCTGG	104	N/A	N/A	398
908316	42239	42254	GCCCAAGCCCTCGGCG	147	N/A	N/A	399
908317	42806	42821	ATGCACGCGCTACCAT	106	N/A	N/A	400
908318	43841	43856	ACATATCCTGGCCGGG	112	N/A	N/A	401
908319	44266	44281	CTGGATGTGGGAACGG	94	N/A	N/A	402
908320	44817	44832	CCTCAGGCCGCCCCAT	57	N/A	N/A	403
908321	45179	45194	GGCCATGGAGGGTCAC	111	N/A	N/A	404
908322	45544	45559	GGGACAACTGGCGACA	39	N/A	N/A	405
908323	45952	45967	TGGTAGAGGGCTGGTG	78	N/A	N/A	406
908324	46827	46842	GCCCATCGGCTGCTGT	153	N/A	N/A	407
908325	47604	47619	GGGTAGGCCTGCGCTC	119	N/A	N/A	408
908326	48030	48045	TGCCATGATCAGGCGG	109	N/A	N/A	409
908327	48530	48545	ACCAAGTGGGCACCTA	92	N/A	N/A	410
908328	49088	49103	CCACAAGGCCCCGCCG	103	N/A	N/A	411
908329	49883	49898	GTGACCAGGTGCGGGT	84	N/A	N/A	412
908330	50310	50325	CTGGGCAGAGCCGATC	95	N/A	N/A	413
908331	50840	50855	GACGAGGCTGGCCCTG	36	N/A	N/A	414
908332	51504	51519	CCCCACTGTGCTAAAC	91	N/A	N/A	415
908333	51765	51780	AGTCAGCCGTCCTCGC	58	N/A	N/A	416
908334	52587	52602	CACCAGGCCGAGAGCA	111	N/A	N/A	417
908335	53006	53021	GCCCAGGCACCGACCA	92	N/A	N/A	418
908336	53680	53695	CCCCGGAACCTCAGGC	85	N/A	N/A	419
908337	54271	54286	CAGCACGCTGTGTGCA	65	N/A	N/A	420
908338	54667	54682	CACTCGGCCGCTCTTC	80	N/A	N/A	421
908339	55325	55340	GCGCACTGCCCTGTCG	77	N/A	N/A	422
908340	56452	56467	CAAGAGGGCCCCCTAC	110	N/A	N/A	423
908341	56855	56870	TATGAATCCCCCTCCC	99	N/A	N/A	424
908342	57413	57428	GCGCATGGACTGCGGG	150	N/A	N/A	425
908343	57695	57710	TGGAAGTACACAGGCT	40	N/A	N/A	426
908344	58949	58964	GTCTATGGCCCCGGGC	102	N/A	N/A	427
908345	59713	59728	GCATAGGCCAACGCAG	88	N/A	N/A	428
908346	60635	60650	AAACAGGCCCGCAGCC	95	N/A	N/A	429
908347	61004	61019	CCTACAGCGGCCATGG	115	N/A	N/A	430
908348	61545	61560	GTGCTAACCGTGTGTG	85	N/A	N/A	431
908349	62025	62040	GTCCAGTTGGCCCTGA	84	N/A	N/A	432
908350	62964	62979	AACCACCGAAGCTGGG	125	N/A	N/A	433
908351	63324	63339	GGAAGATGGCCGGGTG	111	N/A	N/A	434
908352	63675	63690	GCTACAATGCCTAGGA	85	N/A	N/A	435
908353	64393	64408	GGTCAACGCAGGCTCA	48	N/A	N/A	436
908354	64657	64672	AGCCAGGAGCAATCGC	78	N/A	N/A	437

908355	65114	65129	GGCAACCAAGGTCTGA	15	N/A	N/A	438
908356	65639	65654	CGCCTAGCCTGGGTTC	67	N/A	N/A	439
908357	66042	66057	CACCATCACACACGGA	44	N/A	N/A	440
908358	66433	66448	GGGAGAGGTGCCGGTC	99	N/A	N/A	441
908359	66885	66900	CACCGAGAAGGAGGTA	99	N/A	N/A	442
908360	67650	67665	AAAATCTCGGCCGGGA	101	N/A	N/A	443
908361	67903	67918	GCCAAGTGGACCTGGC	84	N/A	N/A	444
908362	68192	68207	GCCTGAAACAAGTGCC	75	N/A	N/A	445
908363	68628	68643	CCCCAGGCAATGCATA	125	N/A	N/A	446
908364	68993	69008	AGAACGATAGGCCAGG	52	N/A	N/A	447
908365	69310	69325	TCTTTTCCCGGCCCCC	48	N/A	N/A	448
908366	71364	71379	CGGCACGGAGCTGCCC	126	N/A	N/A	449
908367	71557	71572	GGTCAGTTGCTGCAGG	40	N/A	N/A	450
908368	72040	72055	GGCCGGCCAATGCTCA	118	N/A	N/A	451
908369	73315	73330	TTGCACTGGCCGGGCT	75	N/A	N/A	452
908370	73937	73952	CCCTTAGCCCACGACC	92	N/A	N/A	453
908371	74402	74417	CTGCCAGTTTGTCCCC	25	N/A	N/A	454
908372	74408	74423	TGTAATCTGCCAGTTT	53	N/A	N/A	455
908373	74410	74425	CTTGTAATCTGCCAGT	55	N/A	N/A	456
908374	74415	74430	GGCACCTTGTAATCTG	96	N/A	N/A	457
908375	74908	74923	TGTGATGGGCATCCCC	56	N/A	N/A	458
908376	75761	75776	ATACATGAGGTCCGGG	106	N/A	N/A	459
908377	76583	76598	GCCCAACCCACGCTGC	79	N/A	N/A	460
908378	77237	77252	CCCCAACTGGGAGAGG	107	N/A	N/A	461
908379	77517	77532	TAGAACGGGCCTGGCC	93	N/A	N/A	462
908380	78331	78346	TCCATAGGTTCCCGCC	89	N/A	N/A	463
908381	78849	78864	GGGCACTACCTTCACC	138	N/A	N/A	464
908382	79488	79503	TCCCACGGATTATAGG	140	N/A	N/A	465
908383	80002	80017	GCCCAGGAAGGTCGAA	105	N/A	N/A	466
908384	80333	80348	ATGCATGGAGGCACCC	93	N/A	N/A	467
908385	80626	80641	TGCAATGGACGCAGGA	37	N/A	N/A	468
908386	80968	80983	GGCCGGGTCCCCAACA	113	N/A	N/A	469
908387	81643	81658	GGCCATTCCCGGAGCT	114	N/A	N/A	470
908388	82021	82036	CCTTTTCTAATCGAAG	116	N/A	N/A	471
908389	82046	82061	ACCTGTTTGGACTGTT	5	N/A	N/A	472
908390	82049	82064	CCAACCTGTTTGGACT	74	N/A	N/A	473
908391	82051	82066	TTCCAACCTGTTTGGA	54	N/A	N/A	474
908392	82055	82070	CGTTTTCCAACCTGTT	3	N/A	N/A	475
908393	82069	82084	GGCTCTAGGACGAGCG	55	N/A	N/A	476
908394	82072	82087	CCTGGCTCTAGGACGA	41	N/A	N/A	477
908395	82083	82098	TGTCCATGACACCTGG	66	N/A	N/A	478

908396	82086	82101	TCATGTCCATGACACC	8	N/A	N/A	479
908397	82088	82103	ATTCATGTCCATGACA	25	N/A	N/A	480
908398	82704	82719	CCCCACGGGCAGCCAC	127	N/A	N/A	481
908399	83290	83305	GGGCACCGTGGACCGG	112	N/A	N/A	482
908400	83646	83661	CATATGCAGCTGTCAG	27	N/A	N/A	483
	83734	83749			N/A	N/A	
	83822	83837			N/A	N/A	
908401	83647	83662	CCATATGCAGCTGTCA	2	N/A	N/A	484
	83735	83750			N/A	N/A	
	83823	83838			N/A	N/A	
908402	83649	83664	TGCCATATGCAGCTGT	27	N/A	N/A	485
	83737	83752			N/A	N/A	
	83825	83840			N/A	N/A	
908403	83650	83665	TTGCCATATGCAGCTG	18	N/A	N/A	486
	83738	83753			N/A	N/A	
	83826	83841			N/A	N/A	
908404	83651	83666	TTTGCCATATGCAGCT	17	N/A	N/A	487
	83739	83754			N/A	N/A	
	83827	83842			N/A	N/A	
908405	83658	83673	GGGTTACTTTGCCATA	7	N/A	N/A	488
	83746	83761			N/A	N/A	
	83834	83849			N/A	N/A	
908406	83659	83674	AGGGTTACTTTGCCAT	74	N/A	N/A	489
	83747	83762			N/A	N/A	
	83835	83850			N/A	N/A	
908407	83660	83675	AAGGGTTACTTTGCCA	7	N/A	N/A	490
	83748	83763			N/A	N/A	
	83836	83851			N/A	N/A	
908408	83661	83676	TAAGGGTTACTTTGCC	2	N/A	N/A	491
	83749	83764			N/A	N/A	
	83837	83852			N/A	N/A	
908409	83662	83677	GTAAGGGTTACTTTGC	8	N/A	N/A	492
	83750	83765			N/A	N/A	
	83838	83853			N/A	N/A	
908410	83663	83678	GGTAAGGGTTACTTTG	12	N/A	N/A	493
	83751	83766			N/A	N/A	
	83839	83854			N/A	N/A	
908411	83664	83679	AGGTAAGGGTTACTTT	17	N/A	N/A	494
	83752	83767			N/A	N/A	
	83840	83855			N/A	N/A	
908412	83665	83680	GAGGTAAGGGTTACTT	12	N/A	N/A	495

	83753	83768			N/A	N/A	
	83841	83856			N/A	N/A	
908413	83666	83681	TGAGGTAAGGGTTACT	3	N/A	N/A	496
	83754	83769			N/A	N/A	
	83842	83857			N/A	N/A	
908414	83667	83682	TTGAGGTAAGGGTTAC	5	N/A	N/A	497
	83755	83770			N/A	N/A	
	83843	83858			N/A	N/A	
908415	83669	83684	AACCCTTACCTCAATC	3	N/A	N/A	498
	83757	83772			N/A	N/A	
	83845	83860			N/A	N/A	
908416	83670	83685	TGATTGAGGTAAGGGT	4	N/A	N/A	499
	83758	83773			N/A	N/A	
	83846	83861			N/A	N/A	
908417	83671	83686	TTGATTGAGGTAAGGG	2	N/A	N/A	500
	83759	83774			N/A	N/A	
	83847	83862			N/A	N/A	
908418	83672	83687	CTTGATTGAGGTAAGG	8	N/A	N/A	501
	83760	83775			N/A	N/A	
	83848	83863			N/A	N/A	
908419	83673	83688	TCTTGATTGAGGTAAG	5	N/A	N/A	502
	83761	83776			N/A	N/A	
	83849	83864			N/A	N/A	
908420	83674	83689	ATCTTGATTGAGGTAA	2	N/A	N/A	503
	83762	83777			N/A	N/A	
	83850	83865			N/A	N/A	
908421	83684	83699	ACCGCTCTGTATCTTG	3	N/A	N/A	504
	83772	83787			N/A	N/A	
	83860	83875			N/A	N/A	
908422	83685	83700	AACCGCTCTGTATCTT	3	N/A	N/A	505
	83773	83788			N/A	N/A	
	83861	83876			N/A	N/A	
908423	83686	83701	AGATACAGAGCGGTTC	28	N/A	N/A	506
	83774	83789			N/A	N/A	
	83862	83877			N/A	N/A	
908424	83687	83702	GGAACCGCTCTGTATC	8	N/A	N/A	507
	83775	83790			N/A	N/A	
	83863	83878			N/A	N/A	
908425	83688	83703	CGGAACCGCTCTGTAT	13	N/A	N/A	508
	83776	83791			N/A	N/A	
	83864	83879			N/A	N/A	

908426	83689	83704	ACGGAACCGCTCTGTA	47	N/A	N/A	509
	83777	83792			N/A	N/A	
	83865	83880			N/A	N/A	
908427	83690	83705	GACGGAACCGCTCTGT	21	N/A	N/A	510
	83778	83793			N/A	N/A	
	83866	83881			N/A	N/A	
908428	83691	83706	TGACGGAACCGCTCTG	33	N/A	N/A	511
	83779	83794			N/A	N/A	
	83867	83882			N/A	N/A	
908429	83692	83707	GTGACGGAACCGCTCT	44	N/A	N/A	512
	83780	83795			N/A	N/A	
	83868	83883			N/A	N/A	
908430	83693	83708	GGTGACGGAACCGCTC	27	N/A	N/A	513
	83781	83796			N/A	N/A	
	83869	83884			N/A	N/A	
908431	83694	83709	AGCGGTTCCGTCACCT	67	N/A	N/A	514
	83782	83797			N/A	N/A	
	83870	83885			N/A	N/A	
908432	83695	83710	GAGGTGACGGAACCGC	69	N/A	N/A	515
	83783	83798			N/A	N/A	
	83871	83886			N/A	N/A	
908433	83696	83711	GGAGGTGACGGAACCG	62	N/A	N/A	516
	83784	83799			N/A	N/A	
	83872	83887			N/A	N/A	
908434	83697	83712	AGGAGGTGACGGAACC	6	N/A	N/A	517
	83785	83800			N/A	N/A	
	83873	83888			N/A	N/A	
908435	83698	83713	TAGGAGGTGACGGAAC	16	N/A	N/A	518
	83786	83801			N/A	N/A	
	83874	83889			N/A	N/A	
908436	83699	83714	TTAGGAGGTGACGGAA	14	N/A	N/A	519
	83787	83802			N/A	N/A	
	83875	83890			N/A	N/A	
908437	83709	83724	GACAGGGATTTTAGGA	29	N/A	N/A	520
	83885	83900			N/A	N/A	
908438	83710	83725	GGACAGGGATTTTAGG	49	N/A	N/A	521
	83886	83901			N/A	N/A	
908439	83719	83734	CCTGTCCCTATCATGC	3	N/A	N/A	522
	83807	83822			N/A	N/A	
908440	83720	83735	AGCATGATAGGGACAG	4	N/A	N/A	523
	83808	83823			N/A	N/A	

908441	83721	83736	CAGCATGATAGGGACA	2	N/A	N/A	524
	83809	83824			N/A	N/A	
908442	83722	83737	TCAGCATGATAGGGAC	4	N/A	N/A	525
	83810	83825			N/A	N/A	
908443	83723	83738	GTCAGCATGATAGGGA	4	N/A	N/A	526
	83811	83826			N/A	N/A	
908444	83724	83739	TGTCAGCATGATAGGG	4	N/A	N/A	527
	83812	83827			N/A	N/A	
908445	83725	83740	CTGTCAGCATGATAGG	44	N/A	N/A	528
	83813	83828			N/A	N/A	
908446	83726	83741	GCTGTCAGCATGATAG	70	N/A	N/A	529
	83814	83829			N/A	N/A	
908447	83727	83742	TATCATGCTGACAGCT	55	N/A	N/A	530
	83815	83830			N/A	N/A	
908448	83910	83925	GAGGTTGACTACAAAG	12	N/A	N/A	531
908449	83913	83928	TGAGAGGTTGACTACA	6	N/A	N/A	532
908450	83915	83930	TTTGAGAGGTTGACTA	17	N/A	N/A	533
908451	83921	83936	TGGGTTTTTGAGAGGT	9	N/A	N/A	534
908452	84177	84192	GGCGATGGCACGACCA	71	N/A	N/A	535
908453	84938	84953	GTATAAGGACGGCCCA	45	N/A	N/A	536
908454	85500	85515	TCAGATCCGGCCTGGC	191	N/A	N/A	537
908455	86165	86180	GTGGTGTGGCGTGCGC	75	N/A	N/A	538
908456	86583	86598	GAACTTACTGTCTCCC	14	N/A	N/A	539
908457	87056	87071	AGGCAGGGCCGCTGTC	100	N/A	N/A	540
908458	87386	87401	AGGATTGGTGCCGCCC	36	N/A	N/A	541
908459	87906	87921	AATCAGCGGGTGATGC	118	N/A	N/A	542
908460	88179	88194	GCCCAGTGGCCGCCCT	70	N/A	N/A	543
908461	88831	88846	CTACAGCTGGTGCGGT	40	N/A	N/A	544
908462	89400	89415	CGCCAGGCTTGGGCCC	100	N/A	N/A	545
908463	89711	89726	GCCCAGATAAGAAGCC	38	N/A	N/A	546
908464	90096	90111	GGCTAGTTCATGCCGG	63	N/A	N/A	547
908465	90743	90758	ACGGCCTGGGCACACG	52	N/A	N/A	548
908466	90747	90762	GGAAACGGCCTGGGCA	64	N/A	N/A	549
908467	90750	90765	AAGGGAAACGGCCTGG	76	N/A	N/A	550
908468	90753	90768	CGCAAGGGAAACGGCC	108	N/A	N/A	551
908469	90755	90770	TGCGCAAGGGAAACGG	87	N/A	N/A	552
908470	90757	90772	GCTGCGCAAGGGAAAC	124	N/A	N/A	553
908471	90761	90776	CCCTTGCGCAGCTCTG	18	N/A	N/A	554
908472	90765	90780	CACACAGAGCTGCGCA	57	N/A	N/A	555
908473	90778	90793	GAAGCCCCCTGCACAC	37	N/A	N/A	556
908474	90781	90796	AGAGAAGCCCCCTGCA	72	N/A	N/A	557

908475	90809	90824	CCAAGTGAGCAGCCAC	9	N/A	N/A	558
908476	90811	90826	GACCAAGTGAGCAGCC	27	N/A	N/A	559
908477	90813	90828	GGGACCAAGTGAGCAG	63	N/A	N/A	560
908478	91157	91172	CACTAGGCCCTGCCAG	128	N/A	N/A	561
908479	91836	91851	GAGCGGGGGTCTGTGA	58	N/A	N/A	562
908480	92802	92817	CAGCACTTTGTCCGGG	82	N/A	N/A	563
908481	93315	93330	ACCTACGGCAAGCGCA	31	N/A	N/A	564
908482	93568	93583	TACCAGGATCTCCCCC	19	N/A	N/A	565
908483	94077	94092	GCTAGAGGAGCGGCAC	74	N/A	N/A	566
908484	94531	94546	GCCCATCTCACGCCCC	71	N/A	N/A	567
908485	95058	95073	CCAGAGGCCACGGCCA	94	N/A	N/A	568
908486	95635	95650	CCGCACACCCCTCGGT	111	N/A	N/A	569
908487	96522	96537	CAGGCCGCCCTGTGCG	93	N/A	N/A	570
908488	97096	97111	CCCAAGCATTTCCAGC	37	N/A	N/A	571
908489	97109	97124	AGTTCCACCCTGTCCC	23	N/A	N/A	572
908490	97144	97159	TAGAGACACCTCCAGC	47	N/A	N/A	573
908491	97147	97162	CAATAGAGACACCTCC	44	N/A	N/A	574
908492	97150	97165	CCGCAATAGAGACACC	43	N/A	N/A	575
908493	97152	97167	GACCGCAATAGAGACA	64	N/A	N/A	576
908494	97154	97169	GGGACCGCAATAGAGA	94	N/A	N/A	577
908495	97157	97172	CTATTGCGGTCCCTGG	31	N/A	N/A	578
908496	97159	97174	AGCCAGGGACCGCAAT	85	N/A	N/A	579
908497	97426	97441	GCCCACCCGCTCTTCC	80	N/A	N/A	580
908498	98041	98056	TGGAACCCCGGTGCCC	119	N/A	N/A	581
908499	98971	98986	CTTCACCGTTTGGCCA	45	N/A	N/A	582
908500	100149	100164	CGCGGAGCCAGGCCCT	114	N/A	N/A	583
908501	101337	101352	CCCCAGAGTCCCGCAG	72	N/A	N/A	584
908502	101845	101860	ACACGAAGGGCCCCTC	52	N/A	N/A	585
908503	102223	102238	GCAGACTGATAGGGCC	103	N/A	N/A	586
908504	102495	102510	GGATAGCCGGCCCCGC	102	N/A	N/A	587
908505	102955	102970	CGCGGCCGGAAGCTTC	93	N/A	N/A	588
908506	103211	103226	CAGAGCATAGGAGAGG	7	N/A	N/A	589
	103249	103264			N/A	N/A	
908507	103213	103228	AGCAGAGCATAGGAGA	12	N/A	N/A	590
	103251	103266			N/A	N/A	
908508	103216	103231	GGGAGCAGAGCATAGG	16	N/A	N/A	591
	103254	103269			N/A	N/A	
908509	104082	104097	GCCAGCCACGGCTGTC	81	N/A	N/A	592
908510	104495	104510	GCTGACGGCACGCACA	65	N/A	N/A	593
908511	105108	105123	TGGGGATGGCTCGGGG	79	N/A	N/A	594
908512	105526	105541	CACCAGGGCTCCGCCT	107	N/A	N/A	595

908513	106268	106283	GGCACACGGCTCAGGG	93	N/A	N/A	596
908514	106974	106989	CAGCAAGTGGCTGCCC	107	N/A	N/A	597
908515	107645	107660	TGGGAGTGGTACTGCA	70	N/A	N/A	598
908516	108733	108748	TGCCATGGGTCTGGCA	86	N/A	N/A	599
908517	108893	108908	GCTCCTCACCTGGTCC	92	N/A	N/A	600
908518	108899	108914	AGGACGGCTCCTCACC	111	N/A	N/A	601
908519	108902	108917	GAGGAGCCGTCCTGCG	85	N/A	N/A	602
908520	108906	108921	GCTGCGCAGGACGGCT	104	N/A	N/A	603
908521	109226	109241	GGGCGAACCACCCACC	78	N/A	N/A	604
908522	109577	109592	GCCCAAAGGATCTGCC	88	N/A	N/A	605
908523	109968	109983	CCCTATTGTCCCACCA	43	N/A	N/A	606
908524	110612	110627	GTGCACTCTAGGCTTA	100	N/A	N/A	607
908525	111378	111393	GGACACAGCGGCTGCC	78	N/A	N/A	608
908526	111925	111940	CCGCAGGTTTCTGTGG	122	N/A	N/A	609
908527	112198	112213	ACCGATAGGATCGGAG	95	N/A	N/A	610
908528	112578	112593	GGCCGTCACAACTTTT	116	N/A	N/A	611
908529	112910	112925	CTGGAACCTCCTACTG	87	N/A	N/A	612
908530	114292	114307	GGCCGAATGCTTGAGG	97	N/A	N/A	613
908531	114921	114936	TCACAGGGCCCCCTCA	68	N/A	N/A	614
908532	115371	115386	GGCCTTACCTGGGCAC	101	N/A	N/A	615
908533	115837	115852	CCGCAAGCCACCAGGG	87	N/A	N/A	616

*Oligos with an asterisk target an amplicon region.

Each modified oligonucleotide listed in the table below is 100% complementary to human DNM2 nucleic acid sequence GENBANK Number NM_001005361.2 (designated herein as SEQ ID NO: 3). "Start Site" indicates the 5'-most nucleoside of SEQ ID No: 3 to which the oligonucleotide is complementary. "Stop Site" indicates the 3'-most nucleoside of SEQ ID No: 3 to which the oligonucleotide is complementary. 'N/A' indicates that the modified oligonucleotide is not 100% complementary to the particular nucleic acid. As shown below, modified oligonucleotides complementary to DNM2 reduced human DNM2 mRNA expression.

Table 2: DNM2 mRNA Expression

Compound Number	SEQ ID: 3 Start Site	SEQ ID: 3 Stop Site	Sequence	Dynamin2 (%Control)	SEQ ID NO
695118	1728	1743	ATCTCCCCCTGATTGG	60	617
908218	1732	1747	CAGGATCTCCCCCTGA	114	618
908219	1379	1394	GCCCCGTCCTGACTCC	61	619
908220	1381	1396	GAGCCCCGTCCTGACT	92	620
908233	1515	1530	CTGAGCTTCTCGGCAC	70	621

908234	1517	1532	AACTGAGCTTCTCGGC	85	622
908235	1519	1534	GGAACTGAGCTTCTCG	33	623

Example 2: Effect of modified oligonucleotides complementary to dynamin 2 *in vitro*

Modified oligonucleotides complementary to dynamin 2 (DNM2) nucleic acid were designed and tested for their effect on dynamin 2 mRNA *in vitro*. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions.

A431 cells cultured at a density of 10,000 cells per well were treated with 2,000 nM of modified oligonucleotide via free uptake or no oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and DNM2 mRNA levels were measured by quantitative real-time PCR as described in Example 1.

The modified oligonucleotides in the tables below each have a 3-10-3 cEt gapmer motif, wherein the central gap segment contains ten 2'-deoxynucleosides and is flanked by wing segments on the 3' and 5' ends, each containing three cEt nucleosides. All cytosine residues throughout each modified oligonucletoide are 5-methyl cytosines. All internucleoside linkages are phosphorothioate internucleoside linkages.

Each modified oligonucleotide listed in the tables below is 100% complementary to human DNM2 nucleic acid sequence GENBANK Number NC_000019.10, truncated from 10715001 to 1083500 (SEQ ID NO: 1) and/or GENBANK Number NM_004945.3 (SEQ ID NO: 2). As shown below, modified oligonucleotides complementary to human DNM2 inhibited human DNM2 mRNA expression.

Table 3: DNM2 mRNA Expression

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	Sequence	Dynamin2 (%Control)	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	SEQ ID NO
694792	3060	3075	CGACACCCGACCCGAG	26	N/A	N/A	624
694812	3317	3332	GTCCAGGTGGCAGCTC	37	265	280	625
694826	57522	57537	CCGGACTTCATCAAAG	82	469	484	626
694999	115263	115278	GTCCAGGCCGGGATGG	92	2606	N/A	627
695015	116005	116020	GCGGATAATGGTGGGC	12	2749	N/A	628
695016	116011	116026	GGCTGGGCGGATAATG	76	2755	N/A	629
695170	82446	82461	CTTCAAACTCGGCTCT	9	N/A	N/A	630
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	12	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	11	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	121	N/A	N/A	13

695171	82451	82466	ACACACTTCAAACTCG	14	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	31	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	10	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	12	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	11	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	11	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	5	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	12	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	120	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	6	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	8	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	10	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	9	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	10	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	7	N/A	N/A	13
948484	82379	82394	GTGAAGAGCCCCGTCC	42	N/A	N/A	631
948485	82380	82395	GGTGAAGAGCCCCGTC	103	N/A	N/A	632
948486	82443	82458	CAAACTCGGCTCTTTG	99	N/A	N/A	633
948487	82444	82459	TCAAACTCGGCTCTTT	15	N/A	N/A	634
948488	82445	82460	TTCAAACTCGGCTCTT	5	N/A	N/A	635
948489	82448	82463	CACTTCAAACTCGGCT	3	N/A	N/A	636
948490	82449	82464	ACACTTCAAACTCGGC	1	N/A	N/A	637
948491	82450	82465	CACACTTCAAACTCGG	25	N/A	N/A	638
948492	82452	82467	AACACACTTCAAACTC	11	N/A	N/A	639
948493	82453	82468	CAACACACTTCAAACT	51	N/A	N/A	640
948494	82454	82469	TCAACACACTTCAAAC	30	N/A	N/A	641
948495	82458	82473	GAGATCAACACACTTC	19	N/A	N/A	642
948496	82460	82475	ACGAGATCAACACACT	5	N/A	N/A	643
948497	82461	82476	CACGAGATCAACACAC	28	N/A	N/A	644
948498	82463	82478	ACCACGAGATCAACAC	50	N/A	N/A	645
948499	82467	82482	TGAGACCACGAGATCA	55	N/A	N/A	646
948500	82469	82484	TCTGAGACCACGAGAT	107	N/A	N/A	647
948501	82470	82485	CTCTGAGACCACGAGA	119	N/A	N/A	648

948502	82490	82505	TTTTTTATGACCGTGG	18	N/A	N/A	649
948503	82496	82511	GCACACTTTTTTATGA	17	N/A	N/A	650
948504	82497	82512	GGCACACTTTTTTATG	54	N/A	N/A	651
948505	82499	82514	TCGGCACACTTTTTTA	10	N/A	N/A	652
948506	82500	82515	CTCGGCACACTTTTTT	3	N/A	N/A	653
948507	82501	82516	TCTCGGCACACTTTTT	3	N/A	N/A	654
948508	82503	82518	CTTCTCGGCACACTTT	3	N/A	N/A	655
948514	3056	3071	ACCCGACCCGAGCGAC	81	4	19	656
948515	3067	3082	TCTCAGGCGACACCCG	88	15	30	657
948516	3092	3107	CCTCACGGTCGCCGCC	56	40	55	658
948517	3094	3109	GGCCTCACGGTCGCCG	98	42	57	659
948518	3103	3118	TCCCGGCTCGGCCTCA	48	51	66	660
948519	3139	3154	GCTCCCCGCCCGCCCG	71	87	102	661
948520	3141	3156	TTGCTCCCCGCCCGCC	23	89	104	662
948521	3142	3157	GTTGCTCCCCGCCCGC	10	90	105	663
948522	3143	3158	CGTTGCTCCCCGCCCG	50	91	106	664
948523	3145	3160	GCCGTTGCTCCCCGCC	53	93	108	665
948524	3147	3162	TAGCCGTTGCTCCCCG	17	95	110	666
948525	3148	3163	GTAGCCGTTGCTCCCC	14	96	111	667
948526	3150	3165	CTGTAGCCGTTGCTCC	10	98	113	668
948527	3151	3166	TCTGTAGCCGTTGCTC	9	99	114	669
948528	3152	3167	GTCTGTAGCCGTTGCT	13	100	115	670
948529	3168	3183	GACCTGGCCCCGCGGC	76	116	131	671
948530	3169	3184	CGACCTGGCCCCGCGG	83	117	132	672
948531	3170	3185	ACGACCTGGCCCCGCG	36	118	133	673
948532	3172	3187	CAACGACCTGGCCCCG	17	120	135	674
948533	3173	3188	TCAACGACCTGGCCCC	20	121	136	675
948534	3174	3189	CTCAACGACCTGGCCC	30	122	137	676
948535	3175	3190	CCTCAACGACCTGGCC	101	123	138	677
948536	3176	3191	CCCTCAACGACCTGGC	57	124	139	678
948537	3278	3293	CTGCAGTTTGTTGACC	45	226	241	679
948538	3299	3314	GCCGATGGAGCTGAAG	7	247	262	680
948539	3300	3315	GGCCGATGGAGCTGAA	104	248	263	681
948540	N/A	N/A	AAGGAAGTCCCGGCCC	81	346	361	682
948541	N/A	N/A	GAAGGAAGTCCCGGCC	101	347	362	683
948542	44750	44765	GATTCCTGAACCGCGG	106	364	379	684
948543	44752	44767	ACGATTCCTGAACCGC	38	366	381	685
948544	44754	44769	TGACGATTCCTGAACC	18	368	383	686
948545	44755	44770	GTGACGATTCCTGAAC	40	369	384	687
948546	44756	44771	GGTGACGATTCCTGAA	42	370	385	688
948547	44758	44773	CGGGTGACGATTCCTG	111	372	387	689
948548	44761	44776	CGCCGGGTGACGATTC	44	375	390	690
948549	44769	44784	TGAGAGGCCGCCGGGT	11	383	398	691

948550	44771	44786	AATGAGAGGCCGCCGG	76	385	400	692
948551	44772	44787	GAATGAGAGGCCGCCG	67	386	401	693
948552	44775	44790	GCAGAATGAGAGGCCG	99	389	404	694
948553	57480	57495	CAAAAACTCGGCATGT	20	427	442	695
948554	57481	57496	GCAAAAACTCGGCATG	15	428	443	696
948555	57490	57505	ACTTGCAGTGCAAAAA	15	437	452	697
948556	57492	57507	GGACTTGCAGTGCAAA	7	439	454	698
948557	57494	57509	TTGGACTTGCAGTGCA	3	441	456	699
948558	57497	57512	TTTTTGGACTTGCAGT	10	444	459	700
948559	57498	57513	CTTTTTGGACTTGCAG	6	445	460	701
948560	57500	57515	AACTTTTTGGACTTGC	3	447	462	702
948561	57501	57516	AAACTTTTTGGACTTG	92	448	463	703
948562	57502	57517	TAAACTTTTTGGACTT	8	449	464	704
948563	57503	57518	GTAAACTTTTTGGACT	26	450	465	705
948564	57504	57519	TGTAAACTTTTTGGAC	15	451	466	706
948565	57524	57539	TGCCGGACTTCATCAA	31	471	486	707
948566	57525	57540	CTGCCGGACTTCATCA	24	472	487	708
948567	57527	57542	TCCTGCCGGACTTCAT	26	474	489	709
948568	57530	57545	ATCTCCTGCCGGACTT	14	477	492	710
948569	57531	57546	AATCTCCTGCCGGACT	18	478	493	711
948570	57535	57550	CTTCAATCTCCTGCCG	29	482	497	712
948571	57597	57612	TCGAAGGTTGATGGGC	89	544	559	713
948572	57598	57613	CTCGAAGGTTGATGGG	88	545	560	714
948573	57599	57614	ACTCGAAGGTTGATGG	75	546	561	715
948574	60706	60721	ATGAGGGTCAAGTTCA	52	579	594	716
948575	60708	60723	CGATGAGGGTCAAGTT	15	581	596	717
948576	60709	60724	TCGATGAGGGTCAAGT	28	582	597	718
948577	60710	60725	GTCGATGAGGGTCAAG	22	583	598	719
948578	60712	60727	AGGTCGATGAGGGTCA	15	585	600	720
948579	60714	60729	GGAGGTCGATGAGGGT	53	587	602	721
948580	60717	60732	CCGGGAGGTCGATGAG	93	590	605	722
948581	60721	60736	ATACCCGGGAGGTCGA	32	594	609	723
948582	60723	60738	TGATACCCGGGAGGTC	34	596	611	724
948583	60725	60740	GGTGATACCCGGGAGG	32	598	613	725
948584	60726	60741	TGGTGATACCCGGGAG	79	599	614	726
948585	60727	60742	TTGGTGATACCCGGGA	27	600	615	727
948586	60729	60744	CCTTGGTGATACCCGG	44	602	617	728
948587	60774	60789	CCTTGATCTGGTACTC	6	647	662	729
948588	60775	60790	TCCTTGATCTGGTACT	20	648	663	730
948589	60777	60792	TGTCCTTGATCTGGTA	12	650	665	731
948590	60779	60794	CATGTCCTTGATCTGG	13	652	667	732
948591	60781	60796	ATCATGTCCTTGATCT	34	654	669	733
948592	60782	60797	GATCATGTCCTTGATC	57	655	670	734

948593	60783	60798	GGATCATGTCCTTGAT	38	656	671	735
948594	60815	60830	AATGAGGCTGCTCTCC	42	688	703	736
948595	60820	60835	GCCAGAATGAGGCTGC	92	693	708	737
948596	60848	60863	GGCCAGGTCCATGTTG	92	721	736	738
948597	N/A	N/A	GGTCCGTAGGCCTTGG	45	775	790	739
948598	62120	62135	CACCGATGGTCCGTAG	49	782	797	740
948599	62192	62207	ACGGGAGCAACTTGTT	76	854	869	741
948600	62196	62211	CTCAACGGGAGCAACT	48	858	873	742
948601	62197	62212	TCTCAACGGGAGCAAC	45	859	874	743
948602	68004	68019	CACGGATGTCCTTCTT	8	923	938	744
948603	68006	68021	TGCACGGATGTCCTTC	25	925	940	745
948604	68007	68022	CTGCACGGATGTCCTT	5	926	941	746
948605	68009	68024	TGCTGCACGGATGTCC	16	928	943	747
948606	68010	68025	GTGCTGCACGGATGTC	20	929	944	748
948607	68011	68026	AGTGCTGCACGGATGT	22	930	945	749
948608	68012	68027	CAGTGCTGCACGGATG	8	931	946	750
948609	68014	68029	GCCAGTGCTGCACGGA	37	933	948	751
948610	68015	68030	TGCCAGTGCTGCACGG	50	934	949	752
948611	68016	68031	CTGCCAGTGCTGCACG	27	935	950	753
948612	68018	68033	AGCTGCCAGTGCTGCA	107	937	952	754
948613	68056	68071	TGCCGGTAGGCCGGGT	122	975	990	755
948614	71653	71668	CCGAAAGTTCTTGTAC	31	1129	1144	756
948615	71656	71671	GGGCCGAAAGTTCTTG	88	1132	1147	757
948616	71657	71672	CGGGCCGAAAGTTCTT	75	1133	1148	758
948617	71658	71673	TCGGGCCGAAAGTTCT	42	1134	1149	759
948618	71660	71675	CGTCGGGCCGAAAGTT	20	1136	1151	760
948619	71683	71698	GGCTTTGGTTTTGCGG	80	1159	1174	761
948620	78729	78744	ATCCACCCCAAACTGC	45	1192	1207	762
948621	78771	78786	AGTGTCCACCTGATCT	27	1234	1249	763
948622	78773	78788	AGAGTGTCCACCTGAT	11	1236	1251	764
948623	78774	78789	CAGAGTGTCCACCTGA	88	1237	1252	765
948624	78775	78790	CCAGAGTGTCCACCTG	74	1238	1253	766
948625	78777	78792	CTCCAGAGTGTCCACC	51	1240	1255	767
948626	78785	78800	CCGGAGAGCTCCAGAG	98	1248	1263	768
948627	78787	78802	CCCCGGAGAGCTCCAG	44	1250	1265	769
948628	78805	78820	TGCGATTGATTCGGGC	11	1268	1283	770
948629	78806	78821	ATGCGATTGATTCGGG	3	1269	1284	771
948630	78810	78825	GAAGATGCGATTGATT	10	1273	1288	772
948631	78811	78826	GGAAGATGCGATTGAT	3	1274	1289	773
948632	78812	78827	TGGAAGATGCGATTGA	9	1275	1290	774
948633	78813	78828	GTGGAAGATGCGATTG	8	1276	1291	775
948634	78829	78844	CAAATGGGAACCGCTC	60	1292	1307	776
948635	78830	78845	TCAAATGGGAACCGCT	65	1293	1308	777

948636	78831	78846	CTCAAATGGGAACCGC	81	1294	1309	778
948637	78832	78847	GCTCAAATGGGAACCG	58	1295	1310	779
948638	78833	78848	AGCTCAAATGGGAACC	43	1296	1311	780
948639	78837	78852	CACCAGCTCAAATGGG	70	1300	1315	781
948640	80420	80435	CTCCATGGATGTTCTT	42	1367	1382	782
948641	81059	81074	TGAAAAGCCCGGTCCT	38	1385	1400	783
948642	81060	81075	GTGAAAAGCCCGGTCC	37	1386	1401	784
948643	81062	81077	GGGTGAAAAGCCCGGT	120	1388	1403	785
948644	81077	81092	CGAATGCCAAGTCCGG	84	1403	1418	786
948645	81078	81093	TCGAATGCCAAGTCCG	28	1404	1419	787
948646	81080	81095	CCTCGAATGCCAAGTC	13	1406	1421	788
948647	81081	81096	GCCTCGAATGCCAAGT	73	1407	1422	789
948648	81084	81099	ATGGCCTCGAATGCCA	94	1410	1425	790
948649	81088	81103	CACAATGGCCTCGAAT	35	1414	1429	791
948650	81104	81119	TGACGACCTGCTTTTT	15	1430	1445	792
948651	81105	81120	TTGACGACCTGCTTTT	21	1431	1446	793
948652	81108	81123	AGCTTGACGACCTGCT	84	1434	1449	794
948653	81110	81125	TCAGCTTGACGACCTG	61	1436	1451	795
948654	81112	81127	TTTCAGCTTGACGACC	11	1438	1453	796
948655	81114	81129	TCTTTCAGCTTGACGA	27	1440	1455	797
948656	81116	81131	GCTCTTTCAGCTTGAC	3	1442	1457	798
948657	81117	81132	GGCTCTTTCAGCTTGA	59	1443	1458	799
948658	81118	81133	GGGCTCTTTCAGCTTG	73	1444	1459	800
948659	81120	81135	CAGGGCTCTTTCAGCT	75	1446	1461	801
948660	81132	81147	ACACATTTCAGACAGG	3	1458	1473	802
948661	81134	81149	CGACACATTTCAGACA	7	1460	1475	803
948662	81135	81150	TCGACACATTTCAGAC	10	1461	1476	804
948663	81136	81151	GTCGACACATTTCAGA	51	1462	1477	805
948664	81138	81153	AGGTCGACACATTTCA	3	1464	1479	806
948665	81140	81155	CCAGGTCGACACATTT	6	1466	1481	807
948666	81141	81156	ACCAGGTCGACACATT	8	1467	1482	808
948667	81142	81157	AACCAGGTCGACACAT	34	1468	1483	809
948668	81146	81161	GGATAACCAGGTCGAC	34	1472	1487	810
948669	81148	81163	CTGGATAACCAGGTCG	43	1474	1489	811
948670	81149	81164	CCTGGATAACCAGGTC	111	1475	1490	812
948671	81150	81165	TCCTGGATAACCAGGT	100	1476	1491	813
948672	81152	81167	GCTCCTGGATAACCAG	51	1478	1493	814
948673	81159	81174	TTGATTAGCTCCTGGA	2	1485	1500	815
948674	81161	81176	TATTGATTAGCTCCTG	8	1487	1502	816
948675	81162	81177	GTATTGATTAGCTCCT	2	1488	1503	817
948676	81163	81178	TGTATTGATTAGCTCC	1	1489	1504	818
948677	81164	81179	CTGTATTGATTAGCTC	2	1490	1505	819
948678	81165	81180	ACTGTATTGATTAGCT	7	1491	1506	820

948679	81168	81183	CTAACTGTATTGATTA	56	1494	1509	821
948680	81169	81184	CCTAACTGTATTGATT	44	1495	1510	822
948681	81171	81186	TGCCTAACTGTATTGA	25	1497	1512	823
948682	81177	81192	GTACACTGCCTAACTG	23	1503	1518	824
948683	81180	81195	CTGGTACACTGCCTAA	14	1506	1521	825
948684	81181	81196	ACTGGTACACTGCCTA	8	1507	1522	826
948685	81183	81198	TTACTGGTACACTGCC	2	1509	1524	827
948686	81184	81199	CTTACTGGTACACTGC	1	1510	1525	828
948687	N/A	N/A	GCTTACTGGTACACTG	6	1511	1526	829
948688	N/A	N/A	AGCTTACTGGTACACT	26	1512	1527	830
948689	N/A	N/A	GAGCTTACTGGTACAC	12	1513	1528	831
948690	N/A	N/A	ACTGAGCTTACTGGTA	47	1516	1531	832
948691	N/A	N/A	AACTGAGCTTACTGGT	24	1517	1532	833
948692	N/A	N/A	GGAACTGAGCTTACTG	10	1519	1534	834
948693	N/A	N/A	AGGAACTGAGCTTACT	12	1520	1535	835
948694	N/A	N/A	TAGGAACTGAGCTTAC	17	1521	1536	836
948695	N/A	N/A	GTAGGAACTGAGCTTA	15	1522	1537	837
948696	83484	83499	GGGTAGGAACTGAGCT	28	1524	1539	838
948697	83500	83515	CTCCTCTCGCAACCGG	56	1540	1555	839
948698	83503	83518	TGTCTCCTCTCGCAAC	44	1543	1558	840
948699	83504	83519	CTGTCTCCTCTCGCAA	27	1544	1559	841
948700	83506	83521	CTCTGTCTCCTCTCGC	5	1546	1561	842
948701	83507	83522	GCTCTGTCTCCTCTCG	8	1547	1562	843
948702	83508	83523	CGCTCTGTCTCCTCTC	5	1548	1563	844
948703	83510	83525	TTCGCTCTGTCTCCTC	5	1550	1565	845
948704	83514	83529	ACGATTCGCTCTGTCT	69	1554	1569	846
948705	83515	83530	GACGATTCGCTCTGTC	91	1555	1570	847
948706	83516	83531	TGACGATTCGCTCTGT	37	1556	1571	848
948707	83521	83536	AGTGGTGACGATTCGC	5	1561	1576	849
948708	83523	83538	TAAGTGGTGACGATTC	25	1563	1578	850
948709	83525	83540	TGTAAGTGGTGACGAT	21	1565	1580	851
948710	83526	83541	ATGTAAGTGGTGACGA	27	1566	1581	852
948711	83527	83542	GATGTAAGTGGTGACG	37	1567	1582	853
948712	83530	83545	CCGGATGTAAGTGGTG	60	1570	1585	854
948713	83543	83558	TCCCCTCCCGTTCCCG	40	1583	1598	855
948714	83545	83560	TCTCCCCTCCCGTTCC	30	1585	1600	856
948715	83546	83561	TTCTCCCCTCCCGTTC	43	1586	1601	857
948716	83547	83562	GTTCTCCCCTCCCGTT	14	1587	1602	858
948717	N/A	N/A	GCAGAAGAATCTGGTC	27	1607	1622	859
948718	87287	87302	GATCAGCAGAAGAATC	126	1612	1627	860
948719	87289	87304	TCGATCAGCAGAAGAA	70	1614	1629	861
948720	87291	87306	TGTCGATCAGCAGAAG	27	1616	1631	862
948721	87292	87307	ATGTCGATCAGCAGAA	51	1617	1632	863

948722	87293	87308	AATGTCGATCAGCAGA	41	1618	1633	864
948723	87295	87310	TCAATGTCGATCAGCA	17	1620	1635	865
948724	87297	87312	GCTCAATGTCGATCAG	14	1622	1637	866
948725	87298	87313	TGCTCAATGTCGATCA	41	1623	1638	867
948726	87301	87316	GACTGCTCAATGTCGA	91	1626	1641	868
948727	87303	87318	AGGACTGCTCAATGTC	28	1628	1643	869
948728	87305	87320	GTAGGACTGCTCAATG	136	1630	1645	870
948729	87306	87321	TGTAGGACTGCTCAAT	2	1631	1646	871
948730	87307	87322	ATGTAGGACTGCTCAA	18	1632	1647	872
948731	87309	87324	TGATGTAGGACTGCTC	6	1634	1649	873
948732	87310	87325	TTGATGTAGGACTGCT	13	1635	1650	874
948733	87312	87327	TGTTGATGTAGGACTG	39	1637	1652	875
948734	87313	87328	GTGTTGATGTAGGACT	22	1638	1653	876
948735	87314	87329	CGTGTTGATGTAGGAC	3	1639	1654	877
948736	N/A	N/A	GGCATTGGCAAACCCG	106	1672	1687	878
948737	97293	97308	CATCAGGCTGATGTTG	43	1765	1780	879
948738	97296	97311	TTTCATCAGGCTGATG	90	1768	1783	880
948739	97340	97355	AGTGACTCGGCAGTCA	100	1812	1827	881
948740	97342	97357	ACAGTGACTCGGCAGT	25	1814	1829	882
948741	97343	97358	GACAGTGACTCGGCAG	13	1815	1830	883
948742	97344	97359	GGACAGTGACTCGGCA	33	1816	1831	884
948743	97346	97361	CAGGACAGTGACTCGG	23	1818	1833	885
948744	97347	97362	CCAGGACAGTGACTCG	36	1819	1834	886
948745	97348	97363	ACCAGGACAGTGACTC	23	1820	1835	887
948746	97349	97364	TACCAGGACAGTGACT	93	1821	1836	888
948747	105014	105029	TCACGGATCTTGAGGT	27	1884	1899	889
948748	105016	105031	CATCACGGATCTTGAG	52	1886	1901	890
948749	105017	105032	ACATCACGGATCTTGA	43	1887	1902	891
948750	105018	105033	CACATCACGGATCTTG	19	1888	1903	892
948751	105021	105036	CTCCACATCACGGATC	60	1891	1906	893
948752	105024	105039	CTTCTCCACATCACGG	4	1894	1909	894
948753	105061	105076	TGAAGATGGCGAAGAC	52	1931	1946	895
948754	105062	105077	TTGAAGATGGCGAAGA	101	1932	1947	896
948755	105063	105078	GTTGAAGATGGCGAAG	83	1933	1948	897
948756	108794	108809	CCGCAGGTCCTTGTAG	60	1966	1981	898
948757	108796	108811	TGCCGCAGGTCCTTGT	42	1968	1983	899
948758	108809	108824	GGCCAGCTCGATCTGC	85	1981	1996	900
948759	108855	108870	GGAGGAACGAGGCCTT	80	2027	2042	901
948760	108856	108871	CGGAGGAACGAGGCCT	107	2028	2043	902
948761	108858	108873	CTCGGAGGAACGAGGC	111	2030	2045	903
948762	108864	108879	CGCCAGCTCGGAGGAA	125	2036	2051	904
948763	110079	110094	GAGAAGGTGTTCTCCT	98	2094	2109	905
948764	110082	110097	ATGGAGAAGGTGTTCT	112	2097	2112	906

948765	110158	110173	GGACTTGTTGATGATG	9	2173	2188	907
948766	110159	110174	TGGACTTGTTGATGAT	10	2174	2189	908
948767	110161	110176	GATGGACTTGTTGATG	12	2176	2191	909
948768	110162	110177	GGATGGACTTGTTGAT	8	2177	2192	910
948769	110163	110178	CGGATGGACTTGTTGA	10	2178	2193	911
948770	110164	110179	GCGGATGGACTTGTTG	36	2179	2194	912
948771	110165	110180	CGCGGATGGACTTGTT	78	2180	2195	913
948772	110173	110188	CATGAGGTCGCGGATG	25	2188	2203	914
948773	110174	110189	GCATGAGGTCGCGGAT	4	2189	2204	915
948774	110176	110191	TGGCATGAGGTCGCGG	9	2191	2206	916
948775	114037	114052	TGGATGAAGGCCTTCG	6	2238	2253	917
948776	114065	114080	GGAGTATAGGTAGGCC	15	2266	2281	918
948777	114067	114082	GAGGAGTATAGGTAGG	7	2268	2283	919
948778	114070	114085	GCCGAGGAGTATAGGT	51	2271	2286	920
948779	114071	114086	TGCCGAGGAGTATAGG	17	2272	2287	921
948780	114152	114167	CTTGAGGGCATGGTAC	48	2353	2368	922
948781	114225	114240	TGTCATCGACAGGCGG	32	2426	2441	923
948782	115139	115154	GGACACCGGTCGGCGC	103	2482	2497	924
948783	115140	115155	TGGACACCGGTCGGCG	43	2483	2498	925
948784	115145	115160	TATGCTGGACACCGGT	33	2488	2503	926
948785	115147	115162	TGTATGCTGGACACCG	22	2490	2505	927
948786	115148	115163	GTGTATGCTGGACACC	78	2491	2506	928
948787	115149	115164	GGTGTATGCTGGACAC	79	2492	2507	929
948788	115212	115227	CGGGAACAGGAATCAG	13	2555	2570	930
948789	115213	115228	ACGGGAACAGGAATCA	19	2556	2571	931
948790	115217	115232	CCCCACGGGAACAGGA	101	2560	2575	932
948791	115235	115250	CGAGAAGGAGGCTGCT	45	2578	2593	933
948792	115236	115251	CCGAGAAGGAGGCTGC	37	2579	2594	934
948793	115237	115252	GCCGAGAAGGAGGCTG	124	2580	2595	935
948794	115279	115294	GCAAACACGCTCTGGG	6	2622	2637	936
948795	115280	115295	GGCAAACACGCTCTGG	11	2623	2638	937
948796	115281	115296	TGGCAAACACGCTCTG	31	2624	2639	938
948797	115282	115297	TTGGCAAACACGCTCT	23	2625	2640	939
948798	115284	115299	TGTTGGCAAACACGCT	15	2627	2642	940
948799	115286	115301	ACTGTTGGCAAACACG	66	2629	2644	941
948800	115287	115302	CACTGTTGGCAAACAC	39	2630	2645	942
948801	115288	115303	TCACTGTTGGCAAACA	28	2631	2646	943
948802	115289	115304	GTCACTGTTGGCAAAC	17	2632	2647	944
948803	115290	115305	GGTCACTGTTGGCAAA	16	2633	2648	945
948804	115291	115306	AGGTCACTGTTGGCAA	9	2634	2649	946
948805	115293	115308	AGAGGTCACTGTTGGC	3	2636	2651	947
948806	115294	115309	AAGAGGTCACTGTTGG	7	2637	2652	948
948807	115295	115310	GAAGAGGTCACTGTTG	19	2638	2653	949

948808	115297	115312	GGGAAGAGGTCACTGT	13	2640	2655	950
948809	115321	115336	CGAGATGGGATCTGAG	33	2664	2679	951
948810	115322	115337	CCGAGATGGGATCTGA	18	2665	2680	952
948811	115323	115338	GCCGAGATGGGATCTG	28	2666	2681	953
948812	115327	115342	ACTGGCCGAGATGGGA	13	2670	2685	954
948813	115328	115343	AACTGGCCGAGATGGG	20	2671	2686	955
948814	115330	115345	CGAACTGGCCGAGATG	27	2673	2688	956
948815	115331	115346	CCGAACTGGCCGAGAT	46	2674	2689	957
948816	115333	115348	ATCCGAACTGGCCGAG	35	2676	2691	958
948817	115334	115349	GATCCGAACTGGCCGA	105	2677	2692	959
948818	115991	116006	GCCGGCTGGGCGCAGC	124	2735	2750	960
948819	116000	116015	TAATGGTGGGCCGGCT	83	2744	2759	961
948820	116002	116017	GATAATGGTGGGCCGG	96	2746	2761	962
948821	116003	116018	GGATAATGGTGGGCCG	73	2747	2762	963
948822	116004	116019	CGGATAATGGTGGGCC	41	2748	2763	964
948823	116014	116029	CTCGGCTGGGCGGATA	109	2758	2773	965
948824	116023	116038	CAGGGATGGCTCGGCT	48	2767	2782	966
948825	116028	116043	TCGAGCAGGGATGGCT	84	2772	2787	967
948826	116029	116044	GTCGAGCAGGGATGGC	135	2773	2788	968
948827	116034	116049	GCCTAGTCGAGCAGGG	84	2778	2793	969
948828	116055	116070	CGAGAGCACGCCCCCC	37	2799	2814	970
948829	116058	116073	CCCCGAGAGCACGCCC	73	2802	2817	971
948830	116092	116107	ACTGAAGCTCCTGCGC	75	2836	2851	972
948831	116109	116124	GCGGAGGGCCCCAGAC	94	2853	2868	973
948832	116163	116178	GTTAAGGAAGAGGCCA	27	2907	2922	974
948833	116210	116225	TGCGGTGTCCAGCCAG	42	2954	2969	975
948834	116212	116227	AGTGCGGTGTCCAGCC	24	2956	2971	976
948835	116213	116228	CAGTGCGGTGTCCAGC	9	2957	2972	977
948836	116214	116229	GCAGTGCGGTGTCCAG	11	2958	2973	978
948837	116216	116231	GCGCAGTGCGGTGTCC	60	2960	2975	979
948838	116217	116232	TGCGCAGTGCGGTGTC	58	2961	2976	980
948839	116221	116236	CCTTTGCGCAGTGCGG	57	2965	2980	981
948840	116222	116237	CCCTTTGCGCAGTGCG	21	2966	2981	982
948841	116224	116239	GCCCCTTTGCGCAGTG	104	2968	2983	983
948842	116225	116240	GGCCCCTTTGCGCAGT	98	2969	2984	984
948843	116261	116276	GTGCAACACCCCAGCG	58	3005	3020	985
948844	116266	116281	CCAAAGTGCAACACCC	31	3010	3025	986
948845	116267	116282	CCCAAAGTGCAACACC	82	3011	3026	987
948846	116288	116303	TGCCACCCTGAGACTC	62	3032	3047	988
948847	116310	116325	TCAAGGGTTCTGGTCC	10	3054	3069	989
948848	116311	116326	GTCAAGGGTTCTGGTC	28	3055	3070	990
948849	116313	116328	GTGTCAAGGGTTCTGG	8	3057	3072	991
948850	116315	116330	TGGTGTCAAGGGTTCT	6	3059	3074	992

948851	116316	116331	ATGGTGTCAAGGGTTC	5	3060	3075	993
948852	116317	116332	GATGGTGTCAAGGGTT	6	3061	3076	994
948853	116319	116334	AGGATGGTGTCAAGGG	13	3063	3078	995
948854	116320	116335	CAGGATGGTGTCAAGG	11	3064	3079	996
948855	116321	116336	TCAGGATGGTGTCAAG	13	3065	3080	997
948856	116323	116338	ATTCAGGATGGTGTCA	13	3067	3082	998
948857	116325	116340	TCATTCAGGATGGTGT	20	3069	3084	999
948858	116327	116342	CCTCATTCAGGATGGT	82	3071	3086	1000
948859	116351	116366	GTAGAGTCCCCCCCAG	22	3095	3110	1001
948860	116353	116368	TGGTAGAGTCCCCCCC	44	3097	3112	1002
948861	116354	116369	TTGGTAGAGTCCCCCC	19	3098	3113	1003
948862	116355	116370	CTTGGTAGAGTCCCCC	9	3099	3114	1004
948863	116357	116372	ACCTTGGTAGAGTCCC	4	3101	3116	1005
948864	116358	116373	GACCTTGGTAGAGTCC	94	3102	3117	1006
948865	116361	116376	GAAGACCTTGGTAGAG	6	3105	3120	1007
948866	116363	116378	AAGAAGACCTTGGTAG	17	3107	3122	1008
948867	116364	116379	CAAGAAGACCTTGGTA	60	3108	3123	1009
948868	116365	116380	CCAAGAAGACCTTGGT	62	3109	3124	1010
948869	116366	116381	CCCAAGAAGACCTTGG	70	3110	3125	1011
948870	116367	116382	GCCCAAGAAGACCTTG	60	3111	3126	1012
948871	116384	116399	CTACATGGGCTTTCCC	85	3128	3143	1013
948872	116386	116401	CCCTACATGGGCTTTC	98	3130	3145	1014
948873	116399	116414	TATAGAAGGCCTGCCC	100	3143	3158	1015
948874	116401	116416	CTTATAGAAGGCCTGC	20	3145	3160	1016
948875	116402	116417	ACTTATAGAAGGCCTG	25	3146	3161	1017
948876	116403	116418	CACTTATAGAAGGCCT	34	3147	3162	1018
948877	116405	116420	CGCACTTATAGAAGGC	57	3149	3164	1019
948878	116406	116421	CCGCACTTATAGAAGG	83	3150	3165	1020
948879	116450	116465	CCCTGCACCCCAGCAA	128	3194	3209	1021
948880	116454	116469	ATACCCCTGCACCCCA	18	3198	3213	1022
948881	116456	116471	ATATACCCCTGCACCC	45	3200	3215	1023
948882	116457	116472	GATATACCCCTGCACC	11	3201	3216	1024
948883	116458	116473	TGATATACCCCTGCAC	13	3202	3217	1025
948884	116459	116474	TTGATATACCCCTGCA	9	3203	3218	1026
948885	116460	116475	GTTGATATACCCCTGC	4	3204	3219	1027
948886	116465	116480	GGGAAGTTGATATACC	14	3209	3224	1028
948887	116466	116481	TGGGAAGTTGATATAC	20	3210	3225	1029
948888	116468	116483	AATGGGAAGTTGATAT	59	3212	3227	1030
948889	116469	116484	TAATGGGAAGTTGATA	49	3213	3228	1031
948890	116470	116485	CTAATGGGAAGTTGAT	15	3214	3229	1032
948891	116472	116487	TGCTAATGGGAAGTTG	12	3216	3231	1033
948892	116473	116488	CTGCTAATGGGAAGTT	4	3217	3232	1034
948893	116475	116490	TCCTGCTAATGGGAAG	2	3219	3234	1035

948894	116476	116491	CTCCTGCTAATGGGAA	86	3220	3235	1036
948895	116479	116494	GAGCTCCTGCTAATGG	94	3223	3238	1037
948896	116498	116513	GGCCAGGCTTGCCGCT	99	3242	3257	1038
948897	116512	116527	TACCGAGCCCACTGGG	103	3256	3271	1039
948898	116515	116530	CACTACCGAGCCCACT	82	3259	3274	1040
948899	116517	116532	GGCACTACCGAGCCCA	64	3261	3276	1041
948900	116520	116535	CTGGGCACTACCGAGC	92	3264	3279	1042
948901	116525	116540	GCCAGCTGGGCACTAC	149	3269	3284	1043
948902	116526	116541	TGCCAGCTGGGCACTA	130	3270	3285	1044
948903	116539	116554	TACACCTCAGGCCTGC	28	3283	3298	1045
948904	116540	116555	GTACACCTCAGGCCTG	98	3284	3299	1046
948905	116542	116557	ATGTACACCTCAGGCC	77	3286	3301	1047
948906	116543	116558	TATGTACACCTCAGGC	9	3287	3302	1048
948907	116545	116560	ACTATGTACACCTCAG	5	3289	3304	1049
948908	116546	116561	GACTATGTACACCTCA	16	3290	3305	1050
948909	116548	116563	AGGACTATGTACACCT	125	3292	3307	1051
948910	116549	116564	AAGGACTATGTACACC	5	3293	3308	1052
948911	116551	116566	GGAAGGACTATGTACA	11	3295	3310	1053
948912	116552	116567	GGGAAGGACTATGTAC	28	3296	3311	1054
948913	116553	116568	CGGGAAGGACTATGTA	16	3297	3312	1055
948914	116554	116569	CCGGGAAGGACTATGT	60	3298	3313	1056
948915	116555	116570	GCCGGGAAGGACTATG	40	3299	3314	1057
948916	116560	116575	ATATGGCCGGGAAGGA	21	3304	3319	1058
948917	116562	116577	TAATATGGCCGGGAAG	2	3306	3321	1059
948918	116563	116578	TTAATATGGCCGGGAA	9	3307	3322	1060
948919	116564	116579	GTTAATATGGCCGGGA	16	3308	3323	1061
948920	116566	116581	TGGTTAATATGGCCGG	37	3310	3325	1062
948921	116567	116582	GTGGTTAATATGGCCG	45	3311	3326	1063
948922	116568	116583	TGTGGTTAATATGGCC	10	3312	3327	1064
948923	116570	116585	TGTGTGGTTAATATGG	3	3314	3329	1065
948924	116571	116586	CTGTGTGGTTAATATG	4	3315	3330	1066
948925	116572	116587	GCTGTGTGGTTAATAT	7	3316	3331	1067
948926	116574	116589	AGGCTGTGTGGTTAAT	3	3318	3333	1068
948927	116618	116633	GGCCTAGCAAAGGCAC	118	3362	3377	1069
948928	116631	116646	GCCAACGGCTCCGGGC	119	3375	3390	1070
948929	116637	116652	GCCCGGGCCAACGGCT	96	3381	3396	1071
948930	116645	116660	CAAGGCCGGCCCGGGC	131	3389	3404	1072
948931	116647	116662	GGCAAGGCCGGCCCGG	104	3391	3406	1073
948932	116652	116667	AATAGGGCAAGGCCGG	65	3396	3411	1074
948933	116653	116668	GAATAGGGCAAGGCCG	126	3397	3412	1075
948934	116654	116669	GGAATAGGGCAAGGCC	22	3398	3413	1076
948935	116656	116671	GAGGAATAGGGCAAGG	7	3400	3415	1077
948936	116657	116672	AGAGGAATAGGGCAAG	4	3401	3416	1078

948937	116658	116673	GAGAGGAATAGGGCAA	6	3402	3417	1079
948938	116660	116675	AGGAGAGGAATAGGGC	8	3404	3419	1080
948939	116705	116720	ACATAGCCCAAGCCCA	54	3449	3464	1081
948940	116706	116721	CACATAGCCCAAGCCC	72	3450	3465	1082
948941	116707	116722	CCACATAGCCCAAGCC	90	3451	3466	1083
948942	116709	116724	ACCCACATAGCCCAAG	71	3453	3468	1084
948943	116767	116782	ACCCATCAGGGAGGCA	93	3511	3526	1085
948944	116790	116805	CAGAGAGAGGCCGCCC	43	3534	3549	1086
948945	116793	116808	CCTCAGAGAGAGGCCG	134	3537	3552	1087
948946	116814	116829	AGCGAGGAGTGGGTGA	43	3558	3573	1088
948947	116817	116832	CTGAGCGAGGAGTGGG	57	3561	3576	1089
948948	116818	116833	ACTGAGCGAGGAGTGG	34	3562	3577	1090
948949	116820	116835	AAACTGAGCGAGGAGT	64	3564	3579	1091
948950	116821	116836	CAAACTGAGCGAGGAG	7	3565	3580	1092
948951	116823	116838	GTCAAACTGAGCGAGG	5	3567	3582	1093
948952	116824	116839	GGTCAAACTGAGCGAG	5	3568	3583	1094
948953	116825	116840	TGGTCAAACTGAGCGA	9	3569	3584	1095
948954	116827	116842	AGTGGTCAAACTGAGC	5	3571	3586	1096
948955	116828	116843	CAGTGGTCAAACTGAG	64	3572	3587	1097
948956	116829	116844	ACAGTGGTCAAACTGA	73	3573	3588	1098
948957	116830	116845	TACAGTGGTCAAACTG	69	3574	3589	1099
948958	116831	116846	TTACAGTGGTCAAACT	34	3575	3590	1100
948959	116833	116848	ACTTACAGTGGTCAAA	17	3577	3592	1101
948960	116834	116849	CACTTACAGTGGTCAA	11	3578	3593	1102
948961	116835	116850	GCACTTACAGTGGTCA	4	3579	3594	1103
948962	116836	116851	GGCACTTACAGTGGTC	45	3580	3595	1104
948963	116837	116852	AGGCACTTACAGTGGT	5	3581	3596	1105
948964	116841	116856	GTGCAGGCACTTACAG	43	3585	3600	1106
948965	116844	116859	AGAGTGCAGGCACTTA	7	3588	3603	1107
948966	116846	116861	ACAGAGTGCAGGCACT	8	3590	3605	1108
948967	116847	116862	TACAGAGTGCAGGCAC	12	3591	3606	1109
948968	116848	116863	ATACAGAGTGCAGGCA	6	3592	3607	1110
948969	116850	116865	GAATACAGAGTGCAGG	6	3594	3609	1111
948970	116851	116866	AGAATACAGAGTGCAG	2	3595	3610	1112
948971	116852	116867	TAGAATACAGAGTGCA	1	3596	3611	1113
948972	116854	116869	AATAGAATACAGAGTG	6	3598	3613	1114
948973	3394	3409	GCTCACCGGCCCACGA	72	N/A	N/A	1115
948974	3500	3515	CGCGGGCACGCAAGCG	144	N/A	N/A	1116
948975	3607	3622	CGTGACACCGCCCCTG	71	N/A	N/A	1117
948976	3715	3730	ATCTACCCCAGACCCA	63	N/A	N/A	1118
948977	3725	3740	CAGAAGAGGGATCTAC	99	N/A	N/A	1119
948978	3776	3791	CAATAGATATCTAGAT	144	N/A	N/A	1120
948979	3778	3793	CCCAATAGATATCTAG	59	N/A	N/A	1121

948980	3815	3830	AGATACAAGAACAAGC	67	N/A	N/A	1122
948981	3934	3949	AGCTAGCCAGACAGCA	146	N/A	N/A	1123
948982	4010	4025	CAACAGAGGGACTGCT	85	N/A	N/A	1124
948983	4035	4050	ACAGTAGAGGCCAGCT	96	N/A	N/A	1125
948984	4130	4145	CGGAAGAGAGGAGCCA	84	N/A	N/A	1126
948985	4135	4150	TCACACGGAAGAGAGG	63	N/A	N/A	1127
948986	4142	4157	GAAGAATTCACACGGA	50	N/A	N/A	1128
948987	4262	4277	GTCCAAACCTCCTCCT	63	N/A	N/A	1129
948988	4315	4330	TCCTGAAGTAAGGTAC	96	N/A	N/A	1130
948989	4326	4341	TCGGAAAGGAATCCTG	40	N/A	N/A	1131
948990	4371	4386	AATTTGTAGGCTGTAG	21	N/A	N/A	1132
948991	4388	4403	TCCAAAGGAGGGCCCC	140	N/A	N/A	1133
948992	4476	4491	CACCGCGGCTTCTCAA	38	N/A	N/A	1134
948993	4624	4639	GAGAAGTGGCCGCCCA	75	N/A	N/A	1135
948994	4649	4664	CCACAAATGAGTAGTT	49	N/A	N/A	1136
948995	4730	4745	CATTATCCCTTGACAA	115	N/A	N/A	1137
948996	4742	4757	ATCAAGAAGGGACATT	85	N/A	N/A	1138
948997	4838	4853	GGTGATCACAGTCCCT	72	N/A	N/A	1139
948998	4938	4953	AGAGACAAGGTAGCAA	45	N/A	N/A	1140
948999	4950	4965	AGGCAATGAGCTAGAG	39	N/A	N/A	1141
949000	5049	5064	GAAGATGGTCACTCAA	47	N/A	N/A	1142
949001	5051	5066	AGGAAGATGGTCACTC	32	N/A	N/A	1143
949002	5162	5177	GTCAACCAAGACTTAG	48	N/A	N/A	1144
949003	5545	5560	TAGAATGGCATCTTGT	28	N/A	N/A	1145
949004	5710	5725	CCGGATCTGGTTCTGT	88	N/A	N/A	1146
949005	5810	5825	AACCAGCCAGATAAAC	94	N/A	N/A	1147
949006	5872	5887	GCTTAAGTGTGTAACG	8	N/A	N/A	1148
949007	5873	5888	GGCTTAAGTGTGTAAC	10	N/A	N/A	1149
949008	5898	5913	GATTATAGCAATGCCT	22	N/A	N/A	1150
949009	5940	5955	GCTCAGCTATCTGAGC	107	N/A	N/A	1151
949010	6074	6089	CCAGACACCATGGTAG	33	N/A	N/A	1152
949011	6150	6165	ATATAATGAGCAACTC	47	N/A	N/A	1153
949012	6174	6189	GTGAGACTCGGTGTAA	10	N/A	N/A	1154
949013	6298	6313	GTGGTAACGCGCGCCT	41	N/A	N/A	1155
949014	6455	6470	AATACTCTTAACGAGG	95	N/A	N/A	1156
949015	6556	6571	ACCTTATCTCTTACAC	63	N/A	N/A	1157
949016	6697	6712	TCCAGGCTCGGCGCAA	83	N/A	N/A	1158
949017	6752	6767	AGCTATAGGGCTGAAC	129	N/A	N/A	1159
949018	6816	6831	CGCAGGTAAAACAAAA	38	N/A	N/A	1160
949019	6817	6832	ACGCAGGTAAAACAAA	56	N/A	N/A	1161
949020	6821	6836	AGCTACGCAGGTAAAA	66	N/A	N/A	1162
949021	6824	6839	AAAAGCTACGCAGGTA	27	N/A	N/A	1163
949022	6870	6885	CCGGATATTGACTGGA	46	N/A	N/A	1164

949023	6891	6906	TGTCTTAGAGCCACAA	131	N/A	N/A	1165
949024	6906	6921	CTCTATAGATCTGAGT	123	N/A	N/A	1166
949025	6918	6933	GACAACTCAGAACTCT	93	N/A	N/A	1167
949026	7031	7046	TACCACCCTCAGCTTA	69	N/A	N/A	1168
949027	7131	7146	CGCCAGGTGAAACTGA	86	N/A	N/A	1169
949028	7155	7170	CCACAAGGGACAAAGG	89	N/A	N/A	1170
949029	7170	7185	TCGAAGCCATTACTGC	89	N/A	N/A	1171
949030	7248	7263	TGCTAGGGAGTAGTGG	47	N/A	N/A	1172
949031	7273	7288	GCAAAATGATCTAGGC	26	N/A	N/A	1173
949032	7328	7343	CCGCAGACAAGCCAGG	99	N/A	N/A	1174
949033	7351	7366	CCAAAGTTCTATCTGC	15	N/A	N/A	1175
949034	7395	7410	TGACAAGGGTCAAGAG	91	N/A	N/A	1176
949035	7400	7415	CTAAATGACAAGGGTC	22	N/A	N/A	1177
949036	7402	7417	GGCTAAATGACAAGGG	47	N/A	N/A	1178
949037	7645	7660	GTATAAGACCCTATCT	83	N/A	N/A	1179
949038	7849	7864	ATTTGAGGCGAGGAGG	58	N/A	N/A	1180
949050	8567	8582	TTTTAAAGAAGACGGG	51	N/A	N/A	1181
949051	8584	8599	TGCTATTATAACTCCT	15	N/A	N/A	1182
949052	8671	8686	GAACAACACCTAATGT	47	N/A	N/A	1183
949053	8675	8690	GAACGAACAACACCTA	8	N/A	N/A	1184
949054	8678	8693	AATGAACGAACAACAC	22	N/A	N/A	1185
949055	8705	8720	AGTAAAAGTACTCAGG	8	N/A	N/A	1186
949056	8740	8755	TGGTAACTTGCTCAGG	16	N/A	N/A	1187
949057	8773	8788	GCTGAAAGGCCAGCTC	83	N/A	N/A	1188
949058	8949	8964	CTACAGGTGTCACCAT	100	N/A	N/A	1189
949059	9093	9108	ACTTATCGCCTTTTTT	11	N/A	N/A	1190
949061	9613	9628	CTCCACTGGCCTGCTA	4	N/A	N/A	1191
949062	9724	9739	AGGGACAGCAGTAGCG	69	N/A	N/A	1192
949063	9830	9845	AGAAAAATGGCACGGG	41	N/A	N/A	1193
949064	9883	9898	TAAAAACGCAGCTGGA	79	N/A	N/A	1194
949065	9971	9986	TGCACTGGTGCAGCAC	115	N/A	N/A	1195
949066	10072	10087	GGCTCTAAACTAATAA	143	N/A	N/A	1196
949067	10260	10275	TCGGGATTCACTATGT	28	N/A	N/A	1197
949068	10379	10394	CGCTTACTGCAAGTTC	40	N/A	N/A	1198
949069	10481	10496	CCTAACCGAGCCTTGC	78	N/A	N/A	1199
949070	10675	10690	ACAACAATTTGCTACG	45	N/A	N/A	1200
949071	10677	10692	TCACAACAATTTGCTA	23	N/A	N/A	1201
949072	11266	11281	TGACACCAAACTGAGC	92	N/A	N/A	1202
949073	11356	11371	AAAGAAACTAAGGCCG	87	N/A	N/A	1203
949074	11384	11399	TAATGATGAGTTCCTT	14	N/A	N/A	1204
949075	11392	11407	CAACAGAGTAATGATG	54	N/A	N/A	1205
949076	11496	11511	CGATATTTCAGGATCT	88	N/A	N/A	1206
949077	11597	11612	CTCATCACCGTACACA	9	N/A	N/A	1207

949078	11881	11896	CCCTATCATTGGTTTT	55	N/A	N/A	1208
949079	11984	11999	TAACAGGTCTTGTGCA	55	N/A	N/A	1209
949080	12093	12108	ACGATTCACATGTGGG	11	N/A	N/A	1210
949081	12141	12156	AACCTAATCCCCAAAC	104	N/A	N/A	1211
949082	12195	12210	AGCACTTGGACAGCCT	36	N/A	N/A	1212
949083	12200	12215	GAAAAAGCACTTGGAC	31	N/A	N/A	1213
949084	12214	12229	CAATAAGTAACTCTGA	52	N/A	N/A	1214
949085	12318	12333	ATCTACAACTGTCCCC	25	N/A	N/A	1215
949086	12555	12570	AATAATGAGACCCCAC	145	N/A	N/A	1216
949087	12667	12682	TAAATCTAACCTAGGC	126	N/A	N/A	1217
949088	12778	12793	CAGAAGTTTGGCAGAT	5	N/A	N/A	1218
949089	12788	12803	TCAAATCGGGCAGAAG	22	N/A	N/A	1219
949090	12858	12873	AAATTACGGTTTACAT	71	N/A	N/A	1220
949091	12859	12874	TAAATTACGGTTTACA	20	N/A	N/A	1221
949092	12878	12893	TTGTAGTTGGCAATCC	12	N/A	N/A	1222
949093	12892	12907	GGCTTAATTACAGCTT	86	N/A	N/A	1223
949094	12901	12916	CACAATAAGGGCTTAA	10	N/A	N/A	1224
949095	12902	12917	ACACAATAAGGGCTTA	10	N/A	N/A	1225
949096	12947	12962	CCCTATAAATATCTCA	23	N/A	N/A	1226
949097	13037	13052	ACGCACCCGGAAGCAG	71	N/A	N/A	1227
949098	13140	13155	AAACAGTCATCCAGCT	105	N/A	N/A	1228
949099	13208	13223	TGGCACACGGTGATTC	57	N/A	N/A	1229
949100	13215	13230	GCACATGTGGCACACG	27	N/A	N/A	1230
949101	13273	13288	AGGGATGCTAAGAGCA	69	N/A	N/A	1231
949102	13281	13296	TATAAAGCAGGGATGC	117	N/A	N/A	1232
949103	13391	13406	CCATATGTGTGGCTCT	21	N/A	N/A	1233
949104	13520	13535	GCATATCCAAAGCCAC	38	N/A	N/A	1234
949105	13635	13650	CATTTAACTGTTCACC	28	N/A	N/A	1235
949106	13812	13827	CGACAGACAAGTACCA	46	N/A	N/A	1236
949107	13952	13967	GCATACAGCCTTTTTT	38	N/A	N/A	1237
949108	13953	13968	CGCATACAGCCTTTTT	15	N/A	N/A	1238
949109	13955	13970	ACCGCATACAGCCTTT	9	N/A	N/A	1239
949110	13956	13971	CACCGCATACAGCCTT	46	N/A	N/A	1240
949111	13959	13974	AACCACCGCATACAGC	50	N/A	N/A	1241
949112	13961	13976	TGAACCACCGCATACA	40	N/A	N/A	1242
949113	14262	14277	TGCAACCTTCAAGTAA	94	N/A	N/A	1243
949114	14390	14405	GCAAACCGCTTCTCAC	74	N/A	N/A	1244
949115	14492	14507	CCCCAAGTCCTGGCGG	99	N/A	N/A	1245
949116	14629	14644	GAAAAGTCGGCATTCC	74	N/A	N/A	1246
949117	14757	14772	TGACAGTGGTGCTCCC	66	N/A	N/A	1247
949118	15000	15015	TGGCATGTGGTTGTTG	26	N/A	N/A	1248
949119	15165	15180	AACAAATATATGCACG	20	N/A	N/A	1249
949120	15370	15385	TCGCACCTCGGGATTC	92	N/A	N/A	1250

949121	15507	15522	GTGAAATTCACTCCAT	40	N/A	N/A	1251
949122	15612	15627	GGAAGATGTCCTTGCT	49	N/A	N/A	1252
949123	15643	15658	ATAGATGGAGCAAATC	77	N/A	N/A	1253
949124	15647	15662	TTATATAGATGGAGCA	32	N/A	N/A	1254
949125	15708	15723	ACGCAGATAGACACCC	53	N/A	N/A	1255
949126	15712	15727	GCCAACGCAGATAGAC	93	N/A	N/A	1256
949127	15777	15792	TGCCATACAGGGCCTC	116	N/A	N/A	1257
949128	15859	15874	GAAAGAGCAGTGGTGC	73	N/A	N/A	1258
949129	15973	15988	GGGCATGGAGGTGTCA	90	N/A	N/A	1259
949130	16025	16040	CGCGAAAGTGTGTCAC	64	N/A	N/A	1260
949131	16117	16132	TATCACCCAGCAGGCA	75	N/A	N/A	1261
949132	16275	16290	GGCCAGCTGGTAGGCC	114	N/A	N/A	1262
949134	16714	16729	GTCAAGCTGAGCCAGT	52	N/A	N/A	1263
949135	16815	16830	ACAGAAGCCGGGCTTC	127	N/A	N/A	1264
949136	16926	16941	ATCAATTTTCACCCAG	19	N/A	N/A	1265
949137	16930	16945	GTGCATCAATTTTCAC	127	N/A	N/A	1266
949138	17244	17259	AAAGAGTTTAAGGGCG	57	N/A	N/A	1267
949139	17282	17297	CCACAACGAGTAAACA	15	N/A	N/A	1268
949140	17615	17630	GGACAGGGTGAATTGT	62	N/A	N/A	1269
949141	17723	17738	AGTCACACCTAGAAAT	32	N/A	N/A	1270
949142	17758	17773	GACTTATAGGCTCACT	12	N/A	N/A	1271
949143	17763	17778	TACTAGACTTATAGGC	26	N/A	N/A	1272
949144	17765	17780	GTTACTAGACTTATAG	19	N/A	N/A	1273
949145	17766	17781	TGTTACTAGACTTATA	40	N/A	N/A	1274
949146	17834	17849	ATATAGCAGGGACCTG	70	N/A	N/A	1275
949147	17838	17853	CTAAATATAGCAGGGA	36	N/A	N/A	1276
949148	17840	17855	CACTAAATATAGCAGG	24	N/A	N/A	1277
949149	18278	18293	TTTGAGCCCGAGAGGG	46	N/A	N/A	1278
949150	18486	18501	TTATTTCTAGGCAGGG	13	N/A	N/A	1279
949151	18524	18539	GTAAATTTGAAGCTTA	144	N/A	N/A	1280
949152	18583	18598	AATTAGAGGACACTGG	19	N/A	N/A	1281
949153	18665	18680	GCTTTAACTCCTAGAC	61	N/A	N/A	1282
949154	19040	19055	GTATACCAAGGTTAAT	56	N/A	N/A	1283
949155	19050	19065	CTTAATAGTAGTATAC	96	N/A	N/A	1284
949156	19458	19473	CACACGAGGTCTCACT	44	N/A	N/A	1285
949157	19461	19476	CTACACACGAGGTCTC	72	N/A	N/A	1286
949158	19663	19678	TACATTCTGGCTTTGG	12	N/A	N/A	1287
949159	19763	19778	TCTCAGTATGTATACT	12	N/A	N/A	1288
949160	19814	19829	TGTCCAGTCCTAAGAC	101	N/A	N/A	1289
949161	19816	19831	AATGTCCAGTCCTAAG	81	N/A	N/A	1290
949162	19817	19832	CAATGTCCAGTCCTAA	19	N/A	N/A	1291
949163	19818	19833	GCAATGTCCAGTCCTA	4	N/A	N/A	1292
949164	19820	19835	ATGCAATGTCCAGTCC	13	N/A	N/A	1293

949165	19821	19836	GATGCAATGTCCAGTC	70	N/A	N/A	1294
949166	19822	19837	AGATGCAATGTCCAGT	13	N/A	N/A	1295
949167	19824	19839	CTAGATGCAATGTCCA	12	N/A	N/A	1296
949168	19843	19858	GCTTAAGGAGATCCGA	17	N/A	N/A	1297
949169	19844	19859	GGCTTAAGGAGATCCG	85	N/A	N/A	1298
949170	19872	19887	GGCTGAGTTGCTTCCC	79	N/A	N/A	1299
949171	19935	19950	TTCCAGATAAGCCCTA	32	N/A	N/A	1300
949172	19986	20001	CACCAATGGCCTTCTT	42	N/A	N/A	1301
949173	20328	20343	GAAGATGGCTGGACGA	34	N/A	N/A	1302
949174	20330	20345	CAGAAGATGGCTGGAC	34	N/A	N/A	1303
949175	20378	20393	CAATAATTTATCAGTC	68	N/A	N/A	1304
949176	20440	20455	GGGAAACCTAGCAAGC	80	N/A	N/A	1305
949177	20487	20502	CCCAAAGGATAGAGTA	23	N/A	N/A	1306
949178	20735	20750	TTACATGAGTCTAGGA	50	N/A	N/A	1307
949179	20737	20752	TATTACATGAGTCTAG	68	N/A	N/A	1308
949180	20740	20755	GATTATTACATGAGTC	49	N/A	N/A	1309
949181	20748	20763	GGCAAGAGGATTATTA	53	N/A	N/A	1310
949182	20844	20859	AGCAACTTTAGGGAGA	5	N/A	N/A	1311
949183	20899	20914	GAACAGACAGTTCAGG	76	N/A	N/A	1312
949184	20947	20962	AAGATATGTGGTTTTG	35	N/A	N/A	1313
949185	21341	21356	GAGCATCACCAGCCCA	127	N/A	N/A	1314
949186	21403	21418	TAGAAATGAGTGGGCG	116	N/A	N/A	1315
949187	21416	21431	AGCTACAGCAATATAG	43	N/A	N/A	1316
949188	21449	21464	ACTCACATGGCCTGAT	81	N/A	N/A	1317
949189	21491	21506	CTAGACTAGACAAAAC	91	N/A	N/A	1318
949190	21514	21529	ATATATATGTGGAGGC	4	N/A	N/A	1319
949191	21561	21576	CTAATACACAATGATC	34	N/A	N/A	1320
949192	21591	21606	CAAAAAACTAATACCG	105	N/A	N/A	1321
949193	21698	21713	AACCAGTACCAGCTGG	98	N/A	N/A	1322
949194	21758	21773	AGAAACTGTACTGGTC	25	N/A	N/A	1323
949195	21845	21860	GGATATTCTTAACAGG	26	N/A	N/A	1324
949196	21854	21869	AGCTAGGAAGGATATT	83	N/A	N/A	1325
949197	22009	22024	AAGTATGCGCTGCCAT	38	N/A	N/A	1326
949198	22018	22033	TGGGACTGTAAGTATG	63	N/A	N/A	1327
949199	22133	22148	GGATATAGGGTCTCCC	138	N/A	N/A	1328
949200	22243	22258	CATGAGGTAGGACAGC	54	N/A	N/A	1329
949201	22251	22266	GAAAAAGCCATGAGGT	100	N/A	N/A	1330
949202	22301	22316	CCACAGGGTTATCTGG	119	N/A	N/A	1331
949203	22345	22360	AAGGAGGCTTTTAAGC	92	N/A	N/A	1332
949204	22446	22461	AGGAATGACAAGTGGT	17	N/A	N/A	1333
949205	22466	22481	CGCATAGGTGGAACAA	58	N/A	N/A	1334
949206	22478	22493	CAAGAAACCAAACGCA	81	N/A	N/A	1335
949207	22638	22653	AATATACGGGCATGTT	82	N/A	N/A	1336

949208	22639	22654	AAATATACGGGCATGT	110	N/A	N/A	1337
949209	22641	22656	AAAAATATACGGGCAT	104	N/A	N/A	1338
949210	22643	22658	ACAAAAATATACGGGC	67	N/A	N/A	1339
949211	22644	22659	TACAAAAATATACGGG	33	N/A	N/A	1340
949212	22780	22795	TCAAACAAATAGGCCG	86	N/A	N/A	1341
949213	22862	22877	ATGCAAGGGACTGCGC	66	N/A	N/A	1342
949214	22883	22898	ACCTATCGCATGCCAG	17	N/A	N/A	1343
949215	23000	23015	GTTCAGGTCAGAGCCT	51	N/A	N/A	1344
949216	23297	23312	TCTCAATGAAAGTCTC	10	N/A	N/A	1345
949217	23548	23563	GTAACAACCGCTGGGA	27	N/A	N/A	1346
949218	23555	23570	TTAAAGAGTAACAACC	75	N/A	N/A	1347
949219	23715	23730	GCCCAGCTAACTAACT	108	N/A	N/A	1348
949220	24040	24055	GACTACAGTACAGGCG	74	N/A	N/A	1349
949221	24201	24216	AGAACAAGGGAACACG	80	N/A	N/A	1350
949222	24210	24225	CCCCATAGAAGAACAA	138	N/A	N/A	1351
949223	24289	24304	GATTAGGTATTATGGT	12	N/A	N/A	1352
949224	24296	24311	TCAAAAGGATTAGGTA	25	N/A	N/A	1353
949225	24315	24330	ATCCACTGAATAGTAT	32	N/A	N/A	1354
949226	24364	24379	CTACAAAATCAGATAG	91	N/A	N/A	1355
949227	24438	24453	GACATTAGTGGCTTCC	35	N/A	N/A	1356
949228	24561	24576	AACCAGCATGGATGAA	87	N/A	N/A	1357
949229	24782	24797	TGCAACCTTGCCCCCC	11	N/A	N/A	1358
949230	24934	24949	TAGTATTCAAAAAACG	80	N/A	N/A	1359
949231	25044	25059	CAAATTAAATACACCC	62	N/A	N/A	1360
949232	25058	25073	GAATACTATTCTAACA	118	N/A	N/A	1361
949233	25210	25225	CACCACAATTTGCTCT	63	N/A	N/A	1362
949234	25305	25320	TCAGAAAAGGAGGGTA	109	N/A	N/A	1363
949235	25321	25336	TTCCACTTCAAGAACC	87	N/A	N/A	1364
949236	25696	25711	TGTAAGCAACTGTATT	49	N/A	N/A	1365
949237	25788	25803	TGAGAAGATATGCTGA	26	N/A	N/A	1366
949238	25822	25837	AACCTATGTATCAAAG	87	N/A	N/A	1367
949239	25925	25940	CAAAGTAGTTCCTCCA	34	N/A	N/A	1368
949240	25927	25942	TACAAAGTAGTTCCTC	68	N/A	N/A	1369
949241	26042	26057	CCCAAGAGTAAAATAC	105	N/A	N/A	1370
949242	26084	26099	ACGAAACCAATAAGAC	104	N/A	N/A	1371
949243	26090	26105	GAAAATACGAAACCAA	99	N/A	N/A	1372
949244	26133	26148	TAATAATGGATGGAAC	84	N/A	N/A	1373
949245	26155	26170	TGGTATCAGGCAAGAA	35	N/A	N/A	1374
949246	27033	27048	CATGATGCTGCAATCA	97	N/A	N/A	1375
949247	27177	27192	CACAAGCCTGCGGACC	110	N/A	N/A	1376
949248	27191	27206	GAGCATAGCAGACACA	65	N/A	N/A	1377
949249	27254	27269	GGCAACATCACTCTAA	62	N/A	N/A	1378
949250	27289	27304	CAAAGAGCCTTGGCAC	111	N/A	N/A	1379

949251	27390	27405	CAGGACTAGTTCACTA	78	N/A	N/A	1380
949252	27473	27488	ATGAAATTGGGATAAC	60	N/A	N/A	1381
949253	27509	27524	ATGAAGGCTGCCACTT	103	N/A	N/A	1382
949254	27575	27590	AGCAAGATCATTGGGT	65	N/A	N/A	1383
949255	27634	27649	GGAAACCTTGGACTCC	91	N/A	N/A	1384
949256	27761	27776	GTCTATTGGCACACAG	38	N/A	N/A	1385
949257	27775	27790	GATTAAGTCATCCGGT	70	N/A	N/A	1386
949258	27872	27887	GGGCACTGCACAAAGC	86	N/A	N/A	1387
949259	27975	27990	AGTCAGCGGAGACTGA	98	N/A	N/A	1388
949260	28212	28227	CGGCAAAAGAAGCTGG	133	N/A	N/A	1389
949261	28320	28335	AGCTAGAGCATCAGCT	122	N/A	N/A	1390
949262	28971	28986	CTGGAAACAGTCTCGC	29	N/A	N/A	1391
949263	29116	29131	AGCCGAAGTGTAGTGG	51	N/A	N/A	1392
949264	29258	29273	GGCCAAGTCTCCCATC	117	N/A	N/A	1393
949265	29370	29385	CCGGACCCGTTCTTGA	85	N/A	N/A	1394
949266	29501	29516	AGGTAGTGACCTCCAG	114	N/A	N/A	1395
949267	29557	29572	ACCCACAGTCTGCATT	97	N/A	N/A	1396
949268	29591	29606	GCCCAAGTGAACTAGA	94	N/A	N/A	1397
949269	29625	29640	ATGTATGGATTTCCAG	62	N/A	N/A	1398
949270	29642	29657	TTACAGGGTGGTCAGC	82	N/A	N/A	1399
949271	29721	29736	GTAAAACGGTTGTGGT	30	N/A	N/A	1400
949272	29739	29754	CAACAGGTGTCCTGCT	64	N/A	N/A	1401
949273	29842	29857	TGTCATCCTAACTGCT	57	N/A	N/A	1402
949274	29943	29958	AGAAACTGGCCGGCCC	132	N/A	N/A	1403
949275	30052	30067	TTTATAGTCTCCAACG	34	N/A	N/A	1404
949276	30178	30193	ACGGACTGGATTATGC	27	N/A	N/A	1405
949277	30248	30263	GGCTAAATCAATCTTG	60	N/A	N/A	1406
949278	30282	30297	CGATAATGACCTAAAT	84	N/A	N/A	1407
949279	30283	30298	CCGATAATGACCTAAA	8	N/A	N/A	1408
949280	30406	30421	GAATATCAACACCTTG	35	N/A	N/A	1409
949281	30508	30523	AGTGATATGCTGCCTA	39	N/A	N/A	1410
949282	30705	30720	GGTTTATTTGCACCTC	39	N/A	N/A	1411
949283	30830	30845	TACCAGGGACTCAACT	111	N/A	N/A	1412
949284	30933	30948	GGCCAGACATTGCTGT	142	N/A	N/A	1413
949285	31273	31288	CACATTGGTGGTCAAG	98	N/A	N/A	1414
949286	31373	31388	CTCATAACATTTGACG	45	N/A	N/A	1415
949287	31708	31723	AAAAAAGCCGGCACGG	120	N/A	N/A	1416
949288	32027	32042	AAAATTGGTTGAGTGC	40	N/A	N/A	1417
949289	32161	32176	GTAAAACTCAGGCTGA	81	N/A	N/A	1418
949290	32192	32207	CAAAAGAGAACATTCG	64	N/A	N/A	1419
949291	32264	32279	TGTTATGTGGGAATGA	35	N/A	N/A	1420
949292	32420	32435	AGGGACACAACAGGCT	85	N/A	N/A	1421
949293	32560	32575	CACAATCCACTCCTGG	100	N/A	N/A	1422

949294	32561	32576	CCACAATCCACTCCTG	83	N/A	N/A	1423
949295	32615	32630	TTGCAGAACAATGGGC	105	N/A	N/A	1424
949296	32697	32712	GCGCAGGGTCCCGTAT	95	N/A	N/A	1425
949297	32719	32734	TATTAGAGTGGCAGCC	86	N/A	N/A	1426
949298	32799	32814	TGCCACTCACAACTGG	104	N/A	N/A	1427
949299	32852	32867	CGCCATAGGAAGCTGC	111	N/A	N/A	1428
949300	32895	32910	GAGCAGGCGGGCAGCT	82	N/A	N/A	1429
949301	32899	32914	AACAGAGCAGGCGGGC	92	N/A	N/A	1430
949302	32900	32915	TAACAGAGCAGGCGGG	103	N/A	N/A	1431
949303	32903	32918	CATTAACAGAGCAGGC	119	N/A	N/A	1432
949304	32904	32919	GCATTAACAGAGCAGG	46	N/A	N/A	1433
949305	33006	33021	AGCCACATATGCCTCC	91	N/A	N/A	1434
949306	33148	33163	TGTTATGGGCCCTCCT	82	N/A	N/A	1435
949307	33277	33292	TCCAAGGCTGTCAGCG	106	N/A	N/A	1436
949308	33391	33406	CACGAGGCTGCAGACC	40	N/A	N/A	1437
949309	33454	33469	CCGCAGGTAGGTGCCA	56	N/A	N/A	1438
949310	33488	33503	GCCCAAGCCTTACAGT	117	N/A	N/A	1439
949311	33512	33527	AGCCATTGGTCACCCA	43	N/A	N/A	1440
949312	33618	33633	CCGCACCCACCTCAGG	132	N/A	N/A	1441
949313	33644	33659	CACCAATGAGGCAGAC	69	N/A	N/A	1442
949314	33725	33740	GTGGACTGAGGTTCAG	101	N/A	N/A	1443
949315	33826	33841	CTCTAACCCCATCTCG	81	N/A	N/A	1444
949316	33927	33942	TCGGCAGGAGCCCACA	108	N/A	N/A	1445
949317	34028	34043	CCATATGCTCAGCACA	30	N/A	N/A	1446
949318	34029	34044	ACCATATGCTCAGCAC	45	N/A	N/A	1447
949319	34159	34174	GATAAGCCCACAGAGG	107	N/A	N/A	1448
949320	34164	34179	CAACAGATAAGCCCAC	83	N/A	N/A	1449
949321	34281	34296	ACAGACCACAAGGCTC	65	N/A	N/A	1450
949322	34283	34298	GAACAGACCACAAGGC	82	N/A	N/A	1451
949323	34407	34422	CAGGAAGGCGGTAGGG	92	N/A	N/A	1452
949324	34539	34554	TGGGAGGACACTTCCA	121	N/A	N/A	1453
949325	34546	34561	CATGAAATGGGAGGAC	9	N/A	N/A	1454
949326	34561	34576	ACTGACTTGGCCATCC	68	N/A	N/A	1455
949327	34654	34669	CCAGACTGTGGAGCCA	35	N/A	N/A	1456
949328	34763	34778	GCCAAGACTTCTGCAC	129	N/A	N/A	1457
949329	34873	34888	GCCTACCTGGCCATGG	119	N/A	N/A	1458
949330	34995	35010	GCTGACCGGGTTCCCC	148	N/A	N/A	1459
949331	35150	35165	TCCTATCCATGGGCCC	93	N/A	N/A	1460
949332	35178	35193	TACTATTGCATCATTT	33	N/A	N/A	1461
949333	35385	35400	CCCTAGTGAACTTCCC	38	N/A	N/A	1462
949334	35541	35556	GCAAACCTCAGTCTCG	39	N/A	N/A	1463
949335	35921	35936	GCACAATTAAGTAGTT	36	N/A	N/A	1464
949336	35950	35965	GCATAGAGTAGGGCTG	55	N/A	N/A	1465

949337	35955	35970	CCAAAGCATAGAGTAG	57	N/A	N/A	1466
949338	35956	35971	CCCAAAGCATAGAGTA	62	N/A	N/A	1467
949339	36021	36036	CCCATCTGAGCTGTGT	79	N/A	N/A	1468
949340	36170	36185	TCGAATGACATTTCCT	65	N/A	N/A	1469
949341	36211	36226	AGTAAGACAGGGTAAC	136	N/A	N/A	1470
949342	36311	36326	GTGCACCCAGGCTGCC	105	N/A	N/A	1471
949343	36420	36435	TTCCAGCCTCCGTCAT	90	N/A	N/A	1472
949344	36531	36546	CCTAAGGGTTTTCTGG	109	N/A	N/A	1473
949345	36532	36547	CCCTAAGGGTTTTCTG	144	N/A	N/A	1474
949346	36570	36585	CCAGAAGTCTCCTAGG	108	N/A	N/A	1475
949347	36647	36662	CTAAAAGTTCCCAGAC	86	N/A	N/A	1476
949348	36757	36772	GGAGACGCAGCTCTCA	103	N/A	N/A	1477
949349	36892	36907	GGACAAGCACCCCTCT	26	N/A	N/A	1478
949350	36996	37011	CCCGACCCCGGCCAAT	96	N/A	N/A	1479
949351	37100	37115	GTTCACTACAGACATC	71	N/A	N/A	1480
949352	37105	37120	TTCTAGTTCACTACAG	92	N/A	N/A	1481
949353	37243	37258	CATAGTACCCCACACA	56	N/A	N/A	1482
949354	37300	37315	TTGTAGTGTGGAATAT	40	N/A	N/A	1483
949355	37364	37379	CGCCCAAGAGAACACA	104	N/A	N/A	1484
949356	37481	37496	CTCCACTTTGTGTCTG	58	N/A	N/A	1485
949357	37583	37598	GCCTTCTGAGCAAACA	90	N/A	N/A	1486
949358	37726	37741	AAAATGGGTCTGCTGG	18	N/A	N/A	1487
949359	37730	37745	CATTAAAATGGGTCTG	56	N/A	N/A	1488
949360	37843	37858	ACCTTAAGTTTCTTGT	70	N/A	N/A	1489
949361	37896	37911	TGCAATGGAGTCCAAA	65	N/A	N/A	1490
949362	37970	37985	CCTTAAGTTTTTTGGT	132	N/A	N/A	1491
949363	38144	38159	TCATGATTATTAACCT	29	N/A	N/A	1492
949364	38160	38175	AGGCATTGAGAACTTT	77	N/A	N/A	1493
949365	38190	38205	AGCTATTCAACACTGA	65	N/A	N/A	1494
949366	38206	38221	CATTAGAGTAGCTAAT	141	N/A	N/A	1495
949367	38246	38261	TTGAATTCCGCATCAT	86	N/A	N/A	1496
949368	38313	38328	AACAAAACAGGACCCG	108	N/A	N/A	1497
949369	38353	38368	GAAGAAAGTCTGTACT	86	N/A	N/A	1498
949370	38488	38503	TTGTAGTGATCAGTTT	54	N/A	N/A	1499
949371	38588	38603	ATCCATGCTGCTATGC	63	N/A	N/A	1500
949372	38688	38703	TTGCACAACAAAGAGC	90	N/A	N/A	1501
949373	38948	38963	GATATATTGCTGGGCA	72	N/A	N/A	1502
949374	38949	38964	AGATATATTGCTGGGC	44	N/A	N/A	1503
949375	39017	39032	ACCTAAGGAAGCTGAC	72	N/A	N/A	1504
949376	39062	39077	TTAAAGCCCAGCAACA	93	N/A	N/A	1505
949377	39088	39103	ACGAAAAATTCAGATC	104	N/A	N/A	1506
949378	39089	39104	GACGAAAAATTCAGAT	83	N/A	N/A	1507
949379	39124	39139	ACAGAATTGTTACAAC	104	N/A	N/A	1508

949380	39156	39171	GTACAGGGTGGACATT	90	N/A	N/A	1509
949381	39162	39177	ACAAAAGTACAGGGTG	66	N/A	N/A	1510
949382	39163	39178	TACAAAAGTACAGGGT	86	N/A	N/A	1511
949383	39164	39179	ATACAAAAGTACAGGG	54	N/A	N/A	1512
949384	39195	39210	AGTCAAGGAGAACATG	63	N/A	N/A	1513
949385	39529	39544	TTGTAGTGGGTCACGC	53	N/A	N/A	1514
949386	39644	39659	CATGATTGCGCCGTTG	17	N/A	N/A	1515
949387	39745	39760	GTAATTCACTGCGGAT	32	N/A	N/A	1516
949388	39877	39892	AAACTTGCAGCAGTGG	67	N/A	N/A	1517
949389	39981	39996	AAATGGACTAGAAGGG	59	N/A	N/A	1518
949390	40014	40029	AGATAGAAATCAGGGC	47	N/A	N/A	1519
949391	40058	40073	TCACAGGGTGGACTTG	53	N/A	N/A	1520
949392	40089	40104	GTAGACACATGTCCTT	49	N/A	N/A	1521
949393	40195	40210	GACTACAGTCTGTTCG	96	N/A	N/A	1522
949394	40295	40310	AACACAGGAGCAGCAT	87	N/A	N/A	1523
949395	40306	40321	AACGATAAAACAACAC	70	N/A	N/A	1524
949396	40409	40424	ACTGAATCACCAGCAG	99	N/A	N/A	1525
949397	40837	40852	GCCTTTACTTAAGATA	3	N/A	N/A	1526
949398	40961	40976	ACGCAGTGTCTCAGGT	125	N/A	N/A	1527
949399	41061	41076	CACAAGTAGCCTTGGC	107	N/A	N/A	1528
949400	41107	41122	TCACAGTGGACACCAG	85	N/A	N/A	1529
949401	41162	41177	TGACAGACCCCAAAGT	121	N/A	N/A	1530
949402	41234	41249	GAACAAGCTACATCAA	100	N/A	N/A	1531
949403	41266	41281	TGGAGAGGGTTCTCTG	94	N/A	N/A	1532
949404	41272	41287	GATAATTGGAGAGGGT	84	N/A	N/A	1533
949405	41393	41408	GCGAACCTTTCTCACT	57	N/A	N/A	1534
949406	41447	41462	AAACAGGATACGAGAC	74	N/A	N/A	1535
949407	41451	41466	GCACAAACAGGATACG	86	N/A	N/A	1536
949408	41497	41512	TAATCCCTTTCCGTCA	92	N/A	N/A	1537
949409	41604	41619	TGTCTTCGAGCCACAC	99	N/A	N/A	1538
949410	41708	41723	CCCTACAGACACTTGC	101	N/A	N/A	1539
949411	41814	41829	CCGTAGGCAGATTCCA	62	N/A	N/A	1540
949412	41862	41877	GCGAAACCAGAGAGAT	88	N/A	N/A	1541
949413	41863	41878	GGCGAAACCAGAGAGA	86	N/A	N/A	1542
949414	41962	41977	AGCTTTTAAACCCCCC	87	N/A	N/A	1543
949415	41984	41999	AGCCAGATTATTAACA	58	N/A	N/A	1544
949416	42064	42079	GATGAGGAGGCTGGTC	78	N/A	N/A	1545
949417	42169	42184	ACGAAGACCCCCCAGG	163	N/A	N/A	1546
949418	42203	42218	CATGAGAAAAGGGATC	97	N/A	N/A	1547
949419	42249	42264	CAACAAGTCAGCCCAA	100	N/A	N/A	1548
949420	42252	42267	ACACAACAAGTCAGCC	78	N/A	N/A	1549
949421	42254	42269	CTACACAACAAGTCAG	28	N/A	N/A	1550
949422	42318	42333	TTCTAGCCCGTCAGCC	90	N/A	N/A	1551

949423	42434	42449	TTCCAGAAGACCTGTT	143	N/A	N/A	1552
949424	42507	42522	TAGCACTACAATCATT	71	N/A	N/A	1553
949425	42544	42559	AACGAGACAGCATCCT	64	N/A	N/A	1554
949426	42577	42592	GCAATTGGTACTGTAC	101	N/A	N/A	1555
949427	42584	42599	ACACAGGGCAATTGGT	144	N/A	N/A	1556
949428	42727	42742	TCGAACTCAACCTCAG	70	N/A	N/A	1557
949429	42860	42875	TGCCTCGGGTTCAAGC	64	N/A	N/A	1558
949430	42983	42998	TGAAAGGTTCTAGGCA	64	N/A	N/A	1559
949431	42984	42999	GTGAAAGGTTCTAGGC	57	N/A	N/A	1560
949432	43017	43032	TCGAAAGGAAATTCTG	89	N/A	N/A	1561
949433	43028	43043	ACATTAAAGGCTCGAA	43	N/A	N/A	1562
949434	43030	43045	GTACATTAAAGGCTCG	59	N/A	N/A	1563
949435	43050	43065	GTAGAAACAGTGGGCT	61	N/A	N/A	1564
949436	43094	43109	GTACACTCAGAAAGGA	91	N/A	N/A	1565
949437	43141	43156	GTGAATACACCAGGAT	76	N/A	N/A	1566
949438	43194	43209	ACTCAGGCACAACCAC	123	N/A	N/A	1567
949439	43864	43879	CGACAGAGCTGTTTAA	47	N/A	N/A	1568
949440	43884	43899	GCGGAATGTAAATTAC	40	N/A	N/A	1569
949441	43918	43933	CTAAAGACCACTAATT	122	N/A	N/A	1570
949442	43920	43935	GACTAAAGACCACTAA	53	N/A	N/A	1571
949443	44005	44020	GTACAGAGCCATGACT	113	N/A	N/A	1572
949444	44161	44176	TAAAAGCCTGGACAAG	77	N/A	N/A	1573
949445	44199	44214	TACATCTGGACTATGG	23	N/A	N/A	1574
949446	44271	44286	GATACCTGGATGTGGG	80	N/A	N/A	1575
949447	44336	44351	GACAAAATAGGATGTG	88	N/A	N/A	1576
949448	44351	44366	AGGAAAGTTATTGATG	63	N/A	N/A	1577
949449	44356	44371	ATACGAGGAAAGTTAT	112	N/A	N/A	1578
949450	44359	44374	AAAATACGAGGAAAGT	80	N/A	N/A	1579
949451	44362	44377	GGTAAAATACGAGGAA	23	N/A	N/A	1580
949452	44375	44390	CCACATGTATATGGGT	85	N/A	N/A	1581
949453	44426	44441	CCATACCCAGGAGATC	57	N/A	N/A	1582
949454	44509	44524	AACCATTTCCCTCTGG	58	N/A	N/A	1583
949455	44624	44639	GGCGACCTCAGCAAAG	85	N/A	N/A	1584
949456	44732	44747	AAGGAAGTCCCTGTGA	106	N/A	N/A	1585
949457	44851	44866	GGCAACCACACATCCA	79	N/A	N/A	1586
949458	44953	44968	ACTGAGCCGTTTTTCA	42	N/A	N/A	1587
949459	45279	45294	CCGAAGTGAGAGGGTC	88	N/A	N/A	1588
949460	45364	45379	CAAAATCGGGTTATCT	66	N/A	N/A	1589
949461	45365	45380	GCAAAATCGGGTTATC	38	N/A	N/A	1590
949462	45412	45427	AAGGATGGATGTGTCA	18	N/A	N/A	1591
949463	45503	45518	TGACATGCGGGAATGA	40	N/A	N/A	1592
949464	45523	45538	AGTAGAAACTGGGACG	43	N/A	N/A	1593
949465	45570	45585	AGCTATAAAACCAGCC	106	N/A	N/A	1594

949466	45603	45618	TACAAAAGAGTATAGC	70	N/A	N/A	1595
949467	45705	45720	CACCACTGCACGGCCT	97	N/A	N/A	1596
949468	45850	45865	AACATAACCCCCATCT	88	N/A	N/A	1597
949469	45957	45972	AGCAATGGTAGAGGGC	113	N/A	N/A	1598
949470	46279	46294	GCAATGGTGGCCGGGC	96	N/A	N/A	1599
949471	46323	46338	TTCAACAGGCTGGGTC	44	N/A	N/A	1600
949472	46330	46345	TACTATATTCAACAGG	18	N/A	N/A	1601
949473	46344	46359	CCACACATAGGCCATA	35	N/A	N/A	1602
949474	46382	46397	ATACACTGAGATCAGG	50	N/A	N/A	1603
949475	46431	46446	GCTGGGATATACGCCC	98	N/A	N/A	1604
949476	46505	46520	ACGGAGACCCTTACCT	129	N/A	N/A	1605
949477	46528	46543	TTGCAGATTAGCAGGG	35	N/A	N/A	1606
949478	46560	46575	ACAAACTGAGTGTTGA	73	N/A	N/A	1607
949479	46562	46577	ACACAAACTGAGTGTT	78	N/A	N/A	1608
949480	46577	46592	CGCAAGAAGACATTAA	54	N/A	N/A	1609
949481	46666	46681	GGCAGCATGGCTAAGC	75	N/A	N/A	1610
949482	46764	46779	ACGAAAGTGAGGAGTC	66	N/A	N/A	1611
949483	46766	46781	GGACGAAAGTGAGGAG	15	N/A	N/A	1612
949484	46863	46878	TACGAAATAGCAGAGC	17	N/A	N/A	1613
949485	46885	46900	GCCCATTGGCCCATCG	154	N/A	N/A	1614
949486	47094	47109	GATCACCCGCCACTGT	105	N/A	N/A	1615
949487	47352	47367	CACCAGGGACTCATTA	124	N/A	N/A	1616
949488	47466	47481	ACACAGTGGTGGTCCC	59	N/A	N/A	1617
949489	47517	47532	TGCTTTAAGGCTAACA	82	N/A	N/A	1618
949490	47599	47614	GGCCTGCGCTCTGTGC	87	N/A	N/A	1619
949491	47700	47715	TGCCCTAAGGCAAGTG	91	N/A	N/A	1620
949492	47797	47812	CAACAGCCACAGGATC	77	N/A	N/A	1621
949493	47803	47818	TTCCACCAACAGCCAC	25	N/A	N/A	1622
949494	47924	47939	AACTATGCATCCACCT	122	N/A	N/A	1623
949495	47927	47942	TGCAACTATGCATCCA	130	N/A	N/A	1624
949496	48220	48235	GGCTAGGTGGTGTGCG	116	N/A	N/A	1625
949497	48501	48516	GAGATTGGAGCCTGGT	33	N/A	N/A	1626
949498	48506	48521	AATAAGAGATTGGAGC	89	N/A	N/A	1627
949499	48507	48522	CAATAAGAGATTGGAG	69	N/A	N/A	1628
949500	48508	48523	GCAATAAGAGATTGGA	13	N/A	N/A	1629
949501	48622	48637	GTGAATCCAACAGACA	70	N/A	N/A	1630
949502	48748	48763	CAACATGCCTTCCAGT	124	N/A	N/A	1631
949503	48869	48884	TGCCACTCCCTATCCC	79	N/A	N/A	1632
949504	48972	48987	GCTTAATGCCTTGCCT	128	N/A	N/A	1633
949505	49052	49067	CCGCAATGTGTTCATT	42	N/A	N/A	1634
949506	49095	49110	GTATACCCCACAAGGC	73	N/A	N/A	1635
949507	49171	49186	GTAAAGGGTGGCAGCC	84	N/A	N/A	1636
949508	49196	49211	AGTCACTTTAACAAGT	57	N/A	N/A	1637

949509	49218	49233	GCTACCAAGGCACAGA	72	N/A	N/A	1638
949510	49265	49280	CATGGCCACGATGGCA	92	N/A	N/A	1639
949511	49297	49312	GAAGAGACAGCATACC	69	N/A	N/A	1640
949512	49403	49418	AGTTATGGTTCACTGG	29	N/A	N/A	1641
949513	49511	49526	ACTCAGAGTTTACGGG	91	N/A	N/A	1642
949514	49613	49628	TTCCGGTGAGCACACC	49	N/A	N/A	1643
949515	49770	49785	GAATCAGGAGGGAGAT	101	N/A	N/A	1644
949516	49888	49903	GGCAAGTGACCAGGTG	55	N/A	N/A	1645
949517	49896	49911	ACGAAGGCGGCAAGTG	6	N/A	N/A	1646
949518	50269	50284	GCAGAGAGAGTCCATT	38	N/A	N/A	1647
949519	50271	50286	GCGCAGAGAGAGTCCA	116	N/A	N/A	1648
949520	50402	50417	GCCCAGTAGGCAAGAA	117	N/A	N/A	1649
949521	50423	50438	AAGTAACCCCCATCAC	94	N/A	N/A	1650
949522	50491	50506	CTAGATACAAGGCTGC	62	N/A	N/A	1651
949523	50510	50525	CGCCAGCTTGGTCTGC	70	N/A	N/A	1652
949524	50597	50612	ACGCAAATATCTCCCA	41	N/A	N/A	1653
949525	50612	50627	CTAATCCGAGGCAATA	59	N/A	N/A	1654
949526	50654	50669	GCACACAACACTTCCC	41	N/A	N/A	1655
949527	50713	50728	GGCAGGATCCACTCAT	111	N/A	N/A	1656
949528	50818	50833	AGGAGAGGAGATCTGC	87	N/A	N/A	1657
949529	50847	50862	ACACAATGACGAGGCT	27	N/A	N/A	1658
949530	50945	50960	TGTTAGTCTCAGGGAA	54	N/A	N/A	1659
949531	50961	50976	ACAAACACGGCTCAGC	77	N/A	N/A	1660
949532	51078	51093	CGACACCCAGCTCCGG	95	N/A	N/A	1661
949533	51207	51222	TTGAAATGCCCAGGTC	37	N/A	N/A	1662
949534	51318	51333	TTCAAAGGAGCTTGTG	100	N/A	N/A	1663
949535	51433	51448	TGCAAGCTGCCACCTT	79	N/A	N/A	1664
949536	51496	51511	TGCTAAACAGTCAATC	62	N/A	N/A	1665
949537	51544	51559	AACCTAGGAGGACATC	62	N/A	N/A	1666
949538	51660	51675	CCCTACTGAAGCTGGA	71	N/A	N/A	1667
949539	51787	51802	AATCACGCTGCCAAGG	112	N/A	N/A	1668
949540	51890	51905	TCAGAGAGGTTCGCAG	57	N/A	N/A	1669
949541	51993	52008	CGGCAAACTGCAAAGC	67	N/A	N/A	1670
949542	52114	52129	CAACAAGCCACTGAGC	108	N/A	N/A	1671
949543	52204	52219	TAACAATCCACTGGCC	116	N/A	N/A	1672
949544	52243	52258	GCTCAAGTGCTGGAGA	89	N/A	N/A	1673
949545	52494	52509	CAAGATCCTACATGTA	79	N/A	N/A	1674
949546	52597	52612	TAAAAGCTTCCACCAG	119	N/A	N/A	1675
949547	52610	52625	CCCAATAGAGGTTTAA	100	N/A	N/A	1676
949548	52802	52817	TCTCATACTTCGGCCT	111	N/A	N/A	1677
949549	52918	52933	CAACAGAGGTTTTTTG	67	N/A	N/A	1678
949550	52944	52959	GTGAAAGTAAATGCTG	48	N/A	N/A	1679
949551	53030	53045	AACAGAACCACACCAG	216	N/A	N/A	1680

949552	53066	53081	CCAGAAAACCGTTTCT	93	N/A	N/A	1681
949553	53509	53524	ATGCAGGCTGGGAACC	88	N/A	N/A	1682
949554	53548	53563	TGCCAGACTTTGGAGC	92	N/A	N/A	1683
949555	53611	53626	CCCAAGTCCGCCCAGT	90	N/A	N/A	1684
949556	53712	53727	CTGAATCTAGGTGTCT	54	N/A	N/A	1685
949557	53847	53862	CTTGAATGTCCATGCC	60	N/A	N/A	1686
949558	53863	53878	ATATAGAGAGCTTTAC	104	N/A	N/A	1687
949559	53866	53881	CTAATATAGAGAGCTT	51	N/A	N/A	1688
949560	53867	53882	TCTAATATAGAGAGCT	78	N/A	N/A	1689
949561	53909	53924	CCCCATAACACTTACT	98	N/A	N/A	1690
949562	54006	54021	AGCTACTCTCTCAAGT	53	N/A	N/A	1691
949563	54011	54026	GGGCAAGCTACTCTCT	126	N/A	N/A	1692
949564	54127	54142	AGCTACGGTCTGAGCA	114	N/A	N/A	1693
949565	54237	54252	AGTCAGAGGGCCTGCC	58	N/A	N/A	1694
949566	54341	54356	GCTCACTTTGGATTGT	48	N/A	N/A	1695
949567	54452	54467	GTCTACAAAGCCCAGC	67	N/A	N/A	1696
949568	54562	54577	AAAGAGACCATCTCCC	91	N/A	N/A	1697
949569	54673	54688	GGGAAACACTCGGCCG	142	N/A	N/A	1698
949570	54784	54799	CAATGAGGACATCTGC	59	N/A	N/A	1699
949571	54787	54802	GGGCAATGAGGACATC	54	N/A	N/A	1700
949572	54890	54905	AGGAACTTCGCCTCTT	112	N/A	N/A	1701
949573	54924	54939	TCCTAAGCCAGATAGC	49	N/A	N/A	1702
949574	55043	55058	TCTAAGATCCCCATTT	106	N/A	N/A	1703
949575	55144	55159	TTTCACCGTCCCATCA	72	N/A	N/A	1704
949576	55247	55262	AATAACACAGCCATGC	84	N/A	N/A	1705
949577	55348	55363	ACCCACCCCGGAGATG	100	N/A	N/A	1706
949578	55383	55398	TAATAAGTCACACTGG	47	N/A	N/A	1707
949579	55384	55399	GTAATAAGTCACACTG	107	N/A	N/A	1708
949580	55469	55484	CTATGATCTATGATCA	115	N/A	N/A	1709
949581	55678	55693	TCCGTATAAGATGTGA	34	N/A	N/A	1710
949582	56054	56069	CTATTATCCAGCACTG	56	N/A	N/A	1711
949583	56111	56126	AGCTACTGTAGTGATG	81	N/A	N/A	1712
949584	56167	56182	TCGAATTTTCAGAGTA	26	N/A	N/A	1713
949585	56229	56244	ACGGAAGGTGGCTGCC	61	N/A	N/A	1714
949586	56251	56266	GCAAATATAAGGCATG	60	N/A	N/A	1715
949587	56268	56283	CACAGATTGAGGACAA	47	N/A	N/A	1716
949588	56319	56334	TGACAAGCAGTGTGGG	48	N/A	N/A	1717
949589	56371	56386	GGTATCTGAAAGTCAC	9	N/A	N/A	1718
949590	56530	56545	CCACAAGGTAGAGGGA	154	N/A	N/A	1719
949591	56538	56553	CAAGGAGCCCACAAGG	114	N/A	N/A	1720
949592	56633	56648	GCCCAAGTCCTTGTGG	105	N/A	N/A	1721
949593	56691	56706	GATTAAGGTGATGCTG	61	N/A	N/A	1722
949594	56692	56707	TGATTAAGGTGATGCT	41	N/A	N/A	1723

949595	56734	56749	AGGAAGCACCAGGATA	23	N/A	N/A	1724
949596	56860	56875	CATATTATGAATCCCC	66	N/A	N/A	1725
949597	56863	56878	TGACATATTATGAATC	105	N/A	N/A	1726
949598	56979	56994	ATGACAAGGGTCTTGG	17	N/A	N/A	1727
949599	57373	57388	TAATGACCCAGGCTGG	121	N/A	N/A	1728
949600	57619	57634	GCCTACCGTGTGGCGA	104	N/A	N/A	1729
949601	57654	57669	CCAGAAACGGTCAGTG	132	N/A	N/A	1730
949602	57722	57737	TGTGAATGGGCACATG	102	N/A	N/A	1731
949603	57840	57855	CAAACAACTTCTTGGC	82	N/A	N/A	1732
949604	57948	57963	GAAGACTGGTTCTGGC	60	N/A	N/A	1733
949605	57953	57968	TTACAGAAGACTGGTT	91	N/A	N/A	1734
949606	58891	58906	GGCAAGGTGGCTAAAA	123	N/A	N/A	1735
949607	58993	59008	AGGAACCCATCATGGT	95	N/A	N/A	1736
949608	59092	59107	TGACAAGGTAGGTTTT	57	N/A	N/A	1737
949609	59093	59108	TTGACAAGGTAGGTTT	25	N/A	N/A	1738
949610	59102	59117	CAAAACTGGTTGACAA	47	N/A	N/A	1739
949611	59104	59119	TGCAAAACTGGTTGAC	58	N/A	N/A	1740
949612	59272	59287	GTGAAGTGCAGTAGCT	88	N/A	N/A	1741
949613	59302	59317	TAAGATAGAGGGTCTT	35	N/A	N/A	1742
949614	59399	59414	GCTAACAATTTAAGGA	60	N/A	N/A	1743
949615	59741	59756	CTGAGAGGCATACAAA	66	N/A	N/A	1744
949616	59846	59861	GGAGAAGAAGTGAGCC	109	N/A	N/A	1745
949617	60067	60082	ACAAATGGATGAGGCC	129	N/A	N/A	1746
949618	60068	60083	GACAAATGGATGAGGC	54	N/A	N/A	1747
949619	60379	60394	GACAAACAGATGAGGC	74	N/A	N/A	1748
949620	60427	60442	GAATAAATTTCAGCCC	100	N/A	N/A	1749
949621	60483	60498	TTCAATGGCACAGTTC	73	N/A	N/A	1750
949622	60586	60601	TCAGACTTGAGGATGT	32	N/A	N/A	1751
949623	60639	60654	GCACAAACAGGCCCGC	99	N/A	N/A	1752
949624	60700	60715	GTCAAGTTCAACACTG	25	N/A	N/A	1753
949625	60903	60918	GCTCAGGGTTACCTTG	81	N/A	N/A	1754
949626	61033	61048	AGGAAGTGCCATGTTC	64	N/A	N/A	1755
949627	61134	61149	TCCCACTCTGGCAACA	79	N/A	N/A	1756
949628	61204	61219	AGCTAGATGGGACCTA	102	N/A	N/A	1757
949629	61255	61270	GAAGTTCCCGTTCTGA	47	N/A	N/A	1758
949630	61336	61351	AAATAGACGATCTCAC	87	N/A	N/A	1759
949631	61340	61355	AGGGAAATAGACGATC	96	N/A	N/A	1760
949632	61344	61359	TCGAAGGGAAATAGAC	101	N/A	N/A	1761
949633	61382	61397	GTAGAAGGATCTGACT	114	N/A	N/A	1762
949634	61384	61399	CAGTAGAAGGATCTGA	123	N/A	N/A	1763
949635	61480	61495	GTGAAGATCTCTGGTG	88	N/A	N/A	1764
949636	61485	61500	CCAGAGTGAAGATCTC	119	N/A	N/A	1765
949637	61587	61602	CTGCAGATCAACTGCT	104	N/A	N/A	1766

949638	61636	61651	CCACAAGTCATTCCAG	71	N/A	N/A	1767
949639	61706	61721	TTCCAGGACTACCTCT	76	N/A	N/A	1768
949640	61813	61828	GGCTTTGGGAAACCTC	48	N/A	N/A	1769
949641	61839	61854	TATTAAGGACAACCTC	98	N/A	N/A	1770
949642	61840	61855	TTATTAAGGACAACCT	81	N/A	N/A	1771
949643	61842	61857	TGTTATTAAGGACAAC	125	N/A	N/A	1772
949644	61889	61904	TGGCACACGGCAAATA	96	N/A	N/A	1773
949645	61904	61919	TCATAAGGGTGAGCCT	70	N/A	N/A	1774
949646	61915	61930	TCACAGGGTGGTCATA	68	N/A	N/A	1775
949647	61937	61952	GAAGATGGTCACAGCC	51	N/A	N/A	1776
949648	61944	61959	GTCGAATGAAGATGGT	38	N/A	N/A	1777
949649	62105	62120	GGCCTGAAAGAGCCCA	112	N/A	N/A	1778
949650	62252	62267	GATAAGGACCCCACCC	108	N/A	N/A	1779
949651	62328	62343	AAAGAAGGAGTTACGG	88	N/A	N/A	1780
949652	62378	62393	ACGAATGCATACAAAT	72	N/A	N/A	1781
949653	62384	62399	TGAAAAACGAATGCAT	107	N/A	N/A	1782
949654	62491	62506	CACCAGTGGCTGTCTG	63	N/A	N/A	1783
949655	62887	62902	TCATAATAGGCCGGGT	61	N/A	N/A	1784
949656	62969	62984	ATAATAACCACCGAAG	45	N/A	N/A	1785
949657	62972	62987	ATAATAATAACCACCG	13	N/A	N/A	1786
949658	63350	63365	CCTAGGATTTGTGTTA	101	N/A	N/A	1787
949659	63667	63682	GCCTAGGATTTATAGA	96	N/A	N/A	1788
949660	63759	63774	CCACAAATGAATGGTA	72	N/A	N/A	1789
949661	63780	63795	TGGGATGTGGTCTGGT	98	N/A	N/A	1790
949662	63826	63841	CTAATTACCAGCTAAC	46	N/A	N/A	1791
949663	63880	63895	ACTTAGGTTACTCCTA	76	N/A	N/A	1792
949664	64255	64270	AACTGCTGCTCCGATA	53	N/A	N/A	1793
949665	64313	64328	GGCTATAGGGCTGATA	104	N/A	N/A	1794
949666	64366	64381	AAATGCACCGCTCTGC	137	N/A	N/A	1795
949667	64530	64545	ACAGAATAAGACATCG	55	N/A	N/A	1796
949668	64650	64665	AGCAATCGCACATGCC	92	N/A	N/A	1797
949669	64984	64999	AGTAGATGCCAGAGGG	54	N/A	N/A	1798
949670	65026	65041	GGCTAAGCATGAAGGG	96	N/A	N/A	1799
949671	65086	65101	ATCTATCTCAGACATC	110	N/A	N/A	1800
949672	65109	65124	CCAAGGTCTGAACTTT	69	N/A	N/A	1801
949673	65111	65126	AACCAAGGTCTGAACT	125	N/A	N/A	1802
949674	65112	65127	CAACCAAGGTCTGAAC	110	N/A	N/A	1803
949675	65113	65128	GCAACCAAGGTCTGAA	31	N/A	N/A	1804
949676	65115	65130	TGGCAACCAAGGTCTG	67	N/A	N/A	1805
949677	65116	65131	CTGGCAACCAAGGTCT	120	N/A	N/A	1806
949678	65117	65132	GCTGGCAACCAAGGTC	156	N/A	N/A	1807
949679	65119	65134	ATGCTGGCAACCAAGG	40	N/A	N/A	1808
949680	65192	65207	GAATTTAGCCCTGACA	94	N/A	N/A	1809

949681	65208	65223	AGCTAAACAGGGTTTT	78	N/A	N/A	1810
949682	65343	65358	GTCCAAGGGCAGCCGG	100	N/A	N/A	1811
949683	65383	65398	CCCCAAAGGCCCTTAG	97	N/A	N/A	1812
949684	65458	65473	GTGGACATCAGTGAGT	53	N/A	N/A	1813
949685	65527	65542	CTACAAGTGAGCTGAG	6	N/A	N/A	1814
949686	65543	65558	CAAAACGGGAGCAGGC	83	N/A	N/A	1815
949687	65544	65559	ACAAAACGGGAGCAGG	51	N/A	N/A	1816
949688	65545	65560	CACAAAACGGGAGCAG	76	N/A	N/A	1817
949689	65583	65598	AAAAAGGGTCCAGTGG	91	N/A	N/A	1818
949690	65599	65614	TCATTAGTACGCCAGG	24	N/A	N/A	1819
949691	65686	65701	CCCAACTGTGCTTTCC	26	N/A	N/A	1820
949692	66037	66052	TCACACACGGATTTTT	73	N/A	N/A	1821
949693	66148	66163	TTCTGCATTGCAGTGG	26	N/A	N/A	1822
949694	66218	66233	GTAAAAAGCATCTGGC	83	N/A	N/A	1823
949695	66272	66287	GCCAGAGTCACCATCA	73	N/A	N/A	1824
949696	66327	66342	TGCCAAGGTGAGGTCA	91	N/A	N/A	1825
949697	66373	66388	CGCCAGATCTCTCTTG	104	N/A	N/A	1826
949698	66787	66802	TGCCTACCATTGCACT	86	N/A	N/A	1827
949699	66882	66897	CGAGAAGGAGGTAGAA	82	N/A	N/A	1828
949700	66890	66905	AACTACACCGAGAAGG	101	N/A	N/A	1829
949701	66895	66910	TCCAAAACTACACCGA	72	N/A	N/A	1830
949702	66973	66988	ATCAAACGAGTATATT	91	N/A	N/A	1831
949703	66974	66989	TATCAAACGAGTATAT	101	N/A	N/A	1832
949704	66987	67002	AGCTAAAATCCACTAT	110	N/A	N/A	1833
949705	66998	67013	CAATAGGGAAGAGCTA	57	N/A	N/A	1834
949706	66999	67014	GCAATAGGGAAGAGCT	117	N/A	N/A	1835
949707	67000	67015	AGCAATAGGGAAGAGC	75	N/A	N/A	1836
949708	67377	67392	ATCAAGACTCTGAATA	86	N/A	N/A	1837
949709	67669	67684	TTCAAAGATAGGTGAG	32	N/A	N/A	1838
949710	67762	67777	CATTAAGTATTTGGAG	77	N/A	N/A	1839
949711	67770	67785	AAGAGCAACATTAAGT	111	N/A	N/A	1840
949712	67773	67788	GCGAAGAGCAACATTA	120	N/A	N/A	1841
949713	67793	67808	TGCGAATGCACATGGC	138	N/A	N/A	1842
949714	67803	67818	ACACAGAGGGTGCGAA	153	N/A	N/A	1843
949715	67805	67820	CAACACAGAGGGTGCG	47	N/A	N/A	1844
949716	67823	67838	TAACATGTTACTCAGA	75	N/A	N/A	1845
949717	67870	67885	TCAAGTATAGAGATGG	46	N/A	N/A	1846
949718	68110	68125	AGTACCTGATTCAGCG	147	N/A	N/A	1847
949719	68180	68195	TGCCAGTGAGGATTGC	56	N/A	N/A	1848
949720	68210	68225	AAAACAAGTGCTGCTC	77	N/A	N/A	1849
949721	68491	68506	GAATCAAGTACATTTC	77	N/A	N/A	1850
949722	68541	68556	GTAATAGTAGCAGCAC	29	N/A	N/A	1851
949723	68542	68557	TGTAATAGTAGCAGCA	20	N/A	N/A	1852

949724	68610	68625	GTCTTCTGGGTAAATG	30	N/A	N/A	1853
949725	68624	68639	AGGCAATGCATACAGT	25	N/A	N/A	1854
949726	68992	69007	GAACGATAGGCCAGGC	90	N/A	N/A	1855
949727	68999	69014	AAGAAGAGAACGATAG	67	N/A	N/A	1856
949728	69029	69044	GTTTATGCACCATGTG	20	N/A	N/A	1857
949729	69102	69117	AAAACAGCGAGGAGGA	90	N/A	N/A	1858
949730	69108	69123	TGCTAGAAAACAGCGA	109	N/A	N/A	1859
949731	69206	69221	CAGGAACCTACTCTCG	86	N/A	N/A	1860
949732	69213	69228	ACAAGGACAGGAACCT	97	N/A	N/A	1861
949733	69215	69230	CTACAAGGACAGGAAC	107	N/A	N/A	1862
949734	69361	69376	CTAGACACTGACTTCC	89	N/A	N/A	1863
949735	69486	69501	GGCCAGCTGGACTTTT	74	N/A	N/A	1864
949736	69589	69604	TACTAGGGCACTTAAG	149	N/A	N/A	1865
949737	69591	69606	GATACTAGGGCACTTA	69	N/A	N/A	1866
949738	69692	69707	ACCAAGGGTCCCTGCC	113	N/A	N/A	1867
949739	69781	69796	TACAAAGTGTCTGGCG	53	N/A	N/A	1868
949740	69782	69797	ATACAAAGTGTCTGGC	41	N/A	N/A	1869
949741	70034	70049	GATTAGGAGACAAGCC	87	N/A	N/A	1870
949742	70467	70482	ATCCATTCTGGACAAC	62	N/A	N/A	1871
949743	70664	70679	CACTAGAGGATAGGCG	118	N/A	N/A	1872
949744	70759	70774	GTAAAGCAGAGTTTGG	25	N/A	N/A	1873
949745	70760	70775	TGTAAAGCAGAGTTTG	46	N/A	N/A	1874
949746	70766	70781	GCAAAGTGTAAAGCAG	53	N/A	N/A	1875
949747	70787	70802	CCATAAAATCAGCCTA	71	N/A	N/A	1876
949748	70897	70912	AAAGAACTCGGGAGGT	65	N/A	N/A	1877
949749	71020	71035	TTAAGATCAAGAGATC	115	N/A	N/A	1878
949750	71155	71170	TCAAGATGAGCTCCCC	65	N/A	N/A	1879
949751	71255	71270	GTCCATCCAGACCACG	119	N/A	N/A	1880
949752	71260	71275	GGACAGTCCATCCAGA	84	N/A	N/A	1881
949753	71369	71384	GGAGACGGCACGGAGC	81	N/A	N/A	1882
949754	71371	71386	ACGGAGACGGCACGGA	87	N/A	N/A	1883
949755	71473	71488	ACCAAGGGCCAACACC	70	N/A	N/A	1884
949756	71697	71712	ACATACTGCAGCAGGG	52	N/A	N/A	1885
949757	71797	71812	AATCAATGAGTGGACG	29	N/A	N/A	1886
949758	71827	71842	ACGCAGAAGGCTTGCA	87	N/A	N/A	1887
949759	71908	71923	CCATTCTGAGCACTCC	41	N/A	N/A	1888
949760	72021	72036	TCTAAAGGAGGCTGTT	82	N/A	N/A	1889
949761	72175	72190	AGCCTAATTTTGCAAT	133	N/A	N/A	1890
949762	72938	72953	GGCCAACACTCATCTT	128	N/A	N/A	1891
949763	73188	73203	TGATATGCAGTGACAC	75	N/A	N/A	1892
949764	73296	73311	TCCCACACGGCTCCTG	144	N/A	N/A	1893
949765	73415	73430	GCACAACCTGCTCTAT	80	N/A	N/A	1894
949766	73519	73534	GAGCACCTGAGTCAGT	91	N/A	N/A	1895

949767	73639	73654	ACCAACCAAGTCATGG	137	N/A	N/A	1896
949768	73653	73668	AGCTAAGCAGCTGCAC	133	N/A	N/A	1897
949769	73742	73757	TTACAGGCCAAAAGCC	88	N/A	N/A	1898
949770	73868	73883	GAGGAGGCGGTGTCCT	122	N/A	N/A	1899
949771	73954	73969	CATAAAAGCACTCTGG	87	N/A	N/A	1900
949772	73957	73972	GAGCATAAAAGCACTC	92	N/A	N/A	1901
949773	73970	73985	GTCAAGGCTGTCTGAG	56	N/A	N/A	1902
949774	74231	74246	GCTGAATCTTGTGTTT	47	N/A	N/A	1903
949775	74259	74274	CACAACAACACTTCCT	73	N/A	N/A	1904
949776	74351	74366	CTTTAGAGGTGCAGAA	53	N/A	N/A	1905
949777	74592	74607	ATCCACTGAAGCCTCT	50	N/A	N/A	1906
949778	74872	74887	CTTAACAAGTAGTATT	14	N/A	N/A	1907
949779	74874	74889	GGCTTAACAAGTAGTA	38	N/A	N/A	1908
949780	74962	74977	GGCAACTGGTTACAAA	58	N/A	N/A	1909
949781	74967	74982	TGCAAGGCAACTGGTT	14	N/A	N/A	1910
949782	75001	75016	CTCCATGGTGAGAGTG	73	N/A	N/A	1911
949783	75055	75070	GCTAAAGCAAGAAGGC	87	N/A	N/A	1912
949784	75104	75119	AGAAAGACCGCCCATG	97	N/A	N/A	1913
949785	75219	75234	GCGGAGACAGAAGGCT	121	N/A	N/A	1914
949786	75320	75335	AAGCATCGGTTAAGGC	142	N/A	N/A	1915
949787	75846	75861	CCCAAGTGGTGAGGCT	74	N/A	N/A	1916
949788	76007	76022	GTTCAGGCAGGCGGTT	53	N/A	N/A	1917
949789	76107	76122	AACAAGAGACCTTGTC	47	N/A	N/A	1918
949790	76211	76226	GATCAGGCTACTCAGG	116	N/A	N/A	1919
949791	76415	76430	TCATAGCCAATATAAC	42	N/A	N/A	1920
949792	76430	76445	TATCACAGGGTGTGCT	67	N/A	N/A	1921
949793	76487	76502	TCGGAATGTACTCTTA	23	N/A	N/A	1922
949794	76518	76533	GAATTCGGGTTGAATC	107	N/A	N/A	1923
949795	76636	76651	GACAAAGCACACCTGG	81	N/A	N/A	1924
949796	76637	76652	GGACAAAGCACACCTG	100	N/A	N/A	1925
949797	76731	76746	CACTAAACTAATGACA	98	N/A	N/A	1926
949798	76734	76749	TAGCACTAAACTAATG	88	N/A	N/A	1927
949799	76737	76752	GCATAGCACTAAACTA	83	N/A	N/A	1928
949800	76739	76754	AGGCATAGCACTAAAC	80	N/A	N/A	1929
949801	76744	76759	AGCAAAGGCATAGCAC	91	N/A	N/A	1930
949802	76764	76779	ACCAAACCAGGACCAA	57	N/A	N/A	1931
949803	77124	77139	GTTAATGCTTCACCTG	25	N/A	N/A	1932
949804	77125	77140	GGTTAATGCTTCACCT	104	N/A	N/A	1933
949805	77175	77190	GTAAAGGGTGTGCACA	10	N/A	N/A	1934
949806	77224	77239	AGGCAAGCACAAGCTG	115	N/A	N/A	1935
949807	77245	77260	CCTTCATACCCCAACT	97	N/A	N/A	1936
949808	77343	77358	TACTGAAGTACCTGGG	102	N/A	N/A	1937
949809	77421	77436	TCCTAAGCATTCCTAA	113	N/A	N/A	1938

949810	77450	77465	GTAGGATGATCTTGTT	27	N/A	N/A	1939
949811	77458	77473	GTAAAAAAGTAGGATG	68	N/A	N/A	1940
949812	77502	77517	CCTTAAAAAGAGTCTC	75	N/A	N/A	1941
949813	77561	77576	GCTCATCTAATGGACA	46	N/A	N/A	1942
949814	77634	77649	GGCGAGACAGAGTAAG	12	N/A	N/A	1943
949815	77894	77909	TATACTGGACACGGTG	96	N/A	N/A	1944
949816	77895	77910	ATATACTGGACACGGT	88	N/A	N/A	1945
949817	77897	77912	ATATATACTGGACACG	36	N/A	N/A	1946
949818	78035	78050	GTTTTATTGGCCGGGT	20	N/A	N/A	1947
949819	78144	78159	AGTCACTGATCCTAAA	74	N/A	N/A	1948
949820	78149	78164	CAAGAAGTCACTGATC	69	N/A	N/A	1949
949821	78222	78237	ACAAAATGGGTTGAGG	38	N/A	N/A	1950
949822	78223	78238	TACAAAATGGGTTGAG	50	N/A	N/A	1951
949823	78262	78277	GGACAGGACTTTGCCC	119	N/A	N/A	1952
949824	78348	78363	CCACAATTCAGGTGGC	122	N/A	N/A	1953
949825	78366	78381	GGAAAGGTAGCCACTT	64	N/A	N/A	1954
949826	78470	78485	GCCCACTTATTCCTCC	120	N/A	N/A	1955
949827	78561	78576	CCAAATTCAAGAGCTC	45	N/A	N/A	1956
949828	78611	78626	TACCATTTTTCAGCAG	25	N/A	N/A	1957
949829	78678	78693	TCAAAACGGAGGTTTC	20	N/A	N/A	1958
949830	78711	78726	GACCATCCTATGAGGA	106	N/A	N/A	1959
949831	78878	78893	GACCAGAGACGGGAGG	58	N/A	N/A	1960
949832	78949	78964	GCCTAGAGGTAGGAGC	64	N/A	N/A	1961
949833	78961	78976	CCACAAGTTCAGGCCT	107	N/A	N/A	1962
949834	79024	79039	TCAAAGCTGAGTGTCA	25	N/A	N/A	1963
949835	79143	79158	TGCTAGGGACATCTTC	17	N/A	N/A	1964
949836	79212	79227	GTATATATCAGCTCAG	30	N/A	N/A	1965
949837	79225	79240	ACATAAGGATGTTGTA	126	N/A	N/A	1966
949838	79243	79258	ATCCATGTTCAGTTTC	13	N/A	N/A	1967
949839	79330	79345	CGGAAAAAGAAGTCCC	154	N/A	N/A	1968
949840	79375	79390	TTCAAGCAAATCACAC	96	N/A	N/A	1969
949841	79794	79809	TCAGTATGCACCACCA	6	N/A	N/A	1970
949842	79870	79885	AAGCATGACATGACAC	16	N/A	N/A	1971
949843	80250	80265	CAGAATATTTAACTCG	26	N/A	N/A	1972
949844	80347	80362	GACAAACCAAGCACAT	107	N/A	N/A	1973
949845	80435	80450	GTGGAACTTGCCTGAC	86	N/A	N/A	1974
949846	80542	80557	TCCAAGAGCCCTCTTA	11	N/A	N/A	1975
949847	80662	80677	CCTATTTGATCAGGAG	137	N/A	N/A	1976
949848	80759	80774	TGATTCAGTGCCGCCC	7	N/A	N/A	1977
949849	80769	80784	CCCAAAACCCTGATTC	17	N/A	N/A	1978
949850	80805	80820	TCACGAGGAAGCCATG	54	N/A	N/A	1979
949851	80870	80885	GGCGATGGAAGGGCAG	57	N/A	N/A	1980
949852	80981	80996	TTTCATTGGCCCTGGC	62	N/A	N/A	1981

949853	80987	81002	CAGCAATTTCATTGGC	63	N/A	N/A	1982
949854	81187	81202	TACCTTACTGGTACAC	67	N/A	N/A	1983
949855	81200	81215	GCCGAGGGAGCAATAC	102	N/A	N/A	1984
949856	81201	81216	TGCCGAGGGAGCAATA	49	N/A	N/A	1985
949857	81288	81303	GAAAAGGCACCAGTGG	39	N/A	N/A	1986
949858	81306	81321	CACAAAGCGATATGGG	7	N/A	N/A	1987
949859	81411	81426	GTGCATCTGTCTGGCC	79	N/A	N/A	1988
949860	81445	81460	TGCTAGGCTTGGTATC	95	N/A	N/A	1989
949861	81530	81545	CAGCAGTTGACGCGGG	127	N/A	N/A	1990
949862	81635	81650	CCGGAGCTGAGGGACA	117	N/A	N/A	1991
949863	81738	81753	AAAAATGGGCTGCCCC	103	N/A	N/A	1992
949864	81740	81755	CCAAAAATGGGCTGCC	90	N/A	N/A	1993
949865	81752	81767	GACTAAGTGGATCCAA	2	N/A	N/A	1994
949866	81769	81784	GCGCATAGAGGCACTG	56	N/A	N/A	1995
949867	81845	81860	AACCAGGCCCGCGGCG	90	N/A	N/A	1996
949868	81909	81924	GCGCAAGCACAGACTG	109	N/A	N/A	1997
949869	81953	81968	GCAGAAATTCCCTGGC	92	N/A	N/A	1998
949870	82004	82019	AGCTTAAGCAGCAAAT	111	N/A	N/A	1999
949871	82041	82056	TTTGGACTGTTTTCCC	8	N/A	N/A	2000
949872	82043	82058	TGTTTGGACTGTTTTC	2	N/A	N/A	2001
949873	82044	82059	CTGTTTGGACTGTTTT	1	N/A	N/A	2002
949874	82045	82060	CCTGTTTGGACTGTTT	1	N/A	N/A	2003
949875	82047	82062	AACCTGTTTGGACTGT	4	N/A	N/A	2004
949876	82048	82063	CAACCTGTTTGGACTG	5	N/A	N/A	2005
949877	82050	82065	TCCAACCTGTTTGGAC	27	N/A	N/A	2006
949878	82052	82067	TTTCCAACCTGTTTGG	44	N/A	N/A	2007
949879	82053	82068	TTTTCCAACCTGTTTG	17	N/A	N/A	2008
949880	82054	82069	GTTTTCCAACCTGTTT	4	N/A	N/A	2009
949881	82084	82099	ATGTCCATGACACCTG	17	N/A	N/A	2010
949882	82085	82100	CATGTCCATGACACCT	39	N/A	N/A	2011
949883	82087	82102	TTCATGTCCATGACAC	30	N/A	N/A	2012
949884	82089	82104	CATTCATGTCCATGAC	13	N/A	N/A	2013
949885	82091	82106	AACATTCATGTCCATG	51	N/A	N/A	2014
949886	82154	82169	TACAGAAGGGCCACGG	6	N/A	N/A	2015
949887	82155	82170	TTACAGAAGGGCCACG	10	N/A	N/A	2016
949888	82259	82274	GATTAGTCCATGCATG	99	N/A	N/A	2017
949889	82308	82323	ACACACGCAGGACAGG	85	N/A	N/A	2018
949890	82361	82376	GGTCATGCGGAGGGCA	41	N/A	N/A	2019
949891	82509	82524	TGTTACCTTCTCGGCA	19	N/A	N/A	2020
949892	82529	82544	GCGGAGATGAGAACAA	13	N/A	N/A	2021
949893	82619	82634	CTGGTAGGCGGAAGGG	77	N/A	N/A	2022
949894	82632	82647	CTCTAAGTGACAACTG	18	N/A	N/A	2023
949895	82720	82735	AACAAAGGCTGACCGC	85	N/A	N/A	2024

949896	82827	82842	GATGATGTGTTTCCTG	1	N/A	N/A	2025
949897	82836	82851	GGCTATACAGATGATG	7	N/A	N/A	2026
949898	82948	82963	AACCAGACCTCATGCA	22	N/A	N/A	2027
949899	82953	82968	AACTTAACCAGACCTC	12	N/A	N/A	2028
949900	82994	83009	CGCCAAATGCCCCCAC	29	N/A	N/A	2029
949901	83049	83064	GATAGGAACTCCTTGC	48	N/A	N/A	2030
949902	83051	83066	TCGATAGGAACTCCTT	96	N/A	N/A	2031
949903	83124	83139	CTGAAGGGCCTCGCCA	119	N/A	N/A	2032
949904	83183	83198	TGCCATGCAGGGCTTC	74	N/A	N/A	2033
949905	83283	83298	GTGGACCGGAGACAGC	125	N/A	N/A	2034
949906	83399	83414	TAGAAAATGCGGAGGG	91	N/A	N/A	2035
949907	83424	83439	CGGGAAGCAACATGAA	77	N/A	N/A	2036
949908	83429	83444	TGGCACGGGAAGCAAC	87	N/A	N/A	2037
949909	83464	83479	GAACAAGCAGAGTGGT	51	N/A	N/A	2038
949910	83566	83581	GGCCAGTACCTGGTCC	103	N/A	N/A	2039
949911	83622	83637	GAACAGTACACTTGAC	90	N/A	N/A	2040
949912	83627	83642	GCACAGAACAGTACAC	100	N/A	N/A	2041
949942	83908	83923	GGTTGACTACAAAGGG	5	N/A	N/A	2042
949943	83909	83924	AGGTTGACTACAAAGG	3	N/A	N/A	2043
949944	83911	83926	AGAGGTTGACTACAAA	4	N/A	N/A	2044
949945	83912	83927	GAGAGGTTGACTACAA	2	N/A	N/A	2045
949946	83914	83929	TTGAGAGGTTGACTAC	66	N/A	N/A	2046
949947	83916	83931	TTTTGAGAGGTTGACT	21	N/A	N/A	2047
949948	83918	83933	GTTTTTGAGAGGTTGA	2	N/A	N/A	2048
949949	83919	83934	GGTTTTTGAGAGGTTG	3	N/A	N/A	2049
949950	83920	83935	GGGTTTTTGAGAGGTT	5	N/A	N/A	2050
949951	83922	83937	GTGGGTTTTTGAGAGG	17	N/A	N/A	2051
949952	83923	83938	TGTGGGTTTTTGAGAG	25	N/A	N/A	2052
949953	83924	83939	CTGTGGGTTTTTGAGA	38	N/A	N/A	2053
949954	83926	83941	GCCTGTGGGTTTTTGA	24	N/A	N/A	2054
949955	84164	84179	CCATAACTTACTGAAG	69	N/A	N/A	2055
949956	84276	84291	GTAGGATAGGGAGCGG	31	N/A	N/A	2056
949957	84379	84394	TCCCAAATGCAGACGC	38	N/A	N/A	2057
949958	84397	84412	ACAAACAACACGCTTG	88	N/A	N/A	2058
949959	84399	84414	CAACAAACAACACGCT	88	N/A	N/A	2059
949960	84687	84702	AATTAGGTGGGTAAAG	64	N/A	N/A	2060
949961	84860	84875	GCCTTTGCAAGAAAGC	94	N/A	N/A	2061
949962	85204	85219	GGTTTCAACAAACAGT	11	N/A	N/A	2062
949963	85243	85258	AACAAAGTGACATAGC	8	N/A	N/A	2063
949964	85260	85275	GGAGAGGGACCATTTT	94	N/A	N/A	2064
949965	85323	85338	AATCAAAACTGGGCGC	100	N/A	N/A	2065
949966	85335	85350	AGCAATTGGCCAAATC	55	N/A	N/A	2066
949967	85362	85377	GGCATAGGTGGACTGG	21	N/A	N/A	2067

949968	85379	85394	AGCTACAGCAGCTATG	83	N/A	N/A	2068
949969	85438	85453	CTTACCAACAGTAACA	67	N/A	N/A	2069
949970	85541	85556	GGCTGGTTTAGTAAGG	75	N/A	N/A	2070
949971	85608	85623	GGGCAAGGCACTCGGA	54	N/A	N/A	2071
949972	85618	85633	GAATAAAGTAGGGCAA	44	N/A	N/A	2072
949973	85681	85696	CGTCACTGGACTCCCC	75	N/A	N/A	2073
949974	85784	85799	CCAGGATGAAGTTGGT	94	N/A	N/A	2074
949975	85876	85891	ATCAAGCTAGAAAGGT	19	N/A	N/A	2075
949976	85880	85895	AGCTATCAAGCTAGAA	82	N/A	N/A	2076
949977	85884	85899	CTCAAGCTATCAAGCT	120	N/A	N/A	2077
949978	85946	85961	CCAATTATGAACACTA	7	N/A	N/A	2078
949979	85984	85999	GTTCAAAGTGTTGCAT	9	N/A	N/A	2079
949980	86329	86344	AGCCACTGCCTTGTAT	74	N/A	N/A	2080
949981	86547	86562	AATCATAGCCTCAAAC	85	N/A	N/A	2081
949982	86551	86566	GAACAATCATAGCCTC	14	N/A	N/A	2082
949983	86933	86948	AATAATGTGCAGTTGT	14	N/A	N/A	2083
949984	87041	87056	CCCCAAGGTCTGGAGT	104	N/A	N/A	2084
949985	87160	87175	TCCCAGACAGGAGAAC	80	N/A	N/A	2085
949986	87349	87364	ACCTACTTGGCAAACC	128	N/A	N/A	2086
949987	87359	87374	CTCTAAAAGTACCTAC	127	N/A	N/A	2087
949988	87456	87471	CGACAGAGACTGTCTG	130	N/A	N/A	2088
949989	87574	87589	CTAAACTAACCATGGG	79	N/A	N/A	2089
949990	87595	87610	GAACATAGCACTGCCC	3	N/A	N/A	2090
949991	87597	87612	CTGAACATAGCACTGC	3	N/A	N/A	2091
949992	87598	87613	TCTGAACATAGCACTG	9	N/A	N/A	2092
949993	87680	87695	GCACACTGGTCGCTAA	43	N/A	N/A	2093
949994	87782	87797	TTGAAGCTAGGGAGAC	85	N/A	N/A	2094
949995	87817	87832	ACGGAAGGTTCTGGTT	69	N/A	N/A	2095
949996	87880	87895	GCACACTGAATCGACA	23	N/A	N/A	2096
949997	87882	87897	ACGCACACTGAATCGA	43	N/A	N/A	2097
949998	87893	87908	TGCCTGAGACCACGCA	152	N/A	N/A	2098
949999	88002	88017	TACCAGCGGCACCACC	72	N/A	N/A	2099
950000	88014	88029	AGCGAGAGGGCATACC	30	N/A	N/A	2100
950001	88119	88134	CACTACACCTTAACGC	70	N/A	N/A	2101
950002	88226	88241	CTCTAGAGGCCCTCCC	98	N/A	N/A	2102
950003	88271	88286	CACCGATAAATGTTGT	27	N/A	N/A	2103
950004	88308	88323	CAGCACGGAACAGATC	51	N/A	N/A	2104
950005	88397	88412	AGGGACTTCGGCTCAT	120	N/A	N/A	2105
950006	88497	88512	GCAAACCAAAGATGGG	47	N/A	N/A	2106
950007	88619	88634	GGTAAGTGGGAAGGCC	73	N/A	N/A	2107
950008	88766	88781	CCCCGTAGCTCTTCAG	24	N/A	N/A	2108
950009	88878	88893	TTTAAGGACTCCACCT	86	N/A	N/A	2109
950010	88992	89007	TGGCATCACCTGACTT	99	N/A	N/A	2110

950011	89116	89131	ATCCAAAATCCTCCCC	43	N/A	N/A	2111
950012	89192	89207	TCAAATAGCAGCCCAC	38	N/A	N/A	2112
950013	89231	89246	CCTAAGGGCCTCCTGG	102	N/A	N/A	2113
950014	89335	89350	CACAAGAAGGATTTTC	2	N/A	N/A	2114
950015	89459	89474	CAGCAATCGACCCACC	31	N/A	N/A	2115
950016	89560	89575	GCTGAGATTACGCACC	38	N/A	N/A	2116
950017	89706	89721	CTTATCTGGGCTATTT	7	N/A	N/A	2117
950018	89719	89734	TATTATAGGGCTTCTT	20	N/A	N/A	2118
950019	89813	89828	GAAAGTAGGCTTCTGT	6	N/A	N/A	2119
950020	89966	89981	TGTTACTTATCCATCA	7	N/A	N/A	2120
950021	89980	89995	CAACATATATCTCCTG	8	N/A	N/A	2121
950022	90075	90090	ACAAATCCCACTATAT	58	N/A	N/A	2122
950023	90081	90096	GCATAGACAAATCCCA	3	N/A	N/A	2123
950024	90175	90190	CGACAGGGTGTGTTTC	6	N/A	N/A	2124
950025	90197	90212	AAATTTAGAGGACATC	38	N/A	N/A	2125
950026	90276	90291	AGCCATCCAGTCTTAG	38	N/A	N/A	2126
950027	90541	90556	CTCAAGTAGTTCCCCT	12	N/A	N/A	2127
950028	90642	90657	CACTAGAATCCCGGAG	18	N/A	N/A	2128
950029	90673	90688	ACTTACTAAAGCGCAG	24	N/A	N/A	2129
950030	90722	90737	AGTAAATGTATCTGGT	3	N/A	N/A	2130
950031	90754	90769	GCGCAAGGGAAACGGC	97	N/A	N/A	2131
950032	90804	90819	TGAGCAGCCACAGGTA	31	N/A	N/A	2132
950033	90806	90821	AGTGAGCAGCCACAGG	45	N/A	N/A	2133
950034	90807	90822	AAGTGAGCAGCCACAG	83	N/A	N/A	2134
950035	90808	90823	CAAGTGAGCAGCCACA	27	N/A	N/A	2135
950036	90810	90825	ACCAAGTGAGCAGCCA	14	N/A	N/A	2136
950037	90812	90827	GGACCAAGTGAGCAGC	54	N/A	N/A	2137
950038	90837	90852	GCGAATGTGGCCGTTC	64	N/A	N/A	2138
950039	90889	90904	GAACAGACAGGGTTCA	97	N/A	N/A	2139
950040	90978	90993	CGGGAGACTGCAGAGG	44	N/A	N/A	2140
950041	91083	91098	AGCAGATGGCCTGGTA	18	N/A	N/A	2141
950042	91189	91204	ACATAGGGCCTTCTGG	38	N/A	N/A	2142
950043	91226	91241	AGCCAAGAGTCAAGTT	36	N/A	N/A	2143
950044	91384	91399	CATGAGCCCACCACTC	120	N/A	N/A	2144
950045	91538	91553	CTCCTAACATGCTAGA	75	N/A	N/A	2145
950046	91825	91840	CGCTCAAGGGAAAAAT	25	N/A	N/A	2146
950047	91934	91949	TCCCAAGCTCCCCTGA	51	N/A	N/A	2147
950048	92034	92049	GATACAGCCGTTCATA	11	N/A	N/A	2148
950049	92059	92074	TAATAAGGTACTGAAG	54	N/A	N/A	2149
950050	92634	92649	ACGAAGCTAGGAGGCG	108	N/A	N/A	2150
950051	92635	92650	CACGAAGCTAGGAGGC	35	N/A	N/A	2151
950052	92814	92829	GCATGATAATCCCAGC	98	N/A	N/A	2152
950053	93110	93125	AGCCGCCCAGGCCAGA	96	N/A	N/A	2153

950054	93183	93198	GCAGAAATTTTGCGAA	35	N/A	N/A	2154
950055	93185	93200	AGGCAGAAATTTTGCG	48	N/A	N/A	2155
950056	93235	93250	GGTGGAGTCCCCGCCC	165	N/A	N/A	2156
950057	93248	93263	GTGCAAGGTACATGGT	11	N/A	N/A	2157
950058	93303	93318	CGCAAAAATAAATCAT	83	N/A	N/A	2158
950059	93304	93319	GCGCAAAAATAAATCA	105	N/A	N/A	2159
950060	93322	93337	ATGTATTACCTACGGC	7	N/A	N/A	2160
950061	93383	93398	CATATTCATGGTGTTA	10	N/A	N/A	2161
950062	93496	93511	AGAGATGGAAGGGACG	89	N/A	N/A	2162
950063	93586	93601	CCACACTAAGCATGTA	38	N/A	N/A	2163
950064	93600	93615	TCTAATGTTTGCTACC	7	N/A	N/A	2164
950065	93601	93616	CTCTAATGTTTGCTAC	4	N/A	N/A	2165
950066	93612	93627	ACCACTAGATTCTCTA	56	N/A	N/A	2166
950067	93648	93663	GAACAGGGAATATTAG	79	N/A	N/A	2167
950068	93744	93759	TTATACCCAGGGCAAC	37	N/A	N/A	2168
950069	93854	93869	TAAGTATTTGCCATCC	6	N/A	N/A	2169
950070	93908	93923	GCTTAAGCGAGATCTT	42	N/A	N/A	2170
950071	93921	93936	GAATTCTGGTCTGGCT	26	N/A	N/A	2171
950072	93958	93973	CATAGGAGATAGAAGG	4	N/A	N/A	2172
950073	93960	93975	TGCATAGGAGATAGAA	34	N/A	N/A	2173
950074	94019	94034	CACAAGAGGGCAAGAT	36	N/A	N/A	2174
950075	94050	94065	TGCTAGATCAACTAGC	7	N/A	N/A	2175
950076	94058	94073	GCAAAGAGTGCTAGAT	89	N/A	N/A	2176
950077	94060	94075	AGGCAAAGAGTGCTAG	78	N/A	N/A	2177
950078	94065	94080	GCACAAGGCAAAGAGT	89	N/A	N/A	2178
950079	94078	94093	TGCTAGAGGAGCGGCA	114	N/A	N/A	2179
950080	94153	94168	CTATAGAACAGGAGTG	15	N/A	N/A	2180
950081	94155	94170	TGCTATAGAACAGGAG	9	N/A	N/A	2181
950082	94164	94179	AGCCACATCTGCTATA	89	N/A	N/A	2182
950083	94176	94191	CCTTAATCACTTAGCC	7	N/A	N/A	2183
950084	94200	94215	TATCATATAGGGAGAA	16	N/A	N/A	2184
950085	94215	94230	GCATAGAGAAGAGGGT	6	N/A	N/A	2185
950086	94270	94285	GACAAGAGGCAGCATC	7	N/A	N/A	2186
950087	94333	94348	TCACAGGCCAAGGATA	81	N/A	N/A	2187
950088	94371	94386	TGGCAGGAAACGGTGC	42	N/A	N/A	2188
950089	94450	94465	GCAAATATGATTCATC	1	N/A	N/A	2189
950090	94481	94496	AAGGAGGTGTTACCCA	60	N/A	N/A	2190
950091	94581	94596	CTATGAGTAGCAGGCT	3	N/A	N/A	2191
950092	94652	94667	GTCCAAGTGTAAGAGC	12	N/A	N/A	2192
950093	94695	94710	GCAAAAGGGAGCCCCT	69	N/A	N/A	2193
950094	94696	94711	AGCAAAAGGGAGCCCC	88	N/A	N/A	2194
950095	94770	94785	TGCCAGAAGAGCCCCG	84	N/A	N/A	2195
950096	94791	94806	CTACAAGAAAGACCCT	30	N/A	N/A	2196

950097	94805	94820	TAGGATCGGCTCAGCT	18	N/A	N/A	2197
950098	94810	94825	TGGCATAGGATCGGCT	54	N/A	N/A	2198
950099	94920	94935	GAACACATGAGGAACC	24	N/A	N/A	2199
950100	94977	94992	GTACAAGGGAGAAGCA	100	N/A	N/A	2200
950101	95047	95062	GGCCACGCTCATGACG	97	N/A	N/A	2201
950102	95086	95101	GTAGAGATGGGAACCA	4	N/A	N/A	2202
950103	95155	95170	AAGCAGGGATCCTCTG	114	N/A	N/A	2203
950104	95189	95204	GCGGTATGGGTGGCAG	106	N/A	N/A	2204
950105	95227	95242	GGCTAGGGTGCACAGT	60	N/A	N/A	2205
950106	95278	95293	CTTAGAAGGAAGTAGG	100	N/A	N/A	2206
950107	95378	95393	CCGTTAGCCATCCACC	73	N/A	N/A	2207
950108	95416	95431	CCCTAGGGAGCTGCAA	112	N/A	N/A	2208
950109	95443	95458	CCACACGGGTTCAGAG	43	N/A	N/A	2209
950110	95496	95511	GCACACCAAGCCTTGG	63	N/A	N/A	2210
950111	95645	95660	AGGGATGTGCCCGCAC	87	N/A	N/A	2211
950112	95745	95760	TGACAACCAGGTGAGG	24	N/A	N/A	2212
950113	95854	95869	TGGGAATGCCTCCATT	95	N/A	N/A	2213
950114	95954	95969	AGCCCCTGTGAGGTCA	66	N/A	N/A	2214
950115	96079	96094	GTACAGACTTATCCCT	28	N/A	N/A	2215
950116	96081	96096	GGGTACAGACTTATCC	95	N/A	N/A	2216
950117	96178	96193	GGCTAAAGAGTACCCA	63	N/A	N/A	2217
950118	96181	96196	GGTGGCTAAAGAGTAC	23	N/A	N/A	2218
950119	96298	96313	GACTACCCCGACCCAC	71	N/A	N/A	2219
950120	96399	96414	GCACGGCACGGCAGGA	24	N/A	N/A	2220
950121	96523	96538	ACGCACAGGGCGGCCT	111	N/A	N/A	2221
950122	96527	96542	AGGCACGCACAGGGCG	83	N/A	N/A	2222
950123	96646	96661	CTAACGGCAGGCAGCC	71	N/A	N/A	2223
950124	96752	96767	CATCAGGGTTTCAGGC	11	N/A	N/A	2224
950125	96860	96875	GGCTAGGGTCAAAGGT	21	N/A	N/A	2225
950126	96977	96992	GCCCATGGGAGGAGTC	80	N/A	N/A	2226
950127	97078	97093	GAAACCAACATGAGGC	20	N/A	N/A	2227
950128	97149	97164	CGCAATAGAGACACCT	32	N/A	N/A	2228
950129	97221	97236	GAACCTCGCTCCGTGC	165	N/A	N/A	2229
950130	97453	97468	AGTGACTGAGTTCTGC	22	N/A	N/A	2230
950131	97809	97824	GGTTACGGTTGTTTTT	26	N/A	N/A	2231
950132	97855	97870	GTACAATGTAAGCCTT	3	N/A	N/A	2232
950133	97920	97935	TGCTAGTGACTCCATC	27	N/A	N/A	2233
950134	98046	98061	AGTGATGGAACCCCGG	48	N/A	N/A	2234
950135	98098	98113	CGCAGATAGAAAAACT	26	N/A	N/A	2235
950136	98099	98114	TCGCAGATAGAAAAAC	60	N/A	N/A	2236
950137	98150	98165	GCACACTGTGGCCAAG	70	N/A	N/A	2237
950138	98259	98274	AGTGAACGAGTCCCTC	84	N/A	N/A	2238
950139	98353	98368	TTCTACATAGGACCAT	13	N/A	N/A	2239

950140	98399	98414	AAACATCACAGGGACC	43	N/A	N/A	2240
950141	98508	98523	TCAGAAGAGAGGACCT	42	N/A	N/A	2241
950142	98643	98658	AGACACAGGGTAATGC	35	N/A	N/A	2242
950143	98866	98881	CAACAATGCAACAACG	15	N/A	N/A	2243
950144	99310	99325	CGCCAGATTAATTTTG	46	N/A	N/A	2244
950145	99477	99492	AACAATTGTCTGGTGT	85	N/A	N/A	2245
950146	99478	99493	CAACAATTGTCTGGTG	63	N/A	N/A	2246
950147	99481	99496	TAACAACAATTGTCTG	20	N/A	N/A	2247
950148	99493	99508	TAAGACTATAGTTAAC	63	N/A	N/A	2248
950149	99519	99534	CAACAGAAGAGTAGGG	26	N/A	N/A	2249
950150	99522	99537	GTTCAACAGAAGAGTA	25	N/A	N/A	2250
950151	99626	99641	GATAAATACTAGAGGC	45	N/A	N/A	2251
950152	99810	99825	GATCAGGGCCATAGAA	79	N/A	N/A	2252
950153	99823	99838	CAAGAAACGGGTTGAT	71	N/A	N/A	2253
950154	99830	99845	AATTAAGCAAGAAACG	114	N/A	N/A	2254
950155	99893	99908	CAACAAGCTATCACAC	92	N/A	N/A	2255
950156	99912	99927	CTGGACCGCATCAGAG	92	N/A	N/A	2256
950157	99924	99939	TTGAAAGCCAACCTGG	105	N/A	N/A	2257
950158	100015	100030	TAACACAGCCATGGCT	123	N/A	N/A	2258
950159	100020	100035	CCACATAACACAGCCA	28	N/A	N/A	2259
950160	100125	100140	TTGCAGCACAGGGTCA	56	N/A	N/A	2260
950161	100161	100176	GGCAACAGGAGACGCG	62	N/A	N/A	2261
950162	100227	100242	AGAGGCTACATGGTGA	60	N/A	N/A	2262
950163	100328	100343	GAAACAACCAATATCC	58	N/A	N/A	2263
950164	100399	100414	CACGAAGGGTTGACAC	101	N/A	N/A	2264
950165	100435	100450	GGCCAGAGTCCTGACT	98	N/A	N/A	2265
950166	100535	100550	GTTACCAGGACAAAAC	126	N/A	N/A	2266
950167	100670	100685	TGCCATCCCAGGGACC	105	N/A	N/A	2267
950168	100782	100797	CTACAGAGCATTCCCC	89	N/A	N/A	2268
950169	100811	100826	TGCCAGCAAGTCCCCA	80	N/A	N/A	2269
950170	100929	100944	GCCAAGAGGCCCGCCT	171	N/A	N/A	2270
950171	101038	101053	ACCCGAATAGCAAGCG	54	N/A	N/A	2271
950172	101155	101170	GAGCATGGGCCCGCAG	139	N/A	N/A	2272
950173	101255	101270	GATGATCCTTTCACCC	90	N/A	N/A	2273
950174	101362	101377	CACCACCCTGGGTTTA	132	N/A	N/A	2274
950175	101483	101498	GCAGACCACGCCTGGC	44	N/A	N/A	2275
950176	101603	101618	TGCAAGGCGGAAAGAG	95	N/A	N/A	2276
950177	101718	101733	GGCATTCCCACCCAGG	84	N/A	N/A	2277
950178	101808	101823	GAAAACTAGACTTGCA	31	N/A	N/A	2278
950179	101810	101825	CTGAAAACTAGACTTG	44	N/A	N/A	2279
950180	101850	101865	GAAAAACACGAAGGGC	86	N/A	N/A	2280
950181	101951	101966	TCATTACGGCCGGCGC	109	N/A	N/A	2281
950182	102059	102074	CTAACTTGGGTGGTGG	43	N/A	N/A	2282

950183	102159	102174	AGATATTGATGTCTTG	7	N/A	N/A	2283
950184	102264	102279	GCAGAGGGAGCCCCGA	90	N/A	N/A	2284
950185	102314	102329	TCGCATAGAAGATTCG	38	N/A	N/A	2285
950186	102365	102380	CGGCAGGTGAGTGTCA	30	N/A	N/A	2286
950187	102465	102480	GACTACCTGTTCAGGA	112	N/A	N/A	2287
950188	102585	102600	GAAGAGTGGTGGTTTC	80	N/A	N/A	2288
950189	102639	102654	TGCGAGCCGGCCCCAG	61	N/A	N/A	2289
950190	102716	102731	CACGATCCCAAACCCT	79	N/A	N/A	2290
950191	102830	102845	TGCCGGCACGCACGCG	135	N/A	N/A	2291
950192	102935	102950	CAGCAGGGCCAAGTAA	61	N/A	N/A	2292
950193	103102	103117	GGTAACACAGGGCCTG	119	N/A	N/A	2293
950207	103286	103301	GAGCATAGGAAGAGGG	27	N/A	N/A	2294
950208	103302	103317	GCAAAGAAGTAGGGCA	81	N/A	N/A	2295
950209	103323	103338	GATTAGCCTGCCAGGC	20	N/A	N/A	2296
950210	103425	103440	CCTCATCTATCCAAGG	99	N/A	N/A	2297
950211	103552	103567	GGCACATGGGCTCAGC	119	N/A	N/A	2298
950212	103672	103687	CTCCAAGTTCAGGAGC	119	N/A	N/A	2299
950213	103832	103847	CGCAAGCCACAGCAGG	101	N/A	N/A	2300
950214	103971	103986	ACTCACCCAGTGATGT	111	N/A	N/A	2301
950215	104100	104115	GTTCAGGAAGCACCAA	20	N/A	N/A	2302
950216	104276	104291	AGCCTTACTCCCTTTC	34	N/A	N/A	2303
950217	104326	104341	CGCTTTAGGACATCTT	63	N/A	N/A	2304
950218	104410	104425	TAGGAGTGAGTTACCT	102	N/A	N/A	2305
950219	104458	104473	CACGAAGTGAATGGAA	13	N/A	N/A	2306
950220	104486	104501	ACGCACAACACAACTG	63	N/A	N/A	2307
950221	104560	104575	TGCCACTGGACTGACT	69	N/A	N/A	2308
950222	104606	104621	GACCTAGGTGCCTGAC	27	N/A	N/A	2309
950223	104678	104693	ACTCTACCCGCACCCT	96	N/A	N/A	2310
950224	104783	104798	CTCCATGATGCTCCCT	63	N/A	N/A	2311
950225	104895	104910	GTGTAGCATGCGCCAC	124	N/A	N/A	2312
950226	104953	104968	GGGAAAAGAGTCACCC	113	N/A	N/A	2313
950227	105113	105128	CTTCACCCCGAGCCAT	90	N/A	N/A	2314
950228	105248	105263	CGGGAAGCATCCCTGG	114	N/A	N/A	2315
950229	105253	105268	CAGCACGGGAAGCATC	53	N/A	N/A	2316
950230	105366	105381	TGCAAGCACCTGAGCC	99	N/A	N/A	2317
950231	105479	105494	CCCTATGGGTTCTGGC	78	N/A	N/A	2318
950232	105561	105576	TCACAATTGGTGCCTT	16	N/A	N/A	2319
950233	105622	105637	CCCCACCTCGGCCAAT	59	N/A	N/A	2320
950234	105668	105683	CTAAATGGAGCTCTTG	64	N/A	N/A	2321
950235	105671	105686	GGCCTAAATGGAGCTC	79	N/A	N/A	2322
950236	105727	105742	CATCACACTCCTCGAT	96	N/A	N/A	2323
950237	105864	105879	ATGTACTGTGAGCTTC	12	N/A	N/A	2324
950238	106002	106017	GCTAATCCCTGACTCA	37	N/A	N/A	2325

950239	106118	106133	ACTCAGCTGGAGTTGG	63	N/A	N/A	2326
950240	106174	106189	GACAAATGGGTCTCGA	124	N/A	N/A	2327
950241	106213	106228	GCCTAGAAGAGCTATG	97	N/A	N/A	2328
950242	106218	106233	GGCAAGCCTAGAAGAG	95	N/A	N/A	2329
950243	106269	106284	AGGCACACGGCTCAGG	55	N/A	N/A	2330
950244	106276	106291	GTACAGGAGGCACACG	82	N/A	N/A	2331
950245	106340	106355	TACTACTCTGGGTTTC	53	N/A	N/A	2332
950246	106457	106472	GAACATGCAGGGCCTG	13	N/A	N/A	2333
950247	106838	106853	AAGAAGTAGAAGTCGG	36	N/A	N/A	2334
950248	106946	106961	GGATGAGGTTGTGTGG	82	N/A	N/A	2335
950249	107060	107075	ACGCACATTTTCCTGT	59	N/A	N/A	2336
950250	107115	107130	TGCTAAACAGTGCTTG	76	N/A	N/A	2337
950251	107478	107493	AAAGTTTAGGCATGGT	22	N/A	N/A	2338
950252	107673	107688	CGTCAATACTAAAATA	119	N/A	N/A	2339
950253	108115	108130	GCCCGAATGTGTTTTG	72	N/A	N/A	2340
950254	108434	108449	CACCAGAACTTTATTA	92	N/A	N/A	2341
950255	108584	108599	GGCAAGTGTCTGAGTT	17	N/A	N/A	2342
950256	108685	108700	TCTGACTGATCAGGAA	85	N/A	N/A	2343
950257	108748	108763	GCACAAGCTTGACCCT	92	N/A	N/A	2344
950258	108970	108985	GAAAATGACCTGTCCT	92	N/A	N/A	2345
950259	109080	109095	CCGTGAGGGAACTTTC	69	N/A	N/A	2346
950260	109124	109139	AAGCAAGTGGGACCCC	79	N/A	N/A	2347
950261	109129	109144	GAACAAAGCAAGTGGG	62	N/A	N/A	2348
950262	109183	109198	GGCCAAGGGTGGCCAT	143	N/A	N/A	2349
950263	109205	109220	CGGCAAGGCATTTTAA	88	N/A	N/A	2350
950264	109407	109422	TTTAAGCGATCTCCTG	31	N/A	N/A	2351
950265	109408	109423	GTTTAAGCGATCTCCT	39	N/A	N/A	2352
950266	109516	109531	ACCCAACCTTGGGACA	75	N/A	N/A	2353
950267	109576	109591	CCCAAAGGATCTGCCC	101	N/A	N/A	2354
950268	109649	109664	TGCCTGGGTATGTTTG	76	N/A	N/A	2355
950269	109910	109925	AGATAGGCCTGCTTGC	70	N/A	N/A	2356
950270	109914	109929	CACCAGATAGGCCTGC	74	N/A	N/A	2357
950271	110212	110227	ACTCACATTGTTGATC	92	N/A	N/A	2358
950272	110607	110622	CTCTAGGCTTACCACA	53	N/A	N/A	2359
950273	110885	110900	GCCTAGGGTGCCTGGC	105	N/A	N/A	2360
950274	110899	110914	TACAAACAGGTATGGC	20	N/A	N/A	2361
950275	110900	110915	CTACAAACAGGTATGG	46	N/A	N/A	2362
950276	111043	111058	TCAAATTTGTTGTTGC	14	N/A	N/A	2363
950277	111093	111108	CCAAAGAGGATGGCCG	66	N/A	N/A	2364
950278	111150	111165	AGTTAGTGGACTTGAT	37	N/A	N/A	2365
950279	111166	111181	CTGCAGTGTTCACTCC	64	N/A	N/A	2366
950280	111195	111210	GCCTAAGTTAATTCAG	88	N/A	N/A	2367
950281	111339	111354	GCAACCAGGGTAAACG	94	N/A	N/A	2368

950282	111471	111486	ACTGAAGAGGAGCCCA	57	N/A	N/A	2369
950283	111548	111563	GCCAAAGGCCTGATAC	96	N/A	N/A	2370
950284	111581	111596	GGTTTATAAAGCTTCC	35	N/A	N/A	2371
950285	111781	111796	TCTTACCTCGGTCTTC	66	N/A	N/A	2372
950286	111872	111887	TGAAAGAGGTTCCTGC	36	N/A	N/A	2373
950287	111910	111925	GTTGACATTCATATAC	68	N/A	N/A	2374
950288	112131	112146	TGAGAATGGGAGCAAC	39	N/A	N/A	2375
950289	112147	112162	GAACACTGATCACTAC	32	N/A	N/A	2376
950290	112174	112189	AAACATACCAGGACAC	39	N/A	N/A	2377
950291	112192	112207	TCCTATCGGTATATGA	139	N/A	N/A	2378
950292	112222	112237	TCATAGCAGAAGAACC	28	N/A	N/A	2379
950293	112260	112275	TAAACTTGCAGGGTCA	9	N/A	N/A	2380
950294	112267	112282	CTAAAAGTAAACTTGC	98	N/A	N/A	2381
950295	112360	112375	TCCCATCTTTGGCTGC	37	N/A	N/A	2382
950296	112902	112917	TCCTACTGGATACAGA	58	N/A	N/A	2383
950299	113293	113308	GCCAATCCTGTTATAT	97	N/A	N/A	2384
950300	113614	113629	GCAGAATAATCCTGTT	77	N/A	N/A	2385
950301	113616	113631	TGGCAGAATAATCCTG	69	N/A	N/A	2386
950302	113780	113795	GTTGACACCATGCTTG	14	N/A	N/A	2387
950303	113923	113938	CCCCAGACTTTTTTGA	101	N/A	N/A	2388
950304	114269	114284	AACCAGGCTTCCGGAC	83	N/A	N/A	2389
950305	114450	114465	AGCTGTAGGGCTGGCT	61	N/A	N/A	2390
950306	114637	114652	TCTGGCCACGCCTTGC	93	N/A	N/A	2391
950307	114737	114752	CCTTAAGGAACTCCAT	109	N/A	N/A	2392
950308	114843	114858	CCTAATATCTCTAGGG	82	N/A	N/A	2393
950309	115000	115015	GCGCAGTGGGATCCTC	178	N/A	N/A	2394
950310	115042	115057	TGCCAGAACCTGAGGT	96	N/A	N/A	2395
950311	115081	115096	ATACAGATGGAGTAGG	63	N/A	N/A	2396
950312	115423	115438	ACAGGAGGAGAGACCC	58	N/A	N/A	2397
950313	115497	115512	CCAAATAGGGATGAGG	87	N/A	N/A	2398
950314	115504	115519	TCGCAAGCCAAATAGG	29	N/A	N/A	2399
950315	115538	115553	GAACAAGCCTCTTGGC	142	N/A	N/A	2400
950316	115640	115655	GCCCAGTGTGAGGGTT	102	N/A	N/A	2401
950317	115795	115810	CATCAACTCGCCTGCT	101	N/A	N/A	2402
950318	115915	115930	CCGGGAGCAAGAGGCA	160	N/A	N/A	2403
951323	3692	3707	CCAGATGGCAGACTTC	19	N/A	N/A	2404
951324	3772	3787	AGATATCTAGATGGCC	111	N/A	N/A	2405
951325	3773	3788	TAGATATCTAGATGGC	63	N/A	N/A	2406
951326	3774	3789	ATAGATATCTAGATGG	52	N/A	N/A	2407
951327	3884	3899	CCAAATGGTGGTGGCA	84	N/A	N/A	2408
951328	4373	4388	CCAATTTGTAGGCTGT	9	N/A	N/A	2409
951329	4487	4502	ACAGATGGGCACACCG	91	N/A	N/A	2410
951330	4647	4662	ACAAATGAGTAGTTCC	6	N/A	N/A	2411

951331	4668	4683	TCATTTGGCAGCCACA	41	N/A	N/A	2412
951332	4670	4685	TATCATTTGGCAGCCA	77	N/A	N/A	2413
951333	4673	4688	TGTTATCATTTGGCAG	13	N/A	N/A	2414
951334	4767	4782	CCTTACTTGGGATTCA	64	N/A	N/A	2415
951335	4792	4807	ATGATAACACAGCCTC	47	N/A	N/A	2416
951336	4793	4808	GATGATAACACAGCCT	46	N/A	N/A	2417
951337	4795	4810	GGGATGATAACACAGC	104	N/A	N/A	2418
951338	4917	4932	GAGATTTGTGCTGCTT	16	N/A	N/A	2419
951339	5744	5759	GTAAGTAAGCACTTTT	45	N/A	N/A	2420
951340	5899	5914	GGATTATAGCAATGCC	12	N/A	N/A	2421
951341	5970	5985	TCACTTTACAGCCTCC	9	N/A	N/A	2422
951342	6124	6139	GGATTCTAGGAGGTCG	36	N/A	N/A	2423
951343	6458	6473	ATTAATACTCTTAACG	57	N/A	N/A	2424
951344	6738	6753	ACTAACTGGGCTGTTC	53	N/A	N/A	2425
951345	6740	6755	GAACTAACTGGGCTGT	40	N/A	N/A	2426
951346	6857	6872	GGAAATCTAACACTGG	7	N/A	N/A	2427
951347	6908	6923	AACTCTATAGATCTGA	101	N/A	N/A	2428
951348	6959	6974	AGACATGGTGGAACCA	81	N/A	N/A	2429
951349	7117	7132	GATTACAACAACAGCC	76	N/A	N/A	2430
951350	7175	7190	TGAAATCGAAGCCATT	95	N/A	N/A	2431
951351	7399	7414	TAAATGACAAGGGTCA	83	N/A	N/A	2432
951352	7942	7957	GCTATTATAACTTGTA	8	N/A	N/A	2433
951353	8568	8583	ATTTTAAAGAAGACGG	42	N/A	N/A	2434
951354	8583	8598	GCTATTATAACTCCTA	11	N/A	N/A	2435
951355	8616	8631	CACTTAATCCCTATTC	74	N/A	N/A	2436
951356	9095	9110	ATACTTATCGCCTTTT	5	N/A	N/A	2437
951357	9099	9114	CATCATACTTATCGCC	6	N/A	N/A	2438
951358	9144	9159	TCCAACTGTGATCTCT	8	N/A	N/A	2439
951359	10032	10047	CCAAGGAACACATCAC	25	N/A	N/A	2440
951360	10064	10079	ACTAATAAGATCTGTT	97	N/A	N/A	2441
951361	10131	10146	TGCAATTTGTCTTTGC	78	N/A	N/A	2442
951362	10136	10151	CAAGATGCAATTTGTC	3	N/A	N/A	2443
951363	10700	10715	CGAGATCACAAATGCT	41	N/A	N/A	2444
951364	11386	11401	AGTAATGATGAGTTCC	3	N/A	N/A	2445
951365	11416	11431	CACTGATAGGCACTCC	8	N/A	N/A	2446
951366	11553	11568	ATTACTTGTTTGCAGC	8	N/A	N/A	2447
951367	11556	11571	CCAATTACTTGTTTGC	8	N/A	N/A	2448
951368	11572	11587	TAAATAACTCTCACGG	25	N/A	N/A	2449
951369	11573	11588	GTAAATAACTCTCACG	86	N/A	N/A	2450
951370	11575	11590	GTGTAAATAACTCTCA	10	N/A	N/A	2451
951371	11922	11937	GTTGATAGTCGGTTGT	4	N/A	N/A	2452
951372	11960	11975	GGTCATTAAAGATTCT	4	N/A	N/A	2453
951373	11990	12005	GGTACCTAACAGGTCT	93	N/A	N/A	2454

951374	12062	12077	GTCTTTCCGGTCTTTT	4	N/A	N/A	2455
951375	12148	12163	GATTATAAACCTAATC	121	N/A	N/A	2456
951376	12215	12230	TCAATAAGTAACTCTG	11	N/A	N/A	2457
951377	12216	12231	GTCAATAAGTAACTCT	140	N/A	N/A	2458
951378	12237	12252	ACCTATCAAGGGCTGT	27	N/A	N/A	2459
951379	12244	12259	GTTATGAACCTATCAA	20	N/A	N/A	2460
951380	12245	12260	TGTTATGAACCTATCA	47	N/A	N/A	2461
951381	12850	12865	GTTTACATGATGTTCT	7	N/A	N/A	2462
951382	12860	12875	GTAAATTACGGTTTAC	122	N/A	N/A	2463
951383	12861	12876	AGTAAATTACGGTTTA	14	N/A	N/A	2464
951384	12890	12905	CTTAATTACAGCTTGT	6	N/A	N/A	2465
951385	12934	12949	TCATTATTGGCTTGGA	41	N/A	N/A	2466
951386	12935	12950	CTCATTATTGGCTTGG	4	N/A	N/A	2467
951387	12971	12986	CCTTTATTCAGATTGT	3	N/A	N/A	2468
951388	13136	13151	AGTCATCCAGCTCCCG	54	N/A	N/A	2469
951389	13167	13182	ATAAATGTCCAGCAGC	44	N/A	N/A	2470
951390	13169	13184	TCATAAATGTCCAGCA	63	N/A	N/A	2471
951391	13170	13185	ATCATAAATGTCCAGC	32	N/A	N/A	2472
951392	13392	13407	GCCATATGTGTGGCTC	65	N/A	N/A	2473
951393	13487	13502	TGTAATCTTGGCCCAG	83	N/A	N/A	2474
951394	13521	13536	TGCATATCCAAAGCCA	83	N/A	N/A	2475
951395	14442	14457	CCACATGTGAAGCAGC	21	N/A	N/A	2476
951396	14476	14491	GGCTATTCCACTGCAG	99	N/A	N/A	2477
951397	14694	14709	TCTGTAATGGTTTCCC	5	N/A	N/A	2478
951398	14808	14823	TGTACCTAAGTACAGA	97	N/A	N/A	2479
951399	14824	14839	TCTATAGGTACCAGCA	50	N/A	N/A	2480
951400	15508	15523	AGTGAAATTCACTCCA	47	N/A	N/A	2481
951401	15651	15666	CTCTTTATATAGATGG	58	N/A	N/A	2482
951402	16748	16763	AGAGATACATCAACCC	35	N/A	N/A	2483
951403	17836	17851	AAATATAGCAGGGACC	51	N/A	N/A	2484
951404	17839	17854	ACTAAATATAGCAGGG	30	N/A	N/A	2485
951405	17842	17857	GGCACTAAATATAGCA	71	N/A	N/A	2486
951406	19042	19057	TAGTATACCAAGGTTA	11	N/A	N/A	2487
951407	19043	19058	GTAGTATACCAAGGTT	6	N/A	N/A	2488
951408	19760	19775	CAGTATGTATACTTCC	2	N/A	N/A	2489
951409	19761	19776	TCAGTATGTATACTTC	86	N/A	N/A	2490
951410	20345	20360	TCCTGATAAGATTCAC	17	N/A	N/A	2491
951411	20392	20407	TCAGTTATCACTGTCA	31	N/A	N/A	2492
951412	20458	20473	ACTAGTAACTTTCCAG	37	N/A	N/A	2493
951413	20741	20756	GGATTATTACATGAGT	11	N/A	N/A	2494
951414	20743	20758	GAGGATTATTACATGA	29	N/A	N/A	2495
951415	20864	20879	GCCAACTAATTCCAGA	46	N/A	N/A	2496
951416	21512	21527	ATATATGTGGAGGCAA	10	N/A	N/A	2497

951417	21513	21528	TATATATGTGGAGGCA	104	N/A	N/A	2498
951418	21515	21530	AATATATATGTGGAGG	4	N/A	N/A	2499
951419	21654	21669	CACTATTGGCACACCA	115	N/A	N/A	2500
951420	21655	21670	ACACTATTGGCACACC	122	N/A	N/A	2501
951421	21656	21671	AACACTATTGGCACAC	111	N/A	N/A	2502
951422	21840	21855	TTCTTAACAGGCTCCC	41	N/A	N/A	2503
951423	22010	22025	TAAGTATGCGCTGCCA	31	N/A	N/A	2504
951424	22134	22149	AGGATATAGGGTCTCC	97	N/A	N/A	2505
951425	22135	22150	AAGGATATAGGGTCTC	37	N/A	N/A	2506
951426	22212	22227	GAACATCATGGAGCCT	33	N/A	N/A	2507
951427	23308	23323	TTTGATACTGATCTCA	18	N/A	N/A	2508
951428	24284	24299	GGTATTATGGTATGTG	2	N/A	N/A	2509
951429	24285	24300	AGGTATTATGGTATGT	2	N/A	N/A	2510
951430	24396	24411	TCATATGTATGGGTTT	4	N/A	N/A	2511
951431	24398	24413	CTTCATATGTATGGGT	10	N/A	N/A	2512
951432	25701	25716	ATAGATGTAAGCAACT	51	N/A	N/A	2513
951433	25709	25724	GGAAATTCATAGATGT	113	N/A	N/A	2514
951434	25740	25755	ACTTATGGATGCAGCT	52	N/A	N/A	2515
951435	25741	25756	AACTTATGGATGCAGC	39	N/A	N/A	2516
951436	26160	26175	AGCATTGGTATCAGGC	35	N/A	N/A	2517
951437	26168	26183	TGGATATCAGCATTGG	17	N/A	N/A	2518
951438	26173	26188	ATGGATGGATATCAGC	41	N/A	N/A	2519
951439	26180	26195	TTCAATCATGGATGGA	72	N/A	N/A	2520
951440	27070	27085	GGAATACTTGCAGCTA	41	N/A	N/A	2521
951441	27071	27086	AGGAATACTTGCAGCT	11	N/A	N/A	2522
951442	27224	27239	CAACATGGCACTCCCT	64	N/A	N/A	2523
951443	27231	27246	TCTGATGCAACATGGC	12	N/A	N/A	2524
951444	27569	27584	ATCATTGGGTGAAGAC	43	N/A	N/A	2525
951445	27762	27777	GGTCTATTGGCACACA	32	N/A	N/A	2526
951446	27776	27791	AGATTAAGTCATCCGG	90	N/A	N/A	2527
951447	27777	27792	GAGATTAAGTCATCCG	61	N/A	N/A	2528
951448	27778	27793	AGAGATTAAGTCATCC	73	N/A	N/A	2529
951449	28228	28243	GCAAATGCTAGCTGCA	142	N/A	N/A	2530
951450	29274	29289	CGCTCTAATGTCCTGA	11	N/A	N/A	2531
951451	29308	29323	TGGATATCCAGACCCA	97	N/A	N/A	2532
951452	29321	29336	GCAGATCCTGCCTTGG	92	N/A	N/A	2533
951453	29584	29599	TGAACTAGAGGCAGGC	29	N/A	N/A	2534
951454	29585	29600	GTGAACTAGAGGCAGG	19	N/A	N/A	2535
951455	29974	29989	TGTAACTTTCAGCAGT	25	N/A	N/A	2536
951456	29999	30014	TGTGATTGCAGGCCAG	13	N/A	N/A	2537
951457	30053	30068	TTTTATAGTCTCCAAC	140	N/A	N/A	2538
951458	30107	30122	TGTATGGACAGCAGGC	13	N/A	N/A	2539
951459	30108	30123	GTGTATGGACAGCAGG	10	N/A	N/A	2540

951460	30242	30257	ATCAATCTTGGGAGCT	39	N/A	N/A	2541
951461	30246	30261	CTAAATCAATCTTGGG	40	N/A	N/A	2542
951462	30348	30363	ATATTAATGCAGTGGT	4	N/A	N/A	2543
951463	30349	30364	CATATTAATGCAGTGG	14	N/A	N/A	2544
951464	30350	30365	ACATATTAATGCAGTG	66	N/A	N/A	2545
951465	30407	30422	AGAATATCAACACCTT	69	N/A	N/A	2546
951466	30408	30423	TAGAATATCAACACCT	61	N/A	N/A	2547
951467	30426	30441	TTATCTAACAGTCCCA	45	N/A	N/A	2548
951468	30429	30444	CATTTATCTAACAGTC	104	N/A	N/A	2549
951469	30509	30524	TAGTGATATGCTGCCT	22	N/A	N/A	2550
951470	30852	30867	CACAATCCTGGCTATC	56	N/A	N/A	2551
951471	30931	30946	CCAGACATTGCTGTCG	108	N/A	N/A	2552
951472	31367	31382	ACATTTGACGGTTTGA	15	N/A	N/A	2553
951473	32256	32271	GGGAATGATGCCACCT	110	N/A	N/A	2554
951474	32270	32285	CCAATCTGTTATGTGG	23	N/A	N/A	2555
951475	32336	32351	TGGAATCCAGTATTTC	103	N/A	N/A	2556
951476	32498	32513	AGGAATCCTGCAGCTC	108	N/A	N/A	2557
951477	32722	32737	TCCTATTAGAGTGGCA	49	N/A	N/A	2558
951478	32905	32920	AGCATTAACAGAGCAG	92	N/A	N/A	2559
951479	33017	33032	GGCTTTACTCCAGCCA	104	N/A	N/A	2560
951480	33518	33533	AACAATAGCCATTGGT	107	N/A	N/A	2561
951481	34302	34317	TGTTTATTTACCGTTT	3	N/A	N/A	2562
951482	35180	35195	AGTACTATTGCATCAT	28	N/A	N/A	2563
951483	36041	36056	TCACATACAGACCCCA	59	N/A	N/A	2564
951484	36073	36088	CTAAATGTCACTTAGC	40	N/A	N/A	2565
951485	36087	36102	GGAACTAACACATGCT	23	N/A	N/A	2566
951486	36362	36377	GAAATCTACCTACTCC	105	N/A	N/A	2567
951487	36363	36378	TGAAATCTACCTACTC	121	N/A	N/A	2568
951488	36617	36632	GGCACCAACATTCACC	96	N/A	N/A	2569
951489	36660	36675	TCCGATTTTGCTTCTA	10	N/A	N/A	2570
951490	36665	36680	ACTTATCCGATTTTGC	23	N/A	N/A	2571
951491	36809	36824	TGTTATTCCGAACAGT	43	N/A	N/A	2572
951492	36911	36926	TCTCATGGCGACTGGC	77	N/A	N/A	2573
951493	36948	36963	GGAATAAAGGCTCTCG	22	N/A	N/A	2574
951494	37009	37024	TTAGATTGTATGACCC	9	N/A	N/A	2575
951495	37194	37209	GGCTTTGTTAGATGCC	107	N/A	N/A	2576
951496	37246	37261	ATTCATAGTACCCCAC	62	N/A	N/A	2577
951497	37304	37319	GTATTTGTAGTGTGGA	110	N/A	N/A	2578
951498	37305	37320	GGTATTTGTAGTGTGG	10	N/A	N/A	2579
951499	37446	37461	GACAATGGTGATGCCC	62	N/A	N/A	2580
951500	37566	37581	ATCTTAGGCAGACCCT	42	N/A	N/A	2581
951501	37570	37585	ACACATCTTAGGCAGA	14	N/A	N/A	2582
951502	37729	37744	ATTAAAATGGGTCTGC	77	N/A	N/A	2583

951503	37750	37765	CATTTAACCATGACAG	31	N/A	N/A	2584
951504	37751	37766	CCATTTAACCATGACA	32	N/A	N/A	2585
951505	37971	37986	ACCTTAAGTTTTTTGG	118	N/A	N/A	2586
951506	38196	38211	GCTAATAGCTATTCAA	39	N/A	N/A	2587
951507	38225	38240	CGCATTACTGAGTTCA	12	N/A	N/A	2588
951508	38335	38350	GTGACTAAGACAACCA	40	N/A	N/A	2589
951509	38538	38553	AGACATGTAACTCCCT	39	N/A	N/A	2590
951510	38540	38555	CTAGACATGTAACTCC	72	N/A	N/A	2591
951511	38592	38607	GCCTATCCATGCTGCT	105	N/A	N/A	2592
951512	39123	39138	CAGAATTGTTACAACC	47	N/A	N/A	2593
951513	39140	39155	CCATTAAAATTTGCCC	30	N/A	N/A	2594
951514	39141	39156	TCCATTAAAATTTGCC	44	N/A	N/A	2595
951515	39233	39248	TTAACTATATCTAACT	73	N/A	N/A	2596
951516	39236	39251	CGATTAACTATATCTA	87	N/A	N/A	2597
951517	39547	39562	ATTTATGCGATTGGCC	88	N/A	N/A	2598
951518	39548	39563	GATTTATGCGATTGGC	17	N/A	N/A	2599
951519	39549	39564	AGATTTATGCGATTGG	11	N/A	N/A	2600
951520	39555	39570	TGTTTAAGATTTATGC	41	N/A	N/A	2601
951521	39748	39763	AAAGTAATTCACTGCG	81	N/A	N/A	2602
951522	40198	40213	ATGGACTACAGTCTGT	110	N/A	N/A	2603
951523	40275	40290	TGCAATCACAGACATC	93	N/A	N/A	2604
951524	41080	41095	GTATTAACCTCATGAA	93	N/A	N/A	2605
951525	41081	41096	GGTATTAACCTCATGA	68	N/A	N/A	2606
951526	41125	41140	GTCTTTCCGTCACAGT	40	N/A	N/A	2607
951527	41273	41288	GGATAATTGGAGAGGG	94	N/A	N/A	2608
951528	41274	41289	GGGATAATTGGAGAGG	68	N/A	N/A	2609
951529	42072	42087	GGGATTATGATGAGGA	3	N/A	N/A	2610
951530	42327	42342	GATGATGGGTTCTAGC	85	N/A	N/A	2611
951531	42355	42370	GGGAGATGTGCTCTTT	49	N/A	N/A	2612
951532	42381	42396	GTATTACCCAGTGGCT	62	N/A	N/A	2613
951533	42382	42397	TGTATTACCCAGTGGC	15	N/A	N/A	2614
951534	42387	42402	GGGAATGTATTACCCA	131	N/A	N/A	2615
951535	42501	42516	TACAATCATTCCCAGC	89	N/A	N/A	2616
951536	42506	42521	AGCACTACAATCATTC	82	N/A	N/A	2617
951537	42569	42584	TACTGTACAGCTGTGC	8	N/A	N/A	2618
951538	42578	42593	GGCAATTGGTACTGTA	121	N/A	N/A	2619
951539	42599	42614	GAAAATTTGTACAGGA	55	N/A	N/A	2620
951540	43029	43044	TACATTAAAGGCTCGA	44	N/A	N/A	2621
951541	43843	43858	GTACATATCCTGGCCG	32	N/A	N/A	2622
951542	43871	43886	TACTATTCGACAGAGC	31	N/A	N/A	2623
951543	43873	43888	ATTACTATTCGACAGA	36	N/A	N/A	2624
951544	43876	43891	TAAATTACTATTCGAC	45	N/A	N/A	2625
951545	43877	43892	GTAAATTACTATTCGA	63	N/A	N/A	2626

951546	43878	43893	TGTAAATTACTATTCG	19	N/A	N/A	2627
951547	44416	44431	GAGATCAACACATTTC	57	N/A	N/A	2628
951548	44701	44716	AGAAATTACTCTTGCG	116	N/A	N/A	2629
951549	44902	44917	TCCAATGACAGCCCAG	26	N/A	N/A	2630
951550	44914	44929	GTGAATTCAATGTCCA	11	N/A	N/A	2631
951551	44929	44944	ACACATGTGGAACACG	80	N/A	N/A	2632
951552	45353	45368	TATCTATAACACATGA	44	N/A	N/A	2633
951553	45356	45371	GGTTATCTATAACACA	23	N/A	N/A	2634
951554	45446	45461	GTCTTTATTGCATGGG	8	N/A	N/A	2635
951555	45569	45584	GCTATAAAACCAGCCA	101	N/A	N/A	2636
951556	45590	45605	AGCATTGGATTGAGCA	89	N/A	N/A	2637
951557	46280	46295	AGCAATGGTGGCCGGG	109	N/A	N/A	2638
951558	46328	46343	CTATATTCAACAGGCT	24	N/A	N/A	2639
951559	46329	46344	ACTATATTCAACAGGC	61	N/A	N/A	2640
951560	46335	46350	GGCCATACTATATTCA	102	N/A	N/A	2641
951561	46428	46443	GGGATATACGCCCACC	8	N/A	N/A	2642
951562	46590	46605	TATTTAAAAGGGCCGC	23	N/A	N/A	2643
951563	46591	46606	GTATTTAAAAGGGCCG	97	N/A	N/A	2644
951564	46861	46876	CGAAATAGCAGAGCTC	75	N/A	N/A	2645
951565	46961	46976	TCTATAGTGACTCTCA	9	N/A	N/A	2646
951566	46962	46977	TTCTATAGTGACTCTC	6	N/A	N/A	2647
951567	47624	47639	GTTCATCCGGGTCAGG	36	N/A	N/A	2648
951568	47926	47941	GCAACTATGCATCCAC	141	N/A	N/A	2649
951569	48813	48828	GAACATGGCAGCCAGT	82	N/A	N/A	2650
951570	48973	48988	TGCTTAATGCCTTGCC	82	N/A	N/A	2651
951571	49051	49066	CGCAATGTGTTCATTT	27	N/A	N/A	2652
951572	49192	49207	ACTTTAACAAGTCCCG	36	N/A	N/A	2653
951573	49193	49208	CACTTTAACAAGTCCC	23	N/A	N/A	2654
951574	49227	49242	ACAGATGAAGCTACCA	27	N/A	N/A	2655
951575	49443	49458	GGTTATGGTCTTAGGT	16	N/A	N/A	2656
951576	49674	49689	TCGATTTGATTCTGAG	84	N/A	N/A	2657
951577	50575	50590	GACAAATTGCCACTGG	54	N/A	N/A	2658
951578	50595	50610	GCAAATATCTCCCAGT	19	N/A	N/A	2659
951579	50845	50860	ACAATGACGAGGCTGG	25	N/A	N/A	2660
951580	50979	50994	TCAAATCCCATCAGGA	90	N/A	N/A	2661
951581	51714	51729	TGTACTTGCGGGTTTT	42	N/A	N/A	2662
951582	51790	51805	AGCAATCACGCTGCCA	99	N/A	N/A	2663
951583	51798	51813	AGTCATCCAGCAATCA	43	N/A	N/A	2664
951584	51810	51825	ATTAATCTGGGCAGTC	38	N/A	N/A	2665
951585	51811	51826	GATTAATCTGGGCAGT	67	N/A	N/A	2666
951586	51816	51831	TAAAGGATTAATCTGG	48	N/A	N/A	2667
951587	51977	51992	ATTTTGATAGCTCCAC	33	N/A	N/A	2668
951588	51979	51994	GCATTTTGATAGCTCC	17	N/A	N/A	2669

951589	52601	52616	GGTTTAAAAGCTTCCA	98	N/A	N/A	2670
951590	52938	52953	GTAAATGCTGAATGCC	34	N/A	N/A	2671
951591	53084	53099	GGATATGGACAGCAGG	17	N/A	N/A	2672
951592	53085	53100	AGGATATGGACAGCAG	15	N/A	N/A	2673
951593	53553	53568	TCACATGCCAGACTTT	100	N/A	N/A	2674
951594	53781	53796	CACACTCACGCATGTT	102	N/A	N/A	2675
951595	53852	53867	TTTACCTTGAATGTCC	46	N/A	N/A	2676
951596	54009	54024	GCAAGCTACTCTCTCA	88	N/A	N/A	2677
951597	54160	54175	TCAATACCTGCACAGG	42	N/A	N/A	2678
951598	54161	54176	GTCAATACCTGCACAG	80	N/A	N/A	2679
951599	54177	54192	TGTATGAGGACTCAGA	42	N/A	N/A	2680
951600	54189	54204	ATCATAACAGGCTGTA	28	N/A	N/A	2681
951601	54190	54205	CATCATAACAGGCTGT	94	N/A	N/A	2682
951602	54199	54214	TAAAATGCGCATCATA	51	N/A	N/A	2683
951603	54255	54270	GTAATGAGCTCAGTCT	45	N/A	N/A	2684
951604	55117	55132	GAAACTACGGCACTCT	121	N/A	N/A	2685
951605	55385	55400	GGTAATAAGTCACACT	103	N/A	N/A	2686
951606	55528	55543	GATTAATATCGGCTGA	44	N/A	N/A	2687
951607	55530	55545	TGGATTAATATCGGCT	24	N/A	N/A	2688
951608	55531	55546	ATGGATTAATATCGGC	9	N/A	N/A	2689
951609	56236	56251	GTTCATCACGGAAGGT	120	N/A	N/A	2690
951610	56274	56289	CCGAATCACAGATTGA	71	N/A	N/A	2691
951611	56324	56339	GTAATTGACAAGCAGT	16	N/A	N/A	2692
951612	56327	56342	TAAGTAATTGACAAGC	29	N/A	N/A	2693
951613	56387	56402	GTATATAAGACCCGGG	65	N/A	N/A	2694
951614	56388	56403	TGTATATAAGACCCGG	86	N/A	N/A	2695
951615	56389	56404	GTGTATATAAGACCCG	53	N/A	N/A	2696
951616	56390	56405	AGTGTATATAAGACCC	41	N/A	N/A	2697
951617	56459	56474	GACTATTCAAGAGGGC	70	N/A	N/A	2698
951618	56567	56582	TCTCATGGCACTCACT	42	N/A	N/A	2699
951619	56617	56632	ATTCATGGTCCACCAG	101	N/A	N/A	2700
951620	56685	56700	GGTGATGCTGCAGAGC	36	N/A	N/A	2701
951621	56725	56740	CAGGATACATCACCCA	128	N/A	N/A	2702
951622	56858	56873	TATTATGAATCCCCCT	90	N/A	N/A	2703
951623	56859	56874	ATATTATGAATCCCCC	100	N/A	N/A	2704
951624	56861	56876	ACATATTATGAATCCC	52	N/A	N/A	2705
951625	57375	57390	AGTAATGACCCAGGCT	74	N/A	N/A	2706
951626	57642	57657	AGTGATGGGTCCCCAC	94	N/A	N/A	2707
951627	57738	57753	GTGAATATCAACTGTT	41	N/A	N/A	2708
951628	57916	57931	GCAGATCTGGCTGCCT	71	N/A	N/A	2709
951629	58905	58920	AGGATATTTGGCTGGG	70	N/A	N/A	2710
951630	59003	59018	ACTTATCGCAAGGAAC	71	N/A	N/A	2711
951631	59075	59090	GCGATATACCTTTCTG	26	N/A	N/A	2712

951632	59076	59091	TGCGATATACCTTTCT	19	N/A	N/A	2713
951633	59174	59189	TGAATGACAGGTGTGT	124	N/A	N/A	2714
951634	59346	59361	TACAATCACAATTGCT	47	N/A	N/A	2715
951635	60402	60417	GCCAATACCAAAGAAC	96	N/A	N/A	2716
951636	60469	60484	TCTAAATCAGGACAGT	86	N/A	N/A	2717
951637	61124	61139	GCAACATGGGCACTGC	100	N/A	N/A	2718
951638	61190	61205	TAAGATCGCATCTGGG	93	N/A	N/A	2719
951639	61274	61289	AGCTATCTGGGTTAGG	105	N/A	N/A	2720
951640	61338	61353	GGAAATAGACGATCTC	68	N/A	N/A	2721
951641	61460	61475	CCAATTTGGGCATCAA	102	N/A	N/A	2722
951642	61461	61476	GCCAATTTGGGCATCA	102	N/A	N/A	2723
951643	61530	61545	GTTATATGTGTGGCAT	35	N/A	N/A	2724
951644	61531	61546	TGTTATATGTGTGGCA	40	N/A	N/A	2725
951645	61532	61547	GTGTTATATGTGTGGC	9	N/A	N/A	2726
951646	61680	61695	GCTAAAATTCCACTCT	96	N/A	N/A	2727
951647	61796	61811	CGTAAACATGATTCCT	20	N/A	N/A	2728
951648	61841	61856	GTTATTAAGGACAACC	120	N/A	N/A	2729
951649	61857	61872	CGTTATTGTCATTTGT	46	N/A	N/A	2730
951650	61943	61958	TCGAATGAAGATGGTC	30	N/A	N/A	2731
951651	62255	62270	AATGATAAGGACCCCA	63	N/A	N/A	2732
951652	62257	62272	GTAATGATAAGGACCC	66	N/A	N/A	2733
951653	62258	62273	AGTAATGATAAGGACC	80	N/A	N/A	2734
951654	62398	62413	GTTAATTGTGCACTTG	15	N/A	N/A	2735
951655	62399	62414	TGTTAATTGTGCACTT	80	N/A	N/A	2736
951656	62400	62415	GTGTTAATTGTGCACT	109	N/A	N/A	2737
951657	62526	62541	AGTTATAAACCCTGGG	11	N/A	N/A	2738
951658	63805	63820	ACAATAATTGGCCAAA	86	N/A	N/A	2739
951659	63829	63844	GATCTAATTACCAGCT	128	N/A	N/A	2740
951660	63881	63896	TACTTAGGTTACTCCT	49	N/A	N/A	2741
951661	64400	64415	GACAATGGGTCAACGC	67	N/A	N/A	2742
951662	65042	65057	TGCTCTAAATGACTGC	96	N/A	N/A	2743
951663	65090	65105	CCACATCTATCTCAGA	112	N/A	N/A	2744
951664	65141	65156	AATATCTCAGCAGTGC	54	N/A	N/A	2745
951665	65142	65157	CAATATCTCAGCAGTG	126	N/A	N/A	2746
951666	65354	65369	GGCCTAACAGTGTCCA	105	N/A	N/A	2747
951667	65601	65616	AGTCATTAGTACGCCA	46	N/A	N/A	2748
951668	66403	66418	GTCTTGTGGGATGTGA	66	N/A	N/A	2749
951669	66821	66836	TCAATACACACTGTTG	85	N/A	N/A	2750
951670	66828	66843	GGATAATTCAATACAC	41	N/A	N/A	2751
951671	67824	67839	ATAACATGTTACTCAG	71	N/A	N/A	2752
951672	67825	67840	CATAACATGTTACTCA	87	N/A	N/A	2753
951673	67827	67842	GTCATAACATGTTACT	76	N/A	N/A	2754
951674	67828	67843	TGTCATAACATGTTAC	102	N/A	N/A	2755

951675	67840	67855	GGCACTCACAGCTGTC	119	N/A	N/A	2756
951676	68164	68179	AGCTGTTGTGCAGTGC	73	N/A	N/A	2757
951677	68238	68253	GCTAAATGTGGACTGA	28	N/A	N/A	2758
951678	68623	68638	GGCAATGCATACAGTC	44	N/A	N/A	2759
951679	68650	68665	GTTATTAACCCCCTGT	44	N/A	N/A	2760
951680	69011	69026	TCAATTACTTACAAGA	62	N/A	N/A	2761
951681	69030	69045	TGTTTATGCACCATGT	57	N/A	N/A	2762
951682	69227	69242	GAATTATGCCTTCTAC	25	N/A	N/A	2763
951683	69652	69667	GTCTATGTGGGCTGCC	80	N/A	N/A	2764
951684	69735	69750	ATCTATGGCATGGAGC	82	N/A	N/A	2765
951685	69737	69752	ACATCTATGGCATGGA	75	N/A	N/A	2766
951686	71409	71424	ACAGATAAATCAAGCC	50	N/A	N/A	2767
951687	71450	71465	CACTATGCGGCCACCA	93	N/A	N/A	2768
951688	71699	71714	GTACATACTGCAGCAG	113	N/A	N/A	2769
951689	71700	71715	GGTACATACTGCAGCA	107	N/A	N/A	2770
951690	71857	71872	GCGAATGCCATGCTTA	82	N/A	N/A	2771
951691	71968	71983	GACATTTAACACACTA	7	N/A	N/A	2772
951692	73303	73318	GGCTTAATCCCACACG	97	N/A	N/A	2773
951693	73694	73709	GAATTTGGGATTGTGG	21	N/A	N/A	2774
951694	73828	73843	TCATGCATGGCACTGT	102	N/A	N/A	2775
951695	73956	73971	AGCATAAAAGCACTCT	74	N/A	N/A	2776
951696	74038	74053	GCTATGAATTTCCTCC	10	N/A	N/A	2777
951697	74039	74054	GGCTATGAATTTCCTC	115	N/A	N/A	2778
951698	74365	74380	TGCTATGACCCTCACT	82	N/A	N/A	2779
951699	75020	75035	ACAGATAACAGTGGCG	24	N/A	N/A	2780
951700	75136	75151	GTAATTCCCGTTCTCT	16	N/A	N/A	2781
951701	75145	75160	TCTATTACCGTAATTC	23	N/A	N/A	2782
951702	75247	75262	TACATGAACAGTCTGT	50	N/A	N/A	2783
951703	75327	75342	AACTTACAAGCATCGG	91	N/A	N/A	2784
951704	75329	75344	TGAACTTACAAGCATC	94	N/A	N/A	2785
951705	75417	75432	ATCAATTTTAAACACG	31	N/A	N/A	2786
951706	75765	75780	ACAAATACATGAGGTC	32	N/A	N/A	2787
951707	75894	75909	GTATTATTCCCAGCTA	77	N/A	N/A	2788
951708	75895	75910	TGTATTATTCCCAGCT	102	N/A	N/A	2789
951709	76435	76450	GAGAATATCACAGGGT	10	N/A	N/A	2790
951710	76448	76463	TGTAATCAGTCAAGAG	18	N/A	N/A	2791
951711	76550	76565	GACAATTGTGACCGGC	88	N/A	N/A	2792
951712	76568	76583	CACAATCAGAGCATTC	34	N/A	N/A	2793
951713	76593	76608	TGATTTACAGGCCCAA	37	N/A	N/A	2794
951714	76594	76609	GTGATTTACAGGCCCA	50	N/A	N/A	2795
951715	76725	76740	ACTAATGACAGACAAC	27	N/A	N/A	2796
951716	76728	76743	TAAACTAATGACAGAC	92	N/A	N/A	2797
951717	76775	76790	TTGAATTGTGGACCAA	60	N/A	N/A	2798

951718	77126	77141	AGGTTAATGCTTCACC	54	N/A	N/A	2799
951719	77303	77318	TCAAATGGTGACCACT	112	N/A	N/A	2800
951720	77432	77447	CGTTTTAGTTTTCCTA	14	N/A	N/A	2801
951721	77538	77553	GTAATAACATGTGTCG	45	N/A	N/A	2802
951722	77539	77554	GGTAATAACATGTGTC	27	N/A	N/A	2803
951723	77570	77585	TAAACAATTGCTCATC	59	N/A	N/A	2804
951724	78076	78091	GGTAATTCTGCAAAGA	29	N/A	N/A	2805
951725	78080	78095	TAATGGTAATTCTGCA	43	N/A	N/A	2806
951726	78082	78097	ACTAATGGTAATTCTG	50	N/A	N/A	2807
951727	78166	78181	TTAGATCTCATTACCT	71	N/A	N/A	2808
951728	78206	78221	GTAACAACATCTACCT	88	N/A	N/A	2809
951729	78207	78222	GGTAACAACATCTACC	3	N/A	N/A	2810
951730	78387	78402	TGATTTACAGGATGCT	15	N/A	N/A	2811
951731	78388	78403	TTGATTTACAGGATGC	8	N/A	N/A	2812
951732	78539	78554	GCAAATGCTGGCTACG	85	N/A	N/A	2813
951733	78546	78561	CCCAATGGCAAATGCT	66	N/A	N/A	2814
951734	78848	78863	GGCACTACCTTCACCA	109	N/A	N/A	2815
951735	79046	79061	TCATATTGTTCTGCCC	15	N/A	N/A	2816
951736	79047	79062	TTCATATTGTTCTGCC	11	N/A	N/A	2817
951737	79077	79092	GGCTTTTGTCAGAGGA	8	N/A	N/A	2818
951738	79153	79168	TTCAATGACATGCTAG	19	N/A	N/A	2819
951739	79209	79224	TATATCAGCTCAGTGC	75	N/A	N/A	2820
951740	79211	79226	TATATATCAGCTCAGT	66	N/A	N/A	2821
951741	79214	79229	TTGTATATATCAGCTC	37	N/A	N/A	2822
951742	79229	79244	TCATACATAAGGATGT	91	N/A	N/A	2823
951743	79398	79413	GCTCATTGTAAACAGT	20	N/A	N/A	2824
951744	79462	79477	TGCATTTGGTCTTGCT	118	N/A	N/A	2825
951745	79799	79814	GACTATCAGTATGCAC	118	N/A	N/A	2826
951746	79845	79860	CATCATATTGGTGGGA	11	N/A	N/A	2827
951747	80265	80280	GCTATATTCACAAGGC	70	N/A	N/A	2828
951748	80266	80281	GGCTATATTCACAAGG	39	N/A	N/A	2829
951749	80520	80535	AACGATTAGGGACTCA	4	N/A	N/A	2830
951750	80663	80678	CCCTATTTGATCAGGA	117	N/A	N/A	2831
951751	80845	80860	GCAACTACCTTTGTTA	17	N/A	N/A	2832
951752	80986	81001	AGCAATTTCATTGGCC	105	N/A	N/A	2833
951753	81192	81207	AGCAATACCTTACTGG	46	N/A	N/A	2834
951754	81436	81451	TGGTATCAGGGTCCCA	130	N/A	N/A	2835
951755	81663	81678	CATGATGTCGCTGGCA	41	N/A	N/A	2836
951756	81741	81756	TCCAAAAATGGGCTGC	28	N/A	N/A	2837
951757	82016	82031	TCTAATCGAAGAAGCT	99	N/A	N/A	2838
951758	82262	82277	TCTGATTAGTCCATGC	40	N/A	N/A	2839
951759	82535	82550	ACAAATGCGGAGATGA	41	N/A	N/A	2840
951761	82653	82668	GCCAATGCAAGGTGGC	119	N/A	N/A	2841

951762	82803	82818	TGTTTTGGTGCTGGCT	99	N/A	N/A	2842
951763	82880	82895	TGGAATGGTTACTCTC	3	N/A	N/A	2843
951764	82920	82935	ATCTTCTGCAGTGTGG	2	N/A	N/A	2844
951765	83070	83085	GGTATCTGGGCCATCA	101	N/A	N/A	2845
951766	83419	83434	AGCAACATGAACCACA	26	N/A	N/A	2846
951767	84425	84440	GTAATCAAGGCAGCAA	7	N/A	N/A	2847
951768	85210	85225	AGCTCTGGTTTCAACA	82	N/A	N/A	2848
951769	85217	85232	TTAATTAAGCTCTGGT	12	N/A	N/A	2849
951770	85218	85233	CTTAATTAAGCTCTGG	22	N/A	N/A	2850
951771	85220	85235	GGCTTAATTAAGCTCT	67	N/A	N/A	2851
951772	85238	85253	AGTGACATAGCAAGCA	7	N/A	N/A	2852
951773	85417	85432	AAGAATCAGACTCTTC	110	N/A	N/A	2853
951774	85726	85741	CATTTATAACAGGCCA	82	N/A	N/A	2854
951775	85727	85742	CCATTTATAACAGGCC	94	N/A	N/A	2855
951776	85844	85859	GGCTTATGAGTCCACT	91	N/A	N/A	2856
951777	85973	85988	TGCATTAAAACTGCGA	87	N/A	N/A	2857
951778	86550	86565	AACAATCATAGCCTCA	114	N/A	N/A	2858
951779	86582	86597	AACTTACTGTCTCCCA	37	N/A	N/A	2859
951780	86937	86952	GTTTAATAATGTGCAG	40	N/A	N/A	2860
951781	86938	86953	GGTTTAATAATGTGCA	11	N/A	N/A	2861
951782	86939	86954	GGGTTTAATAATGTGC	27	N/A	N/A	2862
951783	87671	87686	TCGCTAAAGGCTCTGA	10	N/A	N/A	2863
951784	87858	87873	TGAAATCAGGGCTCCC	31	N/A	N/A	2864
951785	88030	88045	CTCTATCACAGGGCCC	92	N/A	N/A	2865
951786	88032	88047	TGCTCTATCACAGGGC	30	N/A	N/A	2866
951787	88258	88273	TGTATCTGGTGACTCC	5	N/A	N/A	2867
951788	88270	88285	ACCGATAAATGTTGTA	65	N/A	N/A	2868
951789	88634	88649	TATAGTAACAGCTGGG	73	N/A	N/A	2869
951790	88637	88652	CAGTATAGTAACAGCT	94	N/A	N/A	2870
951791	88638	88653	TCAGTATAGTAACAGC	41	N/A	N/A	2871
951792	88880	88895	TGTTTAAGGACTCCAC	28	N/A	N/A	2872
951793	88887	88902	GACAATTTGTTTAAGG	5	N/A	N/A	2873
951794	89152	89167	GATCTAATCAGAAGCA	29	N/A	N/A	2874
951795	89558	89573	TGAGATTACGCACCAC	5	N/A	N/A	2875
951796	89718	89733	ATTATAGGGCTTCTTA	30	N/A	N/A	2876
951797	89720	89735	TTATTATAGGGCTTCT	8	N/A	N/A	2877
951798	89721	89736	TTTATTATAGGGCTTC	1	N/A	N/A	2878
951799	89722	89737	GTTTATTATAGGGCTT	1	N/A	N/A	2879
951800	89746	89761	AGTGATATTCCCAACA	19	N/A	N/A	2880
951801	89977	89992	CATATATCTCCTGTTA	20	N/A	N/A	2881
951802	89999	90014	TCATATCACCACTTGC	29	N/A	N/A	2882
951803	90003	90018	ACAATCATATCACCAC	6	N/A	N/A	2883
951804	90004	90019	GACAATCATATCACCA	3	N/A	N/A	2884

951805	90058	90073	TTATATGTGGACACCT	34	N/A	N/A	2885
951806	90059	90074	TTTATATGTGGACACC	10	N/A	N/A	2886
951807	90139	90154	CACAATCCCAGATCTC	7	N/A	N/A	2887
951808	90161	90176	TCTATAAGGTTCCTTA	14	N/A	N/A	2888
951809	90165	90180	TGTTTCTATAAGGTTC	3	N/A	N/A	2889
951810	90199	90214	CCAAATTTAGAGGACA	46	N/A	N/A	2890
951811	90222	90237	ACATATCTTGCATGAC	4	N/A	N/A	2891
951812	90264	90279	TTAGACATCAGACTGT	76	N/A	N/A	2892
951813	90267	90282	GTCTTAGACATCAGAC	115	N/A	N/A	2893
951814	90706	90721	TCAATTGAGGCTTCTA	7	N/A	N/A	2894
951815	90716	90731	TGTATCTGGTTCAATT	11	N/A	N/A	2895
951816	90721	90736	GTAAATGTATCTGGTT	2	N/A	N/A	2896
951817	91071	91086	GGTACTGAGGCTGTGG	28	N/A	N/A	2897
951818	91117	91132	CAGAATTATCAATTCC	145	N/A	N/A	2898
951819	91174	91189	GGTGGGTAAAATGTGC	63	N/A	N/A	2899
951820	91191	91206	GCACATAGGGCCTTCT	79	N/A	N/A	2900
951821	91909	91924	GACAATGTAGTTTCCA	2	N/A	N/A	2901
951822	91939	91954	AACTATCCCAAGCTCC	10	N/A	N/A	2902
951823	91945	91960	GGCTTCAACTATCCCA	39	N/A	N/A	2903
951824	92037	92052	ATTGATACAGCCGTTC	8	N/A	N/A	2904
951825	92827	92842	ATGATAAAGGCTGGCA	21	N/A	N/A	2905
951826	92828	92843	AATGATAAAGGCTGGC	127	N/A	N/A	2906
951827	93169	93184	AAGATTATGGTTTCCT	4	N/A	N/A	2907
951828	93170	93185	GAAGATTATGGTTTCC	6	N/A	N/A	2908
951829	93241	93256	GTACATGGTGGAGTCC	83	N/A	N/A	2909
951830	93321	93336	TGTATTACCTACGGCA	6	N/A	N/A	2910
951831	93392	93407	GCTATTAATCATATTC	18	N/A	N/A	2911
951832	93572	93587	TACTTACCAGGATCTC	24	N/A	N/A	2912
951833	93746	93761	ACTTATACCCAGGGCA	7	N/A	N/A	2913
951834	93747	93762	GACTTATACCCAGGGC	81	N/A	N/A	2914
951835	93923	93938	ATGAATTCTGGTCTGG	2	N/A	N/A	2915
951836	94043	94058	TCAACTAGCCATGTCT	25	N/A	N/A	2916
951837	94169	94184	CACTTAGCCACATCTG	5	N/A	N/A	2917
951838	94174	94189	TTAATCACTTAGCCAC	8	N/A	N/A	2918
951839	94177	94192	ACCTTAATCACTTAGC	5	N/A	N/A	2919
951840	94182	94197	ACAATACCTTAATCAC	7	N/A	N/A	2920
951841	94284	94299	CAATTTATCTGGAGGA	8	N/A	N/A	2921
951842	94350	94365	TCAATTAGTGTTGCCT	119	N/A	N/A	2922
951843	94351	94366	ATCAATTAGTGTTGCC	5	N/A	N/A	2923
951844	94423	94438	GTCAATCGACTGGTAC	41	N/A	N/A	2924
951845	94446	94461	ATATGATTCATCTCGG	2	N/A	N/A	2925
951846	94447	94462	AATATGATTCATCTCG	2	N/A	N/A	2926
951847	94583	94598	AGCTATGAGTAGCAGG	18	N/A	N/A	2927

951848	94885	94900	GCCAACTAATTCCTCC	31	N/A	N/A	2928
951849	96000	96015	GCCATTCACGGGCTGC	104	N/A	N/A	2929
951850	96084	96099	CAAGGGTACAGACTTA	152	N/A	N/A	2930
951851	96224	96239	GGCTGGATGTGAGTGC	63	N/A	N/A	2931
951852	96650	96665	ACAACTAACGGCAGGC	17	N/A	N/A	2932
951853	96755	96770	ACACATCAGGGTTTCA	56	N/A	N/A	2933
951854	97483	97498	TCCTAATGGTGACTCA	40	N/A	N/A	2934
951855	97854	97869	TACAATGTAAGCCTTT	7	N/A	N/A	2935
951856	98522	98537	GTATTTCAAAGTAGTC	4	N/A	N/A	2936
951857	98652	98667	GGTTTTAATAGACACA	6	N/A	N/A	2937
951858	98653	98668	GGGTTTTAATAGACAC	53	N/A	N/A	2938
951859	99483	99498	GTTAACAACAATTGTC	60	N/A	N/A	2939
951860	99712	99727	ACAGATCTTGCATGTT	84	N/A	N/A	2940
951861	99888	99903	AGCTATCACACAGAAG	95	N/A	N/A	2941
951862	100033	100048	GCAAATCCATTGCCCA	78	N/A	N/A	2942
951863	100171	100186	GTGTTAAGGTGGCAAC	43	N/A	N/A	2943
951864	100222	100237	CTACATGGTGATGGGT	20	N/A	N/A	2944
951865	100285	100300	GTTAGCTGGACTCACA	89	N/A	N/A	2945
951866	100375	100390	CAATATCCTGGTGACT	36	N/A	N/A	2946
951867	100514	100529	ACACATGCAGTGAGCC	60	N/A	N/A	2947
951868	101384	101399	TGTATGGTGGCTCAGC	26	N/A	N/A	2948
951869	101385	101400	TTGTATGGTGGCTCAG	44	N/A	N/A	2949
951870	101796	101811	TGCAATGCTGCCAGGC	72	N/A	N/A	2950
951871	102161	102176	AGAGATATTGATGTCT	51	N/A	N/A	2951
951872	102425	102440	GCACATTGGTTAGGCT	93	N/A	N/A	2952
951873	102445	102460	CTCAATGTGTACAGTA	22	N/A	N/A	2953
951874	102885	102900	TGGAACTGTTTACAGT	10	N/A	N/A	2954
951875	102926	102941	CAAGTAACTGAGTCAC	7	N/A	N/A	2955
951876	103421	103436	ATCTATCCAAGGAGGA	93	N/A	N/A	2956
951877	103897	103912	TCAGTTCACGGATCCC	42	N/A	N/A	2957
951878	104120	104135	TGCTTTCTAAGGTTGG	14	N/A	N/A	2958
951879	104441	104456	TTTTATCTGGGCTCCA	39	N/A	N/A	2959
951880	104447	104462	TGGAACTTTTATCTGG	17	N/A	N/A	2960
951881	104452	104467	GTGAATGGAACTTTTA	5	N/A	N/A	2961
951882	104843	104858	TGTATATGAGCCCATC	99	N/A	N/A	2962
951883	105539	105554	TCATATCCATGCCCAC	31	N/A	N/A	2963
951884	105559	105574	ACAATTGGTGCCTTTC	14	N/A	N/A	2964
951885	105560	105575	CACAATTGGTGCCTTT	20	N/A	N/A	2965
951886	105730	105745	GGACATCACACTCCTC	100	N/A	N/A	2966
951887	105777	105792	CGCAATGGTGACTGCC	114	N/A	N/A	2967
951888	105791	105806	TGAAATACCATCCACG	40	N/A	N/A	2968
951889	105793	105808	CTTGAAATACCATCCA	19	N/A	N/A	2969
951890	106015	106030	GCCTTTACTGACAGCT	71	N/A	N/A	2970

951891	106173	106188	ACAAATGGGTCTCGAG	101	N/A	N/A	2971
951892	106195	106210	GGTTTTCACGGCCAGC	44	N/A	N/A	2972
951893	106203	106218	GCTATGAAGGTTTTCA	10	N/A	N/A	2973
951894	106204	106219	AGCTATGAAGGTTTTC	20	N/A	N/A	2974
951895	106233	106248	TGTCATATGGCCAGGG	17	N/A	N/A	2975
951896	106295	106310	TAATATTGTCACCCTC	93	N/A	N/A	2976
951897	106296	106311	ATAATATTGTCACCCT	29	N/A	N/A	2977
951898	106351	106366	GTTTTTGCAGCTACTA	9	N/A	N/A	2978
951899	106371	106386	ACTATCAACCATCTTA	20	N/A	N/A	2979
951900	106391	106406	GGACTTAATTTACACA	12	N/A	N/A	2980
951901	106392	106407	TGGACTTAATTTACAC	30	N/A	N/A	2981
951902	106404	106419	GATACTAAAGTCTGGA	11	N/A	N/A	2982
951903	107100	107115	GCAGATGGTGGTCTAC	69	N/A	N/A	2983
951904	109198	109213	GCATTTTAATATTGGG	31	N/A	N/A	2984
951905	109409	109424	GGTTTAAGCGATCTCC	46	N/A	N/A	2985
951906	109955	109970	CCAATAACTGACCTCA	72	N/A	N/A	2986
951907	109956	109971	ACCAATAACTGACCTC	54	N/A	N/A	2987
951908	111211	111226	AGTTATTCTGATGCCA	3	N/A	N/A	2988
951909	111349	111364	GGGTATGGTTGCAACC	92	N/A	N/A	2989
951910	111384	111399	TCATTAGGACACAGCG	20	N/A	N/A	2990
951911	111385	111400	ATCATTAGGACACAGC	6	N/A	N/A	2991
951912	111494	111509	TACTATCAGTACAGCT	83	N/A	N/A	2992
951913	111496	111511	GATACTATCAGTACAG	42	N/A	N/A	2993
951914	111499	111514	GGAGATACTATCAGTA	115	N/A	N/A	2994
951915	111500	111515	TGGAGATACTATCAGT	27	N/A	N/A	2995
951916	112149	112164	GTGAACACTGATCACT	86	N/A	N/A	2996
951917	112185	112200	GGTATATGAGGAAACA	18	N/A	N/A	2997
951918	112208	112223	CCGTATATGTCTCCGA	8	N/A	N/A	2998
951919	112209	112224	ACCGTATATGTCTCCG	7	N/A	N/A	2999
951920	112293	112308	GGCAATTGTCTCTCTT	47	N/A	N/A	3000
951921	112316	112331	TGTATAAGCTCACTTT	40	N/A	N/A	3001
951922	112318	112333	CATGTATAAGCTCACT	105	N/A	N/A	3002
951923	112320	112335	AGCATGTATAAGCTCA	36	N/A	N/A	3003
951924	112369	112384	ATAATTATGTCCCATC	24	N/A	N/A	3004
951925	112370	112385	GATAATTATGTCCCAT	5	N/A	N/A	3005
951926	112371	112386	GGATAATTATGTCCCA	61	N/A	N/A	3006
951927	112372	112387	TGGATAATTATGTCCC	102	N/A	N/A	3007
951928	112373	112388	ATGGATAATTATGTCC	105	N/A	N/A	3008
951929	112950	112965	ACTACTAGTTTCTGTT	91	N/A	N/A	3009
951930	112951	112966	CACTACTAGTTTCTGT	37	N/A	N/A	3010
951931	113712	113727	GGTTATGAGATTCTTA	4	N/A	N/A	3011
951932	113713	113728	TGGTTATGAGATTCTT	5	N/A	N/A	3012
951933	114474	114489	TTTATTCACAGGGTCC	29	N/A	N/A	3013

951934	114476	114491	TATTTATTCACAGGGT	28	N/A	N/A	3014
951935	114477	114492	GTATTTATTCACAGGG	18	N/A	N/A	3015
951936	114510	114525	GCCAATGGAAGGCACC	129	N/A	N/A	3016
951937	114524	114539	TCCATTTGGGCTGTGC	86	N/A	N/A	3017
951938	114750	114765	TGCGATATCCTCCCCT	15	N/A	N/A	3018
951939	115717	115732	GAGAATAAAGCCTGGC	80	N/A	N/A	3019
908415	83669	83684	GATTGAGGTAAGGGTT	20	N/A	N/A	3020
	83757	83772			N/A	N/A	
	83845	83860			N/A	N/A	
908426	83689	83704	ACGGAACCGCTCTGTA	88	N/A	N/A	509
	83777	83792			N/A	N/A	
	83865	83880			N/A	N/A	
908428	83691	83706	TGACGGAACCGCTCTG	73	N/A	N/A	511
	83779	83794			N/A	N/A	
	83867	83882			N/A	N/A	
908507	103213	103228	AGCAGAGCATAGGAGA	20	N/A	N/A	590
	103251	103266			N/A	N/A	
949039	7946	7961	AAGTGCTATTATAACT	100	N/A	N/A	3021
	8587	8602			N/A	N/A	
949040	7947	7962	GAAGTGCTATTATAAC	8	N/A	N/A	3022
	8588	8603			N/A	N/A	
949041	7948	7963	AGAAGTGCTATTATAA	6	N/A	N/A	3023
	8589	8604			N/A	N/A	
949042	7949	7964	AAGAAGTGCTATTATA	15	N/A	N/A	3024
	8590	8605			N/A	N/A	
949043	7950	7965	AAAGAAGTGCTATTAT	37	N/A	N/A	3025
	8591	8606			N/A	N/A	
949044	7951	7966	GAAAGAAGTGCTATTA	19	N/A	N/A	3026
	8592	8607			N/A	N/A	
949045	7952	7967	GGAAAGAAGTGCTATT	20	N/A	N/A	3027
	8593	8608			N/A	N/A	
949046	7953	7968	GGGAAAGAAGTGCTAT	36	N/A	N/A	3028
	8594	8609			N/A	N/A	
949047	7954	7969	AGGGAAAGAAGTGCTA	64	N/A	N/A	3029
	8595	8610			N/A	N/A	
949048	7955	7970	AAGGGAAAGAAGTGCT	22	N/A	N/A	3030
	8596	8611			N/A	N/A	
949049	7956	7971	AAAGGGAAAGAAGTGC	21	N/A	N/A	3031
	8597	8612			N/A	N/A	
949060	9158	9173	TAAAATGTACCCCCTC	42	N/A	N/A	3032
	9478	9493			N/A	N/A	
949133	16330	16345	GAAAAGAACAACCTGG	21	N/A	N/A	3033
	16655	16670			N/A	N/A	

949913	83642	83657	TGCAGCTGTCAGCATG	61	N/A	N/A	3034
	83730	83745			N/A	N/A	
	83818	83833			N/A	N/A	
949914	83643	83658	ATGCAGCTGTCAGCAT	113	N/A	N/A	3035
	83731	83746			N/A	N/A	
	83819	83834			N/A	N/A	
949915	83644	83659	TATGCAGCTGTCAGCA	59	N/A	N/A	3036
	83732	83747			N/A	N/A	
	83820	83835			N/A	N/A	
949916	83645	83660	ATATGCAGCTGTCAGC	16	N/A	N/A	3037
	83733	83748			N/A	N/A	
	83821	83836			N/A	N/A	
949917	83648	83663	GCCATATGCAGCTGTC	13	N/A	N/A	3038
	83736	83751			N/A	N/A	
	83824	83839			N/A	N/A	
949918	83652	83667	CTTTGCCATATGCAGC	8	N/A	N/A	3039
	83740	83755			N/A	N/A	
	83828	83843			N/A	N/A	
949919	83653	83668	ACTTTGCCATATGCAG	15	N/A	N/A	3040
	83741	83756			N/A	N/A	
	83829	83844			N/A	N/A	
949920	83654	83669	TACTTTGCCATATGCA	4	N/A	N/A	3041
	83742	83757			N/A	N/A	
	83830	83845			N/A	N/A	
949921	83655	83670	TTACTTTGCCATATGC	1	N/A	N/A	3042
	83743	83758			N/A	N/A	
	83831	83846			N/A	N/A	
949922	83656	83671	GTTACTTTGCCATATG	4	N/A	N/A	3043
	83744	83759			N/A	N/A	
	83832	83847			N/A	N/A	
949923	83657	83672	GGTTACTTTGCCATAT	8	N/A	N/A	3044
	83745	83760			N/A	N/A	
	83833	83848			N/A	N/A	
949924	83668	83683	ATTGAGGTAAGGGTTA	4	N/A	N/A	3045
	83756	83771			N/A	N/A	
	83844	83859			N/A	N/A	
949925	83675	83690	TATCTTGATTGAGGTA	6	N/A	N/A	3046
	83763	83778			N/A	N/A	
	83851	83866			N/A	N/A	
949926	83676	83691	GTATCTTGATTGAGGT	2	N/A	N/A	3047
	83764	83779			N/A	N/A	
	83852	83867			N/A	N/A	
949927	83677	83692	TGTATCTTGATTGAGG	1	N/A	N/A	3048

	83765	83780			N/A	N/A	
	83853	83868			N/A	N/A	
949928	83678	83693	CTGTATCTTGATTGAG	4	N/A	N/A	3049
	83766	83781			N/A	N/A	
	83854	83869			N/A	N/A	
949929	83682	83697	CGCTCTGTATCTTGAT	2	N/A	N/A	3050
	83770	83785			N/A	N/A	
	83858	83873			N/A	N/A	
949930	83683	83698	CCGCTCTGTATCTTGA	9	N/A	N/A	3051
	83771	83786			N/A	N/A	
	83859	83874			N/A	N/A	
949931	83700	83715	TTTAGGAGGTGACGGA	6	N/A	N/A	3052
	83788	83803			N/A	N/A	
	83876	83891			N/A	N/A	
949932	83701	83716	TTTTAGGAGGTGACGG	7	N/A	N/A	3053
	83789	83804			N/A	N/A	
	83877	83892			N/A	N/A	
949933	83702	83717	ATTTTAGGAGGTGACG	17	N/A	N/A	3054
	83878	83893			N/A	N/A	
949934	83703	83718	GATTTTAGGAGGTGAC	15	N/A	N/A	3055
	83879	83894			N/A	N/A	
949935	83704	83719	GGATTTTAGGAGGTGA	6	N/A	N/A	3056
	83880	83895			N/A	N/A	
949936	83705	83720	GGGATTTTAGGAGGTG	15	N/A	N/A	3057
	83881	83896			N/A	N/A	
949937	83706	83721	AGGGATTTTAGGAGGT	8	N/A	N/A	3058
	83882	83897			N/A	N/A	
949938	83707	83722	CAGGGATTTTAGGAGG	12	N/A	N/A	3059
	83883	83898			N/A	N/A	
949939	83708	83723	ACAGGGATTTTAGGAG	18	N/A	N/A	3060
	83884	83899			N/A	N/A	
949940	83728	83743	CAGCTGTCAGCATGAT	63	N/A	N/A	3061
	83816	83831			N/A	N/A	
949941	83729	83744	GCAGCTGTCAGCATGA	67	N/A	N/A	3062
	83817	83832			N/A	N/A	
950194	103191	103206	CGGTGGCCATGGAGGG	67	N/A	N/A	3063
	103229	103244			N/A	N/A	
	103267	103282			N/A	N/A	
950195	103192	103207	CCGGTGGCCATGGAGG	98	N/A	N/A	3064
	103230	103245			N/A	N/A	
	103268	103283			N/A	N/A	
950196	103193	103208	CCCGGTGGCCATGGAG	91	N/A	N/A	3065
	103231	103246			N/A	N/A	

	103269	103284			N/A	N/A	
950197	103194	103209	GCCCGGTGGCCATGGA	122	N/A	N/A	3066
	103232	103247			N/A	N/A	
	103270	103285			N/A	N/A	
950198	103195	103210	GGCCCGGTGGCCATGG	106	N/A	N/A	3067
	103233	103248			N/A	N/A	
	103271	103286			N/A	N/A	
950199	103196	103211	GGGCCCGGTGGCCATG	125	N/A	N/A	3068
	103234	103249			N/A	N/A	
	103272	103287			N/A	N/A	
950200	103210	103225	AGAGCATAGGAGAGGG	20	N/A	N/A	3069
	103248	103263			N/A	N/A	
950201	103212	103227	GCAGAGCATAGGAGAG	21	N/A	N/A	3070
	103250	103265			N/A	N/A	
950202	103214	103229	GAGCAGAGCATAGGAG	23	N/A	N/A	3071
	103252	103267			N/A	N/A	
950203	103215	103230	GGAGCAGAGCATAGGA	22	N/A	N/A	3072
	103253	103268			N/A	N/A	
950204	103217	103232	AGGGAGCAGAGCATAG	53	N/A	N/A	3073
	103255	103270			N/A	N/A	
950205	103219	103234	GGAGGGAGCAGAGCAT	50	N/A	N/A	3074
	103257	103272			N/A	N/A	
950206	103221	103236	ATGGAGGGAGCAGAGC	53	N/A	N/A	3075
	103259	103274			N/A	N/A	
950297	113289	113304	ATCCTGTTATATCTTT	3	N/A	N/A	3076
	113606	113621			N/A	N/A	
950298	113290	113305	AATCCTGTTATATCTT	2	N/A	N/A	3077
	113607	113622			N/A	N/A	

Each modified oligonucleotide listed in the table below is 100% complementary to human DNM2 nucleic acid sequence GENBANK Number NM_001005361.2. (SEQ ID No: 3(. As shown below, modified oligonucleotides complementary to human DNM2 inhibited human DNM2 mRNA expression.

Table 4: DNM2 mRNA Expression

Compound Number	SEQ ID: 3 Start Site	SEQ ID: 3 Stop Site	Sequence	Dynamin2 (%Control)	SEQ ID NO
948482	1735	1750	CACCAGGATCTCCCCC	30	3078
948483	1738	1753	GATCACCAGGATCTCC	101	3079
948509	1511	1526	GCTTCTCGGCACACTT	27	3080
948510	1512	1527	AGCTTCTCGGCACACT	48	3081
948511	1514	1529	TGAGCTTCTCGGCACA	111	3082

948512	1520	1535	AGGAACTGAGCTTCTC	39	3083
948513	1521	1536	TAGGAACTGAGCTTCT	37	3084

Example 3: Effect of modified oligonucleotides complementary to dynamin 2 *in vitro*

Modified oligonucleotides complementary to dynamin 2 (DNM2) nucleic acid were designed and tested for their effect on dynamin 2 mRNA *in vitro*. The modified oligonucleotides were tested in a series of experiments that had similar culture conditions.

A431 cells cultured at a density of 10,000 cells per well were treated with only 500 nM of modified oligonucleotide via free uptake or no modified oligonucleotide for untreated controls. After approximately 24 hours, RNA was isolated from the cells and DNM2 mRNA levels were measured by quantitative real-time PCR as described in Example 1.

The modified oligonucleotides described in the tables below each have a 3-10-3 cEt gapmer motif, wherein the central gap segment contains ten 2'-deoxynucleosides and is flanked by wing segments on the 3' and 5' ends, each containing three cEt nucleosides. Each modified oligonucleotide listed in the tables below is 100% complementary to human DNM2 nucleic acid sequence GENBANK Number NC_000019.10, truncated from 10715001 to 1083500 (SEQ ID NO: 1) and/or GENBANK Number NM_004945.3 (SEQ ID NO: 2). As shown below, modified oligonucleotides complementary to human DNM2 inhibited human DNM2 mRNA expression.

Table 5: DNM2 mRNA Expression

Compound Number	SEQ ID: 1 Start Site	SEQ ID: 1 Stop Site	Sequence	DNM2 (% Control)	SEQ ID: 2 Start Site	SEQ ID 2: Stop Site	SEQ ID NO
694824	57496	57511	TTTTGGACTTGCAGTG	25	443	458	3085
695171	82451	82466	ACACACTTCAAACTCG	30	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	26	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	28	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	31	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	27	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	42	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	37	N/A	N/A	13
695171	82451	82466	ACACACTTCAAACTCG	29	N/A	N/A	13
951371	11922	11937	GTTGATAGTCGGTTGT	9	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	8	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	7	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	7	N/A	N/A	2452

951371	11922	11937	GTTGATAGTCGGTTGT	7	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	10	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	19	N/A	N/A	2452
951371	11922	11937	GTTGATAGTCGGTTGT	9	N/A	N/A	2452
988378	82447	82462	ACTTCAAACTCGGCTC	24	N/A	N/A	3086
988379	81166	81181	AACTGTATTGATTAGC	20	1492	1507	3087
988380	116569	116584	GTGTGGTTAATATGGC	2	3313	3328	3088
988381	116853	116868	ATAGAATACAGAGTGC	19	3597	3612	3089
988382	11917	11932	TAGTCGGTTGTCTGGA	21	N/A	N/A	3090
988383	11919	11934	GATAGTCGGTTGTCTG	37	N/A	N/A	3091
988384	11920	11935	TGATAGTCGGTTGTCT	67	N/A	N/A	3092
988385	11921	11936	TTGATAGTCGGTTGTC	26	N/A	N/A	3093
988386	11923	11938	AGTTGATAGTCGGTTG	3	N/A	N/A	3094
988387	11924	11939	GAGTTGATAGTCGGTT	5	N/A	N/A	3095
988388	11925	11940	CGAGTTGATAGTCGGT	9	N/A	N/A	3096
988389	11927	11942	AGCGAGTTGATAGTCG	42	N/A	N/A	3097
988390	24283	24298	GTATTATGGTATGTGA	14	N/A	N/A	3098
988391	24286	24301	TAGGTATTATGGTATG	20	N/A	N/A	3099
988392	24287	24302	TTAGGTATTATGGTAT	31	N/A	N/A	3100
988393	24288	24303	ATTAGGTATTATGGTA	29	N/A	N/A	3101
988394	24290	24305	GGATTAGGTATTATGG	6	N/A	N/A	3102
988395	82040	82055	TTGGACTGTTTTCCCC	39	N/A	N/A	3103
988396	82042	82057	GTTTGGACTGTTTTCC	7	N/A	N/A	3104
988397	82824	82839	GATGTGTTTCCTGTGT	2	N/A	N/A	3105
988398	82825	82840	TGATGTGTTTCCTGTG	3	N/A	N/A	3106
988399	82826	82841	ATGATGTGTTTCCTGT	5	N/A	N/A	3107
988400	82828	82843	AGATGATGTGTTTCCT	4	N/A	N/A	3108
988401	82829	82844	CAGATGATGTGTTTCC	4	N/A	N/A	3109
988402	82830	82845	ACAGATGATGTGTTTC	7	N/A	N/A	3110
988403	82832	82847	ATACAGATGATGTGTT	99	N/A	N/A	3111
988404	83917	83932	TTTTTGAGAGGTTGAC	19	N/A	N/A	3112
988405	89716	89731	TATAGGGCTTCTTATC	61	N/A	N/A	3113
988406	89717	89732	TTATAGGGCTTCTTAT	64	N/A	N/A	3114
988407	89723	89738	AGTTTATTATAGGGCT	8	N/A	N/A	3115
988408	89724	89739	AAGTTTATTATAGGGC	13	N/A	N/A	3116
988409	89725	89740	TAAGTTTATTATAGGG	25	N/A	N/A	3117
988410	89726	89741	GTAAGTTTATTATAGG	24	N/A	N/A	3118
988411	89727	89742	AGTAAGTTTATTATAG	96	N/A	N/A	3119
988412	90717	90732	ATGTATCTGGTTCAAT	34	N/A	N/A	3120
988413	90718	90733	AATGTATCTGGTTCAA	11	N/A	N/A	3121
988414	90719	90734	AAATGTATCTGGTTCA	8	N/A	N/A	3122

988415	90720	90735	TAAATGTATCTGGTTC	11	N/A	N/A	3123
988416	90723	90738	AAGTAAATGTATCTGG	15	N/A	N/A	3124
988417	90724	90739	CAAGTAAATGTATCTG	51	N/A	N/A	3125
988418	90725	90740	ACAAGTAAATGTATCT	45	N/A	N/A	3126
988419	90726	90741	AACAAGTAAATGTATC	109	N/A	N/A	3127
988420	93918	93933	TTCTGGTCTGGCTTAA	16	N/A	N/A	3128
988421	93920	93935	AATTCTGGTCTGGCTT	45	N/A	N/A	3129
988422	93922	93937	TGAATTCTGGTCTGGC	7	N/A	N/A	3130
988423	93924	93939	AATGAATTCTGGTCTG	30	N/A	N/A	3131
988424	93925	93940	GAATGAATTCTGGTCT	80	N/A	N/A	3132
988425	93926	93941	AGAATGAATTCTGGTC	20	N/A	N/A	3133
988426	93928	93943	CAAGAATGAATTCTGG	74	N/A	N/A	3134

Example 4: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested at various doses via free uptake in A431 cells. Cells were cultured at a density of 10,000 cells per well and treated with 62.5, 250, 1,000, or 4,000 nM of modified oligonucleotide, as specified in the table below. After a treatment period of approximately 48 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with ribogreen. As illustrated in the tables below, DNM2 mRNA expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 6: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)				IC_{50} (μM)
	62.5 nM	250nM	1,000 nM	4,000 nM	
694838	31	12	5	3	< 0.1
695171	74	28	11	4	0.1
695171	83	33	11	5	0.2
695171	57	25	7	3	0.1
695171	59	24	9	4	0.1
695171	51	17	9	4	< 0.1
695171	57	28	10	4	0.1
907945	38	10	5	3	< 0.1
907946	70	36	17	11	0.2
907947	48	28	9	6	< 0.1
907948	51	22	9	5	< 0.1
907949	77	43	16	6	0.2
907966	53	30	15	8	< 0.1
907967	32	10	6	4	< 0.1

907968	65	30	14	8	0.1
907969	19	6	3	2	< 0.1
907970	20	5	3	2	< 0.1
907971	59	30	17	12	0.1
907972	72	36	18	17	0.2
907975	35	15	7	4	< 0.1
907979	55	26	14	10	< 0.1
907983	39	16	9	8	< 0.1
907998	40	13	6	4	< 0.1
908000	71	42	19	11	0.2
908011	53	24	13	9	< 0.1
908013	52	25	13	7	< 0.1
908025	69	31	13	6	0.1
908027	38	13	5	2	< 0.1
908028	80	51	22	9	0.3
908029	83	43	19	9	0.3
908031	44	13	4	2	< 0.1
908033	52	18	8	5	< 0.1
908034	63	29	13	8	0.1
908035	26	6	2	1	< 0.1
908036	71	39	20	11	0.2
908037	26	9	3	1	< 0.1
908041	49	19	6	3	< 0.1
908043	28	15	10	8	< 0.1
908044	43	17	7	3	< 0.1
908047	54	28	15	9	< 0.1
908049	49	15	6	3	< 0.1
908052	53	21	7	4	< 0.1
908055	69	36	19	12	0.2
908056	54	23	9	6	< 0.1
908059	35	11	3	2	< 0.1
908061	27	7	2	1	< 0.1
908068	72	41	21	10	0.2
908070	64	35	15	9	0.1
908085	68	33	18	11	0.1
908098	61	28	12	10	0.1
908102	42	28	17	11	< 0.1
908104	44	23	12	8	< 0.1
908107	51	25	11	7	< 0.1
908135	46	23	14	14	< 0.1
908138	50	24	11	6	< 0.1
908146	58	33	19	15	0.1
908147	37	18	10	6	< 0.1

908148	42	15	7	5	< 0.1
908154	28	9	3	2	< 0.1
908164	65	31	16	10	0.1
908166	44	18	9	5	< 0.1
908167	62	28	16	12	0.1
908177	69	37	15	7	0.2
908178	52	22	6	4	< 0.1
908179	47	18	7	4	< 0.1
908183	58	34	15	11	0.1
908184	56	24	11	8	< 0.1
908201	26	13	5	4	< 0.1
908213	37	13	5	3	< 0.1
908214	57	37	17	12	0.1
908215	63	30	12	6	0.1
908217	32	10	3	2	< 0.1
908232	58	26	6	3	0.1
908255	64	28	13	9	0.1
908267	48	28	12	8	< 0.1
908355	83	62	42	26	0.6
908389	43	16	5	3	< 0.1
908392	12	3	1	1	< 0.1
908396	57	19	6	3	< 0.1
908401	26	6	2	1	< 0.1
908404	58	29	15	8	0.1
908405	49	26	9	4	< 0.1
908407	70	30	12	5	0.1
908408	18	2	1	1	< 0.1
908409	67	33	13	5	0.1
908410	71	36	15	7	0.2
908412	58	24	10	6	0.1
908413	33	8	2	1	< 0.1
908414	25	6	3	2	< 0.1
908415	40	11	4	3	< 0.1
908416	42	13	4	1	< 0.1
908417	26	5	2	1	< 0.1
908418	63	33	11	4	0.1
908419	50	11	4	2	< 0.1
908420	17	3	1	1	< 0.1
908421	23	4	1	1	< 0.1
908422	51	16	5	3	< 0.1
908424	57	22	9	7	< 0.1
908425	57	38	20	12	0.1
908434	54	20	8	3	< 0.1

908436	71	40	17	8	0.2
908439	38	9	2	2	< 0.1
908440	25	6	3	3	< 0.1
908441	33	6	2	1	< 0.1
908442	32	9	3	1	< 0.1
908443	56	17	5	2	< 0.1
908444	31	7	2	1	< 0.1
908448	78	44	13	8	0.2
908449	47	20	7	4	< 0.1
908451	45	14	6	5	< 0.1
908475	66	29	12	5	0.1
908506	34	9	4	3	< 0.1
908507	67	39	16	10	0.1
908508	52	30	14	10	< 0.1

Example 5: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested via free uptake at various doses in A431 cells. Cells were cultured at a density of 10,000 cells per well and treated with 31.25, 125, 500, or 2,000 nM of modified oligonucleotide, as specified in the tables below. After approximately 48 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with ribogreen. As illustrated in the tables below, DNM2 mRNA expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 7: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)				IC50 (μM)
	31.25 nM	125 nM	500 nM	2,000 nM	
695015	105	94	89	94	> 2.0
695170	62	30	13	5	0.05
695171	72	33	11	4	0.07
695171	70	33	10	3	0.1
695171	70	35	14	6	0.1
695171	58	22	9	2	< 0.03
695171	71	36	12	4	0.08
695171	70	32	11	4	0.07
695171	74	36	12	4	0.08
695171	71	31	10	3	0.07
695171	73	36	14	4	0.08
695171	73	36	17	7	0.09
695171	54	27	10	3	< 0.03
695171	69	33	10	5	0.06

695171	74	35	12	4	0.08
695171	81	40	14	4	0.11
695171	79	40	14	5	0.11
695171	77	38	14	5	0.10
695171	72	37	13	5	0.08
695171	71	34	11	4	0.07
695171	66	43	11	5	0.08
695171	68	33	11	4	0.06
695171	63	29	12	5	0.05
948488	79	33	12	4	0.09
948489	53	17	5	1	< 0.03
948490	25	5	1	0	< 0.03
948492	67	32	9	4	0.06
948496	72	43	15	6	0.09
948505	67	36	12	5	0.07
948506	58	16	5	2	< 0.03
948507	80	30	9	3	0.1
948508	63	26	7	3	0.0
948521	79	35	19	13	0.11
948524	70	43	19	9	0.09
948525	75	47	19	7	0.12
948526	73	35	12	7	0.08
948527	62	31	14	9	0.05
948528	64	29	11	20	0.04
948538	104	95	96	91	> 2.0
948549	71	38	16	11	0.08
948556	36	11	4	3	< 0.03
948557	23	8	4	3	< 0.03
948558	68	29	14	10	0.06
948559	48	16	7	5	< 0.03
948560	24	7	3	2	< 0.03
948562	69	26	10	5	0.06
948568	57	26	11	7	< 0.03
948575	73	39	20	10	0.1
948587	43	14	7	4	< 0.03
948589	66	21	11	9	0.04
948590	53	35	16	10	0.03
948602	39	15	7	5	< 0.03
948604	42	17	7	4	< 0.03
948608	54	18	6	4	< 0.03
948622	79	47	22	10	0.13
948629	51	13	6	2	< 0.03
948630	67	33	13	5	0.06

948631	46	14	5	3	< 0.03
948632	42	12	5	2	< 0.03
948633	57	21	8	6	< 0.03
948646	63	58	23	10	0.11
948654	68	40	13	4	0.08
948656	69	40	22	13	0.09
948660	47	11	2	1	< 0.03
948661	80	41	14	4	0.11
948662	63	38	16	8	0.06
948664	45	12	2	1	< 0.03
948665	64	25	7	3	0.04
948666	82	37	12	4	0.11
948673	33	9	3	2	< 0.03
948674	75	39	12	5	0.1
948675	43	8	2	0	< 0.03
948676	40	10	2	0	< 0.03
948677	53	11	2	1	< 0.03
948678	69	27	9	4	0.06
948684	61	29	11	4	0.04
948685	52	15	5	2	< 0.03
948686	24	8	2	1	< 0.03
948687	58	19	5	2	< 0.03
948689	73	26	17	8	0.07
948692	49	20	8	6	< 0.03
948693	71	40	18	10	0.09
948695	75	38	20	7	0.1
948700	63	25	7	3	0.04
948701	64	24	9	4	0.04
948702	60	25	6	1	0.04
948703	66	29	7	2	0.05
948707	69	24	7	3	0.05
948729	47	12	2	1	< 0.03
948731	67	33	11	4	0.06
948732	68	40	14	7	0.08
948735	22	9	2	2	< 0.03
948741	49	55	24	15	0.06
948752	64	31	12	5	0.05
948765	61	20	7	3	0.03
948766	78	43	18	7	0.11
948767	76	40	19	12	0.1
948768	67	35	17	12	0.1
948769	60	24	10	5	0.0
948788	57	27	13	10	0.03

948794	51	26	5	2	< 0.03
948804	42	18	8	5	< 0.03
948805	34	13	5	3	< 0.03
948806	16	18	7	5	< 0.03
948807	56	35	18	11	0.04
948812	77	40	20	11	0.11
948835	66	28	7	3	0.05
948836	52	27	11	6	< 0.03
948847	68	32	12	7	0.06
948849	43	13	6	5	< 0.03
948850	43	15	7	5	< 0.03
948851	45	16	5	3	< 0.03
948852	51	16	4	2	< 0.03
948853	84	32	9	5	0.10
948854	58	21	7	3	< 0.03
948855	56	30	12	6	0.03
948856	70	38	14	8	0.08
948862	55	26	10	4	< 0.03
948863	43	8	2	2	< 0.03
948865	57	24	10	6	< 0.03
948880	84	46	26	14	0.16
948882	66	36	19	8	0.07
948883	81	62	29	16	0.21
948884	59	25	9	4	0.03
948885	53	18	6	4	< 0.03
948891	96	52	24	12	0.20
948892	54	24	7	4	< 0.03
948893	93	84	59	44	1.24
948906	81	46	19	9	0.13
948907	65	25	8	4	0.05
948910	62	22	8	4	0.0
948911	48	16	10	4	< 0.03
948917	81	57	30	19	0.20
948918	69	36	14	6	0.07
948922	64	32	12	6	0.05
948923	30	8	4	3	< 0.03
948924	32	11	3	2	< 0.03
948925	58	27	9	6	0.03
948926	109	94	105	111	> 2.0
948935	38	17	6	3	< 0.03
948936	47	12	4	2	< 0.03
948937	48	21	7	3	< 0.03
948938	49	19	8	5	< 0.03

948950	54	27	8	3	< 0.03
948951	32	13	5	3	< 0.03
948952	46	13	4	2	< 0.03
948953	69	41	14	7	0.08
948954	43	15	8	4	< 0.03
948960	41	14	8	7	< 0.03
948961	48	17	6	3	< 0.03
948963	51	23	8	4	< 0.03
948965	96	77	53	28	0.57
948966	63	32	11	4	0.05
948967	71	38	13	6	0.08
948968	60	29	9	3	0.04
948969	47	18	6	4	< 0.03
948970	31	9	3	2	< 0.03
948971	34	9	2	2	< 0.03
948972	72	32	9	3	0.07
949006	79	53	19	8	0.1
949007	84	37	9	6	0.1
949012	81	38	17	10	0.11
949040	80	36	11	4	0.10
949041	101	50	14	5	0.18
949051	74	45	16	8	0.10
949053	89	54	18	5	0.2
949055	68	24	8	4	0.0
949059	73	40	15	5	0.09
949061	109	99	83	73	> 2.0
949077	82	47	15	5	0.1
949080	48	20	7	5	< 0.03
949088	73	24	8	3	0.06
949092	66	24	13	14	0.05
949094	79	48	17	6	0.13
949095	90	66	19	6	0.20
949109	95	55	26	13	0.22
949139	72	47	24	11	0.12
949158	54	20	10	8	< 0.03
949159	75	40	15	25	0.10
949163	52	15	4	2	< 0.03
949164	42	30	15	10	< 0.03
949167	78	39	17	21	0.11
949168	67	36	19	12	0.07
949182	65	27	8	4	0.05
949190	57	15	3	2	< 0.03
949216	74	42	14	5	0.10

949223	87	28	16	6	0.1
949229	125	101	92	78	> 2.0
949279	85	41	15	5	0.12
949325	98	112	86	75	> 2.0
949397	94	96	100	106	> 2.0
949483	71	43	21	11	0.10
949500	78	56	24	10	0.16
949517	103	98	97	80	> 2.0
949589	111	89	57	42	1.06
949685	101	82	58	40	0.99
949778	90	55	20	9	0.18
949805	106	88	66	48	1.73
949814	59	51	22	8	0.08
949841	87	46	11	4	0.13
949846	48	30	11	7	< 0.03
949848	57	18	4	2	< 0.03
949858	66	23	10	6	0.04
949865	61	11	3	1	< 0.03
949871	70	26	7	3	0.1
949872	47	13	3	1	< 0.03
949873	45	10	2	1	< 0.03
949874	14	3	1	0	< 0.03
949875	54	23	5	2	< 0.03
949876	79	32	10	5	0.09
949880	52	20	6	3	< 0.03
949884	87	41	16	7	0.13
949886	62	22	6	3	0.04
949887	87	64	21	8	0.19
949892	83	49	22	13	0.2
949896	13	1	1	0	< 0.03
949897	67	32	15	7	0.06
949899	80	49	20	6	0.14
949917	80	48	22	10	0.1
949918	84	46	15	4	0.1
949920	59	20	3	2	< 0.03
949921	67	19	2	1	0.04
949922	56	21	6	2	< 0.03
949923	70	34	15	7	0.07
949924	112	106	5	2	0.31
949925	59	27	6	2	0.04
949926	44	7	1	1	< 0.03
949927	37	4	1	1	< 0.03
949928	68	20	4	2	0.04

949929	66	18	3	1	0.04
949930	61	30	10	4	0.04
949931	68	27	6	2	0.05
949932	72	31	6	2	0.07
949934	66	42	22	12	0.08
949935	52	20	8	6	< 0.03
949937	69	27	7	5	0.06
949938	66	35	14	5	0.06
949942	69	30	8	3	0.06
949943	52	21	6	2	< 0.03
949944	60	20	4	3	0.03
949945	54	16	5	3	< 0.03
949948	34	5	1	1	< 0.03
949949	46	10	2	1	< 0.03
949950	46	12	3	2	< 0.03
949962	70	34	16	9	0.1
949963	71	43	15	6	0.1
949978	65	35	9	2	0.06
949979	72	35	11	5	0.08
949983	89	66	25	12	0.23
949990	61	23	5	2	0.04
949991	55	21	5	1	< 0.03
949992	56	29	11	6	0.03
950014	60	28	8	3	0.04
950017	68	38	11	5	0.07
950019	52	20	8	5	< 0.03
950020	84	43	13	5	0.12
950021	80	46	15	6	0.12
950023	57	17	5	2	< 0.03
950024	51	17	7	5	< 0.03
950030	37	7	1	0	< 0.03
950048	57	40	16	6	0.05
950057	65	38	21	9	0.07
950060	26	16	3	2	< 0.03
950061	55	34	10	5	0.04
950064	74	32	11	4	0.08
950065	72	30	8	2	0.07
950069	68	31	8	4	0.06
950072	49	20	6	3	< 0.03
950075	87	38	13	5	0.12
950080	69	40	15	7	0.08
950081	60	28	8	4	0.04
950083	65	29	12	4	0.1

950085	53	14	6	4	< 0.03
950086	76	43	15	4	0.10
950089	46	10	2	1	< 0.03
950091	45	12	2	1	< 0.03
950092	80	42	14	8	0.11
950102	81	37	9	3	0.10
950124	69	31	14	8	0.06
950132	55	14	4	1	< 0.03
950139	87	59	24	9	0.19
950183	44	23	5	2	< 0.03
950219	84	37	18	11	0.12
950237	83	48	17	8	0.14
950246	76	33	15	7	0.09
951328	76	37	12	4	0.09
951330	76	40	13	5	0.10
951333	89	45	22	9	0.16
951340	74	42	15	6	0.10
951341	92	58	21	4	0.19
951346	49	22	4	3	< 0.03
951352	67	19	7	3	0.04
951354	67	36	12	6	0.07
951356	57	23	6	2	< 0.03
951357	62	35	10	4	0.05
951358	76	36	12	5	0.09
951362	53	15	3	1	< 0.03
951364	58	18	4	2	< 0.03
951365	78	47	16	6	0.12
951366	61	34	12	6	0.05
951367	69	28	8	4	0.06
951370	74	41	16	7	0.10
951371	30	7	2	2	< 0.03
951372	61	21	6	4	0.03
951374	62	17	4	2	0.03
951376	67	47	15	5	0.09
951381	63	28	11	6	0.05
951384	63	27	6	2	0.05
951386	66	22	6	3	0.04
951387	68	20	3	1	0.04
951397	69	35	8	4	0.07
951406	73	52	19	9	0.12
951407	56	21	6	3	< 0.03
951408	47	15	3	1	< 0.03
951413	68	46	20	9	0.09

951416	63	42	17	7	0.07
951418	60	22	6	3	0.03
951428	28	4	1	1	< 0.03
951429	32	6	2	2	< 0.03
951430	59	25	6	2	0.03
951431	46	32	9	5	< 0.03
951441	100	82	67	42	1.33
951450	71	36	12	6	0.08
951458	63	32	15	10	0.05
951459	77	44	17	9	0.11
951462	74	28	6	2	0.07
951463	74	35	15	6	0.09
951481	91	47	26	13	0.18
951489	59	17	8	3	< 0.03
951494	64	32	10	5	0.05
951498	58	27	10	7	0.03
951519	60	32	8	3	0.05
951529	90	35	24	18	0.15
951537	103	101	105	168	> 2.0
951550	66	42	15	6	0.08
951554	83	36	10	5	0.10
951561	88	59	74	100	> 2.0
951565	65	38	13	4	0.07
951566	77	36	9	3	0.09
951608	73	25	8	4	0.06
951645	64	29	12	7	0.05
951657	107	91	64	62	> 2.0
951691	58	28	9	3	0.04
951696	58	19	9	5	< 0.03
951700	76	40	16	9	0.10
951709	52	25	9	6	< 0.03
951729	73	74	88	89	> 2.0
951731	70	34	10	4	0.07
951737	57	24	5	4	< 0.03
951746	68	31	17	11	0.06
951749	71	27	4	2	0.06
951763	44	11	4	2	< 0.03
951764	40	9	2	1	< 0.03
951767	87	48	16	5	0.14
951772	62	30	10	7	0.05
951781	95	42	15	7	0.15
951783	56	31	12	5	0.04
951787	53	20	7	4	< 0.03
951793	44	11	4	2	< 0.03

951795	64	24	7	3	0.04
951797	40	15	6	4	< 0.03
951798	31	5	1	1	< 0.03
951799	27	5	1	1	< 0.03
951803	67	29	9	4	0.06
951804	45	13	3	1	< 0.03
951806	65	43	15	7	0.07
951807	59	30	10	4	0.04
951808	69	46	18	6	0.10
951809	47	13	3	1	< 0.03
951811	57	22	7	3	< 0.03
951814	60	25	10	7	0.04
951815	58	37	15	7	0.05
951816	46	10	2	1	< 0.03
951821	41	14	4	2	< 0.03
951822	86	44	15	7	0.13
951824	67	23	5	3	0.05
951827	51	17	5	2	< 0.03
951828	63	23	9	4	0.04
951830	61	26	10	5	0.04
951833	59	39	9	4	0.05
951835	23	4	1	0	< 0.03
951837	53	16	4	1	< 0.03
951838	80	51	22	8	0.14
951839	56	25	8	2	< 0.03
951840	76	37	12	4	0.09
951841	69	27	11	2	0.06
951843	63	29	8	4	0.05
951845	39	9	3	1	< 0.03
951846	45	14	3	1	< 0.03
951855	87	65	19	5	0.19
951856	61	18	4	2	< 0.03
951857	57	27	7	2	0.03
951874	74	73	68	47	> 2.0
951875	66	33	10	4	0.06
951881	49	22	3	2	< 0.03
951893	53	26	10	5	< 0.03
951898	46	18	5	2	< 0.03
951902	61	34	13	7	0.05
951938	85	51	20	11	0.16

Example 6: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested at various doses via free uptake in A431 cells. Cells were cultured at a density of 10,000 cells per well and treated with 8, 40, 200, or 1,000 nM of modified oligonucleotide, as specified in the table below. After approximately 48 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with GADPH. As illustrated in the tables below, DNM2 mRNA expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 8: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)				IC50 (μM)
	8 nM	40 nM	200 nM	1,000 nM	
695171	90	84	54	26	0.24
951371	105	67	25	9	0.10
951371	101	70	27	11	0.10
951371	109	63	16	4	0.08
951371	91	61	23	8	0.07
951371	94	78	25	9	0.10
951371	91	63	23	8	0.07
951371	59	66	23	8	0.04
951371	94	56	20	7	0.07
951371	88	67	26	10	0.08
988380	77	33	5	1	0.02
988386	93	70	21	6	0.08
988387	101	46	5	1	0.05
988388	97	80	39	11	0.13
988394	120	81	23	5	0.12
988396	113	87	30	9	0.14
988397	77	29	7	2	0.02
988398	86	46	11	3	0.04
988399	81	47	13	3	0.04
988400	88	54	15	3	0.05
988401	98	65	16	6	0.07
988402	94	48	11	2	0.05
988407	99	77	30	8	0.11
988413	84	58	23	7	0.06
988414	95	73	23	6	0.09
988415	82	62	25	7	0.06
988422	91	60	17	7	0.06

Example 7: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested at various doses via free uptake in A431 cells. Cells were cultured at a density of 10,000 cells per well treated with 7.8, 31.25, 125, 500, or 2,000 nM of modified oligonucleotide, as specified in the tables below. After approximately 48 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with GADPH. As illustrated in the tables below, DNM2 expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 9: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908166	106	97	57	28	16	0.22
908213	139	85	56	30	16	0.21
908408	98	80	33	7	2	0.08
908420	91	86	45	13	4	0.11
948660	105	90	51	13	2	0.14
948677	101	101	61	23	8	0.21
948951	97	79	35	14	8	0.09
949190	107	101	54	22	8	0.18
949865	94	80	40	16	7	0.10
949935	88	84	58	31	19	0.20
950023	89	75	45	13	4	0.09
950060	81	79	48	29	11	0.13
950089	84	79	53	18	5	0.12
950132	87	83	44	19	9	0.11
950183	88	83	58	35	15	0.21

Table 10: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908408	98	80	34	10	2	0.08
951356	190	79	60	28	10	0.23
951362	97	85	63	30	11	0.21
951372	87	80	55	23	10	0.14
951431	100	90	68	38	21	0.31
951797	89	77	42	19	10	0.10
951798	89	58	23	6	1	0.04
951799	90	68	23	6	2	0.05
951816	100	77	38	10	3	0.09

951821	87	57	45	16	6	0.07
951827	94	79	45	17	5	0.11
951839	95	90	69	38	14	0.29
951845	92	71	31	8	2	0.06
951846	91	85	50	19	5	0.13
951856	97	86	54	22	7	0.15

Example 8: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested at various doses in HSMM cells (human myoblast, Lonza CC-2580). Cells were cultured at a density of 20,000 cells per well and transfected via electroporation with 7.8, 31.25, 125, 500, or 2,000 nM of modified oligonucleotide, as specified in the tables below. After approximately 16 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with ribogreen. As illustrated in the tables below, DNM2 mRNA expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 11: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908166	104	95	98	66	42	1.29
908213	93	82	70	42	19	0.33
908408	111	100	74	38	17	0.36
908420	91	93	67	39	17	0.30
948660	88	86	83	42	15	0.40
948677	90	80	87	51	22	0.54
948951	88	74	57	31	12	0.16
949190	99	88	82	47	23	0.49
949865	132	106	92	39	19	0.50
949935	90	92	94	60	25	0.77
950023	113	97	86	40	15	0.43
950060	109	105	78	69	32	0.95
950089	111	102	80	54	21	0.58
950132	117	98	79	51	19	0.51
950183	95	110	84	59	23	0.70

Table 12: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908408	98	102	81	55	20	0.58
951356	95	102	94	74	41	1.45
951362	95	67	85	56	29	0.62
951372	95	91	86	60	27	0.75
951431	87	90	89	55	35	0.77
951797	94	94	98	72	41	1.40
951798	103	95	79	40	21	0.40
951799	104	100	81	47	20	0.50
951816	106	91	89	53	30	0.70
951821	122	106	66	32	22	0.32
951827	100	87	51	38	20	0.21
951839	123	94	99	72	31	1.17
951845	104	94	75	51	20	0.48
951846	112	91	80	59	27	0.69
951856	113	101	77	50	22	0.52

Example 9: Dose Response of modified oligonucleotides complementary to dynamin 2 *in vitro*

Selected oligonucleotides listed in the Examples above were tested at various doses in SkMC cells (human skeletal muscle, Lonza CC-2561). Cells were cultured at a density of 20,000 cells per well and transfected via electroporation with 7.8, 31.25, 125, 500, or 2,000 nM of modified oligonucleotide, as specified in the tables below. After approximately 16 hours, total RNA was isolated and analyzed by RT-PCR with primer probe set RTS36027 (described in Example 1), normalized with ribogreen. As illustrated in the tables below, DNM2 mRNA expression was inhibited in a dose-dependent manner by modified oligonucleotides complementary to DNM2.

Table 13: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908166	90	84	87	43	13	0.41
908213	101	79	59	21	5	0.15
908408	94	72	57	21	3	0.13
908420	84	72	53	9	4	0.10
948660	95	90	64	12	2	0.16
948677	88	77	58	15	4	0.13

948951	83	67	41	12	5	0.07
949190	103	84	61	16	4	0.16
949865	130	106	55	10	4	0.17
949935	118	100	86	33	7	0.36
950023	129	98	57	11	3	0.17
950060	101	103	72	26	5	0.26
950089	112	78	65	20	4	0.17
950132	115	93	53	14	3	0.15
950183	114	92	70	24	5	0.23

Table 14: DNM2 mRNA Expression

Compound Number	DNM2 expression (% control)					IC50 (μM)
	7.8 nM nM	31.25 nM	125 nM	500 nM	2,000 nM	
908408	91	80	46	10	3	0.10
951356	103	98	90	52	15	0.55
951362	90	88	65	22	4	0.19
951372	99	88	65	16	4	0.18
951431	103	97	70	25	6	0.24
951797	102	94	69	25	7	0.23
951798	99	90	46	8	3	0.12
951799	101	90	49	12	3	0.13
951816	96	78	63	13	4	0.14
951821	104	79	47	12	3	0.11
951827	94	71	44	8	3	0.08
951839	114	103	76	32	6	0.32
951845	97	88	55	12	4	0.14
951846	90	86	41	18	4	0.11
951856	102	91	62	15	4	0.17

Example 10: Administration of modified oligonucleotides complementary to human dynamin 2 to CD1 mice

CD1® mice (Charles River, MA) were treated with modified oligonucleotides selected from Examples above and evaluated for changes in the levels of various plasma chemistry markers. Groups of 6 week old male CD1 mice were injected subcutaneously once a week for 6 weeks with 50 mg/kg of a modified oligonucleotide listed in the tables below (50 mg/kg/week dose). Each group contained 4 mice. One control group of male CD1 mice was injected subcutaneously once a week for 6 weeks with PBS. Mice were sacrificed 48 hours after the last dose, and organs and plasma were harvested for further analysis.

Levels of transaminases, albumin, BUN, and billirubin were measured using an automated clinical chemistry analyzer (Hitachi Olympus AU400e, Melville, NY). Kidney, liver, and spleen weights were also measured. The results, presented in the tables below, show that many of the modified oligonucleotides complementary to DNM2 were well tolerated *in vivo*.

Table 15: Levels of plasma markers

	ALT (U/L)	AST (U/L)	Albumin (mg/dL)	BUN (mg/d)	Creatine (mg/dL)	T.Bil. (g/dL)
PBS	48	82	3.36	27.2	0.12	0.66
549144	72	68	3.23	23.6	0.12	0.47
908166	259	108	3.16	20.4	0.11	0.38
908213	93	85	2.95	23.9	0.10	0.34
908389	1073	636	3.17	22.7	0.09	0.55
908408	67	70	2.97	26.2	0.11	0.32
908415	286	209	2.60	26.2	0.10	0.28
908416	425	336	2.35	26.4	0.07	0.19
908420	105	144	2.50	26.5	0.06	0.38
948660	112	165	2.59	21.8	0.08	0.26
948673	225	263	2.15	27.2	0.04	0.82
948675	100	132	2.25	21.4	0.06	0.22
948677	65	91	2.32	17.7	0.05	0.21
948951	107	126	2.46	21.4	0.07	0.22
949158	713	608	2.99	18.6	0.01	0.27
949190	64	62	2.52	22.1	0.07	0.20
949865	45	58	2.62	23.2	0.06	0.22
949873	89	163	2.33	20.7	0.04	0.21
949874	1079	853	2.77	20.7	0.05	0.46
949935	98	81	2.63	22.9	0.07	0.20
950023	42	57	2.52	22.2	0.04	0.20
950030	59	77	2.44	20.6	0.05	0.21

Table 16: Levels of plasma markers

Compound No.	ALT (U/L)	AST (U/L)	Albumin (mg/dL)	BUN (mg/d)	Creatine (mg/dL)	T.Bil. (g/dL)
PBS	37	62	2.78	22.0	0.08	0.46
549144	64	79	2.64	24.0	0.08	0.29
950060	47	63	2.47	22.0	0.09	0.33
950089	40	56	2.65	21.0	0.10	0.22
950132	58	58	2.58	20.0	0.07	0.24
950183	49	62	2.38	21.0	0.06	0.29

951356	64	80	2.39	23.0	0.10	0.25
951362	60	63	2.74	22.0	0.09	0.18
951371	312	209	2.32	20.0	0.09	0.18
951372	59	99	2.54	25.0	0.07	0.21
951407	172	200	2.72	24.0	0.07	0.24
951431	64	80	2.48	23.0	0.08	0.22
951793	319	238	2.5	19.0	0.10	0.20
951797	41	63	2.6	24.0	0.11	0.26
951798	53	97	2.57	26.0	0.10	0.19
951799	44	97	2.44	25.0	0.08	0.19
951816	121	113	2.63	19.0	0.10	0.20
951821	79	80	2.39	23.0	0.07	0.17
951827	56	88	2.46	25.0	0.10	0.21
951839	45	50	2.52	23.0	0.08	0.20
951845	117	132	2.51	21.0	0.08	0.25
951846	35	47	2.59	21.0	0.10	0.21
951856	112	412	2.25	20.0	0.09	0.17

Table 17: Organ weights

	kidney (g)	**liver (g)**	**spleen (g)**
PBS	0.55	1.9	0.09
549144	0.52	1.9	0.10
908166	0.48	2.0	0.08
908213	0.52	2.0	0.12
908389	0.54	2.6	0.14
908408	0.49	2.2	0.13
908415	0.51	2.2	0.12
908416	0.51	2.1	0.16
908420	0.52	2.0	0.13
948660	0.44	1.8	0.14
948673	0.51	3.9	0.62
948675	0.48	2.1	0.21
948677	0.54	2.0	0.15
948951	0.45	1.9	0.11
949158	0.59	2.3	0.18
949190	0.53	2.2	0.14
949865	0.53	2.1	0.14
949873	0.47	1.8	0.20
949874	0.52	2.3	0.16

949935	0.57	2.0	0.13
950023	0.53	1.9	0.16
950030	0.59	2.1	0.20

Table 18: Organ weights

Compound No.	**kidney (g)**	**liver (g)**	**spleen (g)**
PBS	0.57	2.1	0.11
549144	0.57	2.0	0.09
950060	0.57	2.3	0.12
950089	0.60	2.4	0.15
950132	0.59	2.3	0.16
950183	0.60	2.4	0.14
951356	0.57	2.4	0.19
951362	0.58	2.3	0.16
951371	0.51	2.7	0.16
951372	0.55	2.5	0.17
951407	0.53	2.2	0.17
951431	0.54	2.2	0.18
951793	0.55	2.6	0.17
951797	0.52	2.1	0.15
951798	0.57	2.4	0.18
951799	0.54	2.4	0.16
951816	0.50	2.4	0.16
951821	0.50	2.0	0.13
951827	0.47	1.8	0.13
951839	0.51	2.2	0.15
951845	0.55	2.0	0.17
951846	0.57	2.2	0.17
951856	0.60	2.5	0.19