

## COMPOUNDS AND METHODS FOR REDUCING PSD3 EXPRESSION

### Sequence Listing

5           The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled 201185-WO-PCT Sequence Listing, created on September 8, 2022 which is 3319 KB in size. The information in the electronic format of the sequence listing is incorporated herein by reference in its entirety. 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  
10   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 base could be described as a DNA having a modified sugar (2’-OH in place of one 2’-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) in place of an uracil of RNA). Accordingly, nucleic acid sequences provided herein, including, but not limited to those in the sequence listing, are intended to encompass nucleic  
15   acids containing any combination of natural or modified RNA and/or DNA, unless otherwise stated, including, but not limited to such nucleic acids having modified nucleobases.

### Field

20           Provided are oligomeric agents, oligomeric compounds, methods, and pharmaceutical compositions for reducing the amount or activity of PSD3 RNA in a cell or animal, and in certain instances reducing the amount of PSD3 protein in a cell or animal. Such oligomeric agents, oligomeric compounds, methods, and pharmaceutical compositions are useful to treat liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH),  
25   HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

### Background

          Non-alcoholic fatty liver disease (NAFLD) covers a spectrum of liver disease from steatosis to nonalcoholic steatohepatitis (NASH) and cirrhosis. NAFLD is defined as fat accumulation in the liver exceeding 5% by weight, in the  
30   absence of significant alcohol consumption, steatogenic medication, or hereditary disorders (Kotronen et al, Arterioscler Thromb. Vasc. Biol. 2008, 28: 27-38).

          Non-alcoholic steatohepatitis (NASH) is NAFLD with signs of inflammation and hepatic injury. NASH is defined histologically by macrovesicular steatosis, hepatocellular ballooning, and lobular inflammatory infiltrates (Sanyal, Hepatol. Res. 2011. 41: 670-4). NASH is estimated to affect 2-3% of the general population. In the presence of  
35   other pathologies, such as obesity or diabetes, the estimated prevalence increases to 7% and 62% respectively (Hashimoto et al, J. Gastroenterol. 2011. 46(1): 63-69).

### Summary

Oligomeric agents, oligomeric compounds, methods, and pharmaceutical compositions of certain embodiments described herein are useful for reducing or inhibiting PSD3 expression in a cell or animal. In certain embodiments, PSD3 RNA or protein levels can be reduced in a cell or animal.

Also provided are methods of treating liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

### 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. 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. Also, terms such as “element” or “component” encompass both elements and components comprising one unit and elements and components that comprise more than one subunit, unless specifically stated otherwise.

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, and treatises, are hereby expressly incorporated-by-reference for the portions of the document discussed herein, as well as in their entirety.

### DEFINITIONS

Unless specific definitions are provided, the nomenclature used in connection with, and the procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art.

Unless otherwise indicated, the following terms have the following meanings:

As used herein, “2'-deoxynucleoside” means a nucleoside comprising a 2'-H(H) deoxyfuranosyl sugar moiety. In certain embodiments, a 2'-deoxynucleoside is a 2'-β-D-deoxynucleoside and comprises a 2'-β-D-deoxyribose sugar moiety, which has the β-D ribosyl configuration 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'-MOE” means a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> group in place of the 2'-OH group of a furanosyl sugar moiety. A “2'-MOE sugar moiety” means a sugar moiety with a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> group in place of the 2'-OH group of a furanosyl sugar moiety. Unless otherwise indicated, a 2'-MOE sugar moiety is in the β-D-ribose configuration. “MOE” means O-methoxyethyl.

As used herein, “2'-MOE nucleoside” means a nucleoside comprising a 2'-MOE sugar moiety.

As used herein, “2'-OMe” means a 2'-OCH<sub>3</sub> group in place of the 2'-OH group of a furanosyl sugar moiety. A “2'-O-methyl sugar moiety” or “2'-OMe sugar moiety” means a sugar moiety with a 2'-OCH<sub>3</sub> group in place of the 2'-OH group of a furanosyl sugar moiety. Unless otherwise indicated, a 2'-MOE sugar moiety is in the β-D-ribose configuration.

As used herein, “2'-OMe nucleoside” means a nucleoside comprising a 2'-OMe sugar moiety.

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

As used herein, “3′ target site” refers to the 3′-most nucleotide of a target nucleic acid which is complementary to an antisense oligonucleotide, when the antisense oligonucleotide is hybridized to the target nucleic acid.

As used herein, “5′ target site” refers to the 5′-most nucleotide of a target nucleic acid which is complementary to an antisense oligonucleotide, when the antisense oligonucleotide is hybridized to the target nucleic acid.

As used herein, “5-methylcytosine” means a cytosine modified with a methyl group attached to the 5 position. A 5-methyl cytosine is a modified nucleobase.

As used herein, “abasic sugar moiety” means a sugar moiety of a nucleoside that is not attached to a nucleobase. Such abasic sugar moieties are sometimes referred to in the art as “abasic nucleosides.”

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, “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 stereorandom chiral centers. In certain embodiments, the molecules are modified oligonucleotides. In certain embodiments, the molecules are oligomeric compounds comprising modified oligonucleotides.

As used herein, “cleavable moiety” means a bond or group of atoms that is cleaved under physiological conditions, for example, inside a cell, an animal, or a human.

As used herein, “complementary” in reference to an oligonucleotide means that at least 70% of the nucleobases of the oligonucleotide 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 region” in reference to a region of an oligonucleotide means that at least 70% of the nucleobases of that region 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 mean nucleobases 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 (mC) and guanine (G). Certain modified nucleobases that pair with natural nucleobases or with other modified nucleobases are known in the art and are not considered complementary nucleobases as defined herein unless indicated otherwise. For example, inosine can pair, but is not considered complementary, with adenosine, cytosine, or uracil. 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 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 attached to an oligonucleotide. Conjugate groups include a conjugate moiety and a conjugate linker that attaches the conjugate moiety to the  
5 oligonucleotide.

As used herein, “conjugate linker” means a single bond or 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 modifies one or more properties of a molecule compared to the identical molecule lacking the conjugate moiety, including but not limited to pharmacodynamics, pharmacokinetics, stability, binding, absorption, tissue distribution, cellular distribution, cellular uptake, charge and  
10 clearance.

As used herein, “constrained ethyl” or “cEt” or “cEt modified sugar moiety” means a  $\beta$ -D ribosyl bicyclic sugar moiety wherein the second ring of the bicyclic sugar is formed via a bridge connecting the 4'-carbon and the 2'-carbon of the  $\beta$ -D ribosyl sugar moiety, wherein the bridge has the formula 4'-CH(CH<sub>3</sub>)-O-2', and wherein the methyl group of  
15 the bridge is in the *S* configuration.

As used herein, “cEt nucleoside” means a nucleoside comprising a cEt modified sugar moiety.

As used herein, “deoxy region” means a region of 5-12 contiguous nucleotides, wherein at least 70% of the nucleosides comprise a  $\beta$ -D-2'-deoxyribose sugar moiety. In certain embodiments, a deoxy region is the gap of a  
gapmer.

As used herein, “hotspot region” is a range of nucleobases on a target nucleic acid that is amenable to oligomeric agent or oligomeric compound-mediated reduction of the amount or activity of the target nucleic acid.  
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As used herein, “internucleoside linkage” is the covalent linkage between adjacent nucleosides in an oligonucleotide. As used herein “modified internucleoside linkage” means any internucleoside linkage other than a phosphodiester internucleoside linkage.

As used herein, “linked nucleosides” are nucleosides that are connected in a contiguous sequence (i.e., no additional nucleosides are presented between those that are linked).  
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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  
30 with the oligonucleotide.

As used herein, “mismatch” or “non-complementary” means a nucleobase of a first nucleic acid sequence that is not complementary with the corresponding nucleobase of a second nucleic acid sequence or target nucleic acid when the first and second nucleic acid sequences are aligned.

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

As used herein, “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, "nucleobase" means an unmodified nucleobase or a modified nucleobase. A nucleobase is a heterocyclic moiety. As used herein an "unmodified nucleobase" is adenine (A), thymine (T), cytosine (C), uracil (U), or guanine (G). As used herein, a "modified nucleobase" is a group of atoms other than unmodified A, T, C, U, or G capable of pairing with at least one other nucleobase. A "5-methyl cytosine" is a modified nucleobase. A universal base is a modified 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. By way of example and without limitation, an oligomeric compound having the nucleobase sequence "ATCGATCG" encompasses any compounds 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<sup>m</sup>CGAUCG," wherein <sup>m</sup>C indicates a cytosine base comprising a methyl group at the 5-position. Finally, for clarity, unless otherwise indicated, the phrase "nucleobase sequence of SEQ ID NO: X", refers only to the sequence of nucleobases in that SEQ ID NO.: X, independent of any sugar or internucleoside linkage modifications also described in such SEQ ID.

As used herein, "nucleoside" means a compound or fragment of a compound comprising a nucleobase and a sugar moiety. The nucleobase and sugar moiety are each, independently, unmodified or modified.

As used herein, "oligomeric agent" means an oligomeric compound and optionally one or more additional features, such as a second oligomeric compound. An oligomeric agent may be a single-stranded oligomeric compound or may be an oligomeric duplex formed by two complementary oligomeric compounds.

As used herein, "oligomeric compound" means an oligonucleotide and optionally one or more additional features, such as a conjugate group or terminal group. An oligomeric compound may be paired with a second oligomeric compound that is complementary to the first oligomeric compound or may be unpaired. A "singled-stranded oligomeric compound" is an unpaired oligomeric compound.

The term "oligomeric duplex" means a duplex formed by two oligomeric compounds having complementary nucleobase sequences.

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, tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspension and lozenges for the oral ingestion by a subject. In certain embodiments, a pharmaceutically acceptable carrier or diluent is sterile water, sterile saline, sterile buffer solution or sterile artificial cerebrospinal fluid.

As used herein "pharmaceutically acceptable salts" means physiologically and pharmaceutically acceptable salts of compounds. Pharmaceutically acceptable salts 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 oligomeric compound and a sterile aqueous solution. In certain embodiments, a pharmaceutical composition shows activity in free uptake assay in certain cell lines.

As used herein “prodrug” means a therapeutic agent in a first form outside the body that is converted to a second form within an animal or cells thereof. Typically, conversion of a prodrug within the animal 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. In certain embodiments, the first form of the prodrug is less active than the second form.

As used herein, “stabilized phosphate group” means a 5'-phosphate analog that is metabolically more stable than a 5'-phosphate as naturally occurs on DNA or RNA.

As used herein, “standard cell assay” means the assays described in the Examples 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) deoxyribosyl sugar moiety, as found in DNA (an “unmodified DNA sugar moiety”). Unmodified sugar moieties have one hydrogen at each of the 1', 3', and 4' positions, an oxygen at the 3' position, and two hydrogens at the 5' position. As used herein, “modified sugar moiety” or “modified sugar” means a modified furanosyl sugar moiety or a sugar surrogate.

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 target nucleic acids.

As used herein, “target nucleic acid” and “target RNA” mean a nucleic acid that an oligomeric compound is designed to affect. Target RNA means an RNA transcript and includes pre-mRNA and mRNA unless otherwise specified.

As used herein, “target region” means a portion of a target nucleic acid to which an oligomeric 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, “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. In certain embodiments, antisense activity is the modulation of splicing of a target pre-mRNA.

As used herein, “antisense agent” means an antisense compound and optionally one or more additional features, such as a sense compound.

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

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

10 As used herein, “antisense oligonucleotide” means an oligonucleotide, including the oligonucleotide portion of an antisense compound, that is capable of hybridizing to a target nucleic acid and is capable of at least one antisense activity. Antisense oligonucleotides include but are not limited to antisense RNAi oligonucleotides and antisense RNase H oligonucleotides.

As used herein, “sense oligonucleotide” means an oligonucleotide, including the oligonucleotide portion of a sense compound, that is capable of hybridizing to an antisense oligonucleotide.

15 As used herein, “gapmer” means a modified oligonucleotide comprising an internal region positioned between external regions having one or more nucleosides, wherein the nucleosides comprising the internal region are chemically distinct from the nucleoside or nucleosides comprising the external regions, and wherein the modified oligonucleotide supports RNase H cleavage. The internal region may be referred to as the “gap” and the external regions may be referred to as the “wings.” In certain embodiments, the internal region is a deoxy region. The positions of the internal region or gap refer to the order of the nucleosides of the internal region and are counted starting from the 5'-end of the internal region. Unless otherwise indicated, “gapmer” refers to a sugar motif. In certain embodiments, each nucleoside of the gap is a 2'-β-D-deoxynucleoside. In certain embodiments, the gap comprises one 2'-substituted nucleoside at position 1, 2, 3, 4, or 5 of the gap, and the remainder of the nucleosides of the gap are 2'-β-D-deoxynucleosides. As used herein, the term “MOE gapmer” indicates a gapmer having a gap comprising 2'-β-D-deoxynucleosides and wings comprising 2'-  
20 MOE nucleosides. As used herein, the term “mixed wing gapmer” indicates a gapmer having wings comprising modified nucleosides comprising at least two different sugar modifications. Unless otherwise indicated, a gapmer may comprise one or more modified internucleoside linkages and/or modified nucleobases and such modifications do not necessarily follow the gapmer pattern of the sugar modifications.

25 As used herein, “cell-targeting moiety” means a conjugate group or portion of a conjugate group that is capable of binding to a particular cell type or particular cell types.

30 As used herein, “hybridization” means the annealing of oligonucleotides and/or nucleic acids. While not limited to a particular mechanism, the most common mechanism of hybridization involves hydrogen bonding, which may be Watson-Crick, Hoogsteen or reversed Hoogsteen hydrogen bonding, between complementary nucleobases. In certain embodiments, complementary nucleic acid molecules include, but are not limited to, an antisense compound and a nucleic acid target. In certain embodiments, complementary nucleic acid molecules include, but are not limited to, an  
35 oligonucleotide and a nucleic acid target.

As used herein, “RNAi agent” means an antisense agent 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 agents include, but are not limited to double-stranded siRNA, single-stranded RNAi (ssRNAi), and microRNA, including microRNA mimics. RNAi agents

may comprise conjugate groups and/or terminal groups. In certain embodiments, an RNAi agent modulates the amount and/or activity, of a target nucleic acid. The term RNAi agent excludes antisense agents that act through RNase H.

As used herein, "RNase H agent" means an antisense agent that acts through RNase H to modulate a target nucleic acid and/or protein encoded by a target nucleic acid. In certain embodiments, RNase H agents are single-stranded. In certain embodiments, RNase H agents are double-stranded. RNase H compounds may comprise conjugate groups and/or terminal groups. In certain embodiments, an RNase H agent modulates the amount and/or activity of a target nucleic acid. The term RNase H agent excludes antisense agents that act principally through RISC/Ago2.

As used herein, "reducing" or "inhibiting" PSD3 means reducing expression of PSD3 RNA and/or protein levels in the presence of an oligomeric compound or oligomeric agent described herein compared to expression of PSD3 RNA and/or protein levels in the absence of an oligomeric compound or oligomeric agent described herein.

As used herein, "treating" means improving a subject's disease or condition by administering an oligomeric agent or oligomeric compound described herein. In certain embodiments, treating a subject improves a symptom relative to the same symptom in the absence of the treatment. In certain embodiments, treatment reduces in the severity or frequency of a symptom, or delays the onset of a symptom, slows the progression of a symptom, or slows the severity or frequency of a symptom.

As used herein, "therapeutically effective amount" means an amount of a pharmaceutical agent or composition that has been observed to provide a therapeutic benefit to an animal. For example, a therapeutically effective amount may be observed to improve a symptom of a disease.

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#### **CERTAIN EMBODIMENTS**

Embodiment 1. An oligomeric compound comprising a modified oligonucleotide consisting of 8 to 80 linked nucleosides, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion of a PSD3 nucleic acid, and wherein the modified oligonucleotide has at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

Embodiment 2. The oligomeric compound of embodiment 1, wherein the PSD3 nucleic acid has the nucleobase sequence of any of SEQ ID NOs: 1 or 2.

Embodiment 3. The oligomeric compound of embodiment 1 or 2, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 82205-82220, 181927-181942, 184997-185012, 217663-217678, 218081-218096, 218085-218100, 222016-222031, 222028-222043, 222044-222059, 244765-244780, 285152-285167, 285254-285269, 288678-288693, 288680-288695, 288681-288696, 291274-291289, 330574-330589, 344743-344758, or 463909-463924 of SEQ ID NO: 1.

Embodiment 4. The oligomeric compound of any of embodiments 1-3, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 629-644, 1047-1062, 1051-1066, 1426-1441, 1438-1453, 1454-1469, 1787-1802, 1889-1904, 2073-2088, 2075-2090, or 2076-2091 of SEQ ID NO: 2.

Embodiment 5. The oligomeric compound of any of embodiments 1-4, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 222044-222059, 288678-288693, or 288680-288695 of SEQ ID NO: 1.

Embodiment 6. The oligomeric compound of any of embodiments 1-5, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of the PSD3 nucleic acid.

5 Embodiment 7. An oligomeric compound comprising a modified oligonucleotide consisting of 8 to 80 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 contiguous nucleobases of any of the nucleobase sequences of any of SEQ ID NOs: 20-3034.

Embodiment 8. The oligomeric compound of embodiment 7, wherein the modified oligonucleotide has a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 20-3034.

10 Embodiment 9. The oligomeric compound of embodiment 8, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any of SEQ ID NOs: 20-3034.

Embodiment 10. The oligomeric compound of any of embodiments 7-9, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

15 Embodiment 11. The oligomeric compound of embodiment 10, wherein the modified oligonucleotide consists of 16 to 80 linked nucleosides and has a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

Embodiment 12. The oligomeric compound of embodiment 11, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any one of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

Embodiment 13. The oligomeric compound of any of embodiments 7-11, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of a PSD3 nucleic acid, wherein the PSD3 nucleic acid has the nucleobase sequence of SEQ ID NOs: 1 or 2.

25 Embodiment 14. The oligomeric compound of any of embodiments 1-13, wherein the modified oligonucleotide consists of 10 to 25, 10 to 30, 10 to 50, 12 to 20, 12 to 25, 12 to 30, 12 to 50, 13 to 20, 13 to 25, 13 to 30, 13 to 50, 14 to 20, 14 to 25, 14 to 30, 14 to 50, 15 to 20, 15 to 25, 15 to 30, 15 to 50, 16 to 18, 16 to 20, 16 to 25, 16 to 30, 16 to 50, 17 to 20, 17 to 25, 17 to 30, 17 to 50, 18 to 20, 18 to 25, 18 to 30, 18 to 50, 19 to 20, 19 to 25, 19 to 30, 19 to 50, 20 to 25, 20 to 30, 20 to 50, 21 to 25, 21 to 30, 21 to 50, 22 to 25, 22 to 30, 22 to 50, 23 to 25, 23 to 30, or 23 to 50 linked nucleosides.

Embodiment 15. The oligomeric compound of any of embodiments 1-14, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar moiety.

Embodiment 16. The oligomeric compound of embodiment 15, wherein the modified sugar moiety comprises a bicyclic sugar moiety.

35 Embodiment 17. The oligomeric compound of embodiment 16, wherein the bicyclic sugar moiety comprises a 2'-4' bridge selected from -O-CH<sub>2</sub>-; and -O-CH(CH<sub>3</sub>)-.

Embodiment 18. The oligomeric compound of embodiment 15, wherein the modified sugar moiety comprises a non-bicyclic modified sugar moiety.

Embodiment 19. The oligomeric compound of embodiment 18, wherein the non-bicyclic modified sugar moiety is a 2'-MOE sugar moiety or 2'-OMe sugar moiety.

Embodiment 20. The oligomeric compound of any of embodiments 1-19, wherein at least one nucleoside of the modified oligonucleotide compound comprises a sugar surrogate.

5 Embodiment 21. The oligomeric compound of any of embodiments 1-20, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

Embodiment 22. The oligomeric compound of embodiment 21, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

10 Embodiment 23. The oligomeric compound of embodiment 21 or 22, wherein each internucleoside linkage is a modified internucleoside linkage.

Embodiment 24. The oligomeric compound of embodiment 24, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

Embodiment 25. The oligomeric compound of any of embodiments 21-23, wherein at least one internucleoside linkage of the modified oligonucleotide is a phosphodiester internucleoside linkage.

15 Embodiment 26. The oligomeric compound of any of embodiments 1-21, wherein each internucleoside linkage of the modified oligonucleotide is independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

20 Embodiment 27. The oligomeric compound of any of embodiments 1-21, wherein each internucleoside linkage of the modified oligonucleotide is independently selected from a phosphodiester internucleoside linkage, a phosphorothioate internucleoside linkage, or a mesyl phosphoramidate internucleoside linkage.

Embodiment 28. The oligomeric compound of any of embodiments 1-23 or 25-27, wherein at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 internucleoside linkages of the modified oligonucleotide are phosphorothioate internucleoside linkages.

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

Embodiment 30. The oligomeric compound of embodiment 29, wherein the modified nucleobase is 5-methylcytosine.

Embodiment 31. The oligomeric compound of embodiment 29, wherein each cytosine is a 5-methylcytosine.

30 Embodiment 32. The oligomeric compound of any of embodiments 31, wherein the modified oligonucleotide comprises a deoxy region comprising of 5-12 contiguous 2'-deoxynucleosides.

Embodiment 33. The oligomeric compound of embodiment 32, wherein the deoxy region consists of 6, 7, 8, 9, 10, or 6-10 linked nucleosides.

Embodiment 34. The oligomeric compound of embodiment 32 or 33, wherein each nucleoside of the deoxy region is a 2'-β-D-deoxynucleoside.

35 Embodiment 35. The oligomeric compound of embodiment 32 or 33, wherein one nucleoside of the deoxy region comprises a 2'-OMe sugar moiety.

Embodiment 36. The oligomeric compound of any of embodiments 32-35, wherein each nucleoside immediately adjacent to the deoxy region comprises a modified sugar moiety.

Embodiment 37. The oligomeric compound of any of embodiments 32-36, wherein the deoxy region is flanked on the 5'-side by a 5'-region consisting of 1-6 linked 5'-region nucleosides and on the 3'-side by a 3'-region consisting of 1-6 linked 3'-region nucleosides; wherein

- the 3'-most nucleoside of the 5' external region comprises a modified sugar moiety; and  
 5 the 5'-most nucleoside of the 3' external region comprises a modified sugar moiety.

Embodiment 38. The oligomeric compound of embodiment 37, wherein each nucleoside of the 3' external region comprises a modified sugar moiety.

Embodiment 39. The oligomeric compound of embodiment 37 or 38, wherein each nucleoside of the 5' external region comprises a modified sugar moiety.

- 10 Embodiment 40. The oligomeric compound of embodiment 39, wherein the modified oligonucleotide has:  
 a 5' external region consisting of 3 linked nucleosides;  
 a deoxy region consisting of 10 linked nucleosides; and  
 a 3' external region consisting of 3 linked nucleosides;

wherein each of the 5'-region nucleosides and each of the 3'-region nucleosides is a cEt nucleoside.

- 15 Embodiment 41. The oligomeric compound of embodiment 39, wherein the modified oligonucleotide has:  
 a 5' external region consisting of 1-6 linked nucleosides;  
 a deoxy region consisting of 6-10 linked nucleosides; and  
 a 3' external region consisting of 1-6 linked nucleosides;

- wherein each of the 5' external region nucleosides and each of the 3' external region nucleosides is a cEt nucleoside or a  
 20 2'-MOE nucleoside; and each of the deoxy region nucleosides is a 2'-β-D-deoxynucleoside.

Embodiment 42. An oligomeric compound of any of embodiments 1-32, wherein the modified oligonucleotide has a sugar motif (5' to 3') selected from: kkkdddddskkk, kkkdydddddskkk, kkkdddddskkek, and kkkdddddskkke.

- Embodiment 43. An oligomeric compound comprising a modified oligonucleotide according to the following  
 25 chemical notation:  $A_{ks}T_{ks}^mC_{ks}T_{ds}A_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ks}T_{ks}G_k$  (SEQ ID NO:3036), wherein

- A = an adenine nucleobase,  
 $^mC$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 30 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribose sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

- Embodiment 44. An oligomeric compound comprising a modified oligonucleotide according to the following  
 chemical notation:  $A_{ks}G_{ks}T_{ks}A_{ds}T_{ds}A_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}T_{ds}G_{ks}T_{ks}T_k$  (SEQ ID NO: 3038), wherein

- 35 A = an adenine nucleobase,  
 $^mC$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,

k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

Embodiment 45. An oligomeric compound comprising a modified oligonucleotide according to the following  
 5 chemical notation:  ${}^m\text{C}_{\text{ks}}\text{T}_{\text{ks}}\text{A}_{\text{ds}}\text{T}_{\text{ds}}\text{T}_{\text{ds}}\text{G}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ds}}\text{A}_{\text{ds}}\text{G}_{\text{ks}}\text{T}_{\text{es}}\text{G}_{\text{ks}}\text{T}_{\text{es}}\text{A}_{\text{k}}$  (SEQ ID NO: 3040), wherein

A = an adenine nucleobase,  
 ${}^m\text{C}$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 10 e = a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> modified ribosyl sugar moiety,  
 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

Embodiment 46. The oligomeric compound of any of embodiments 1-45, wherein the oligomeric compound  
 15 comprises a conjugate group.

Embodiment 47. The oligomeric compound of embodiment 46, wherein the conjugate group comprises a  
 conjugate linker and a conjugate moiety.

Embodiment 48. The oligomeric compound of embodiment 46 or 47, wherein the conjugate linker consists of  
 a single bond.

Embodiment 49. The oligomeric compound of any of embodiments 46-48, wherein the conjugate linker is  
 20 cleavable.

Embodiment 50. The oligomeric compound of any of embodiments 46-49, wherein the conjugate linker  
 comprises 1-3 linker-nucleosides.

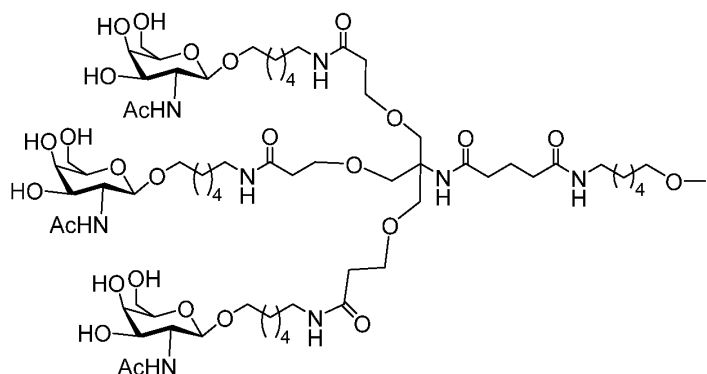
Embodiment 51. The oligomeric compound of any of embodiments 46-49, wherein the conjugate linker is a  
 25 phosphate.

Embodiment 52. The oligomeric compound of any of embodiments 46-51, wherein the conjugate group is  
 attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.

Embodiment 53. The oligomeric compound of any of embodiments 46-51, wherein the conjugate group is  
 attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.

Embodiment 54. The oligomeric compound of any of embodiments 46-53, wherein the conjugate group  
 30 comprises N-acetyl galactosamine.

Embodiment 55. The oligomeric compound of embodiment 54, wherein the conjugate group has the following  
 structure:



Embodiment 56. The oligomeric compound of any of embodiments 46-55, wherein the conjugate group comprises a cell-targeting moiety.

Embodiment 57. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation:  $\text{THA-GalNAc-}_o\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ks}\text{T}_{ks}\text{G}_k$  (SEQ ID NO: 3037), wherein

A = an adenine nucleobase,

${}^m\text{C}$  = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

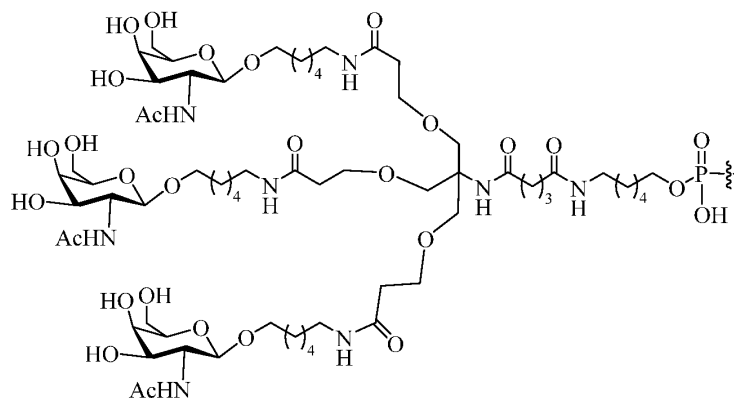
T = a thymine nucleobase,

k = a cEt sugar moiety,

d = a 2'-β-D-deoxyribose sugar moiety,

s = a phosphorothioate internucleoside linkage, and

THA-GalNAc-<sub>o</sub> =

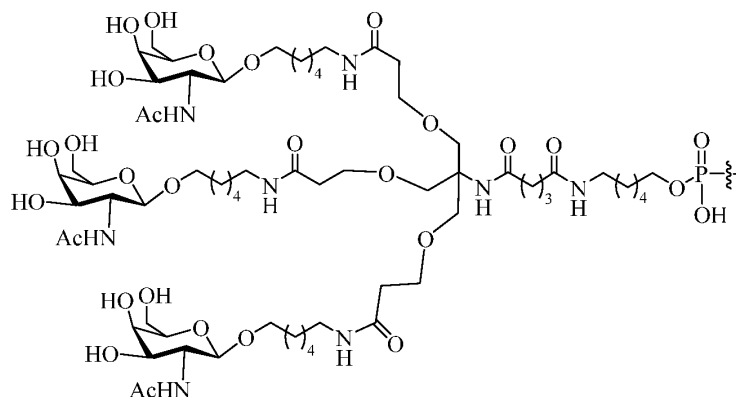


Embodiment 58. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation:  $\text{THA-GalNAc-}_o\text{A}_{ks}\text{G}_{ks}\text{T}_{ks}\text{A}_{ds}\text{T}_{ds}\text{A}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{A}_{ds}\text{G}_{ds}\text{T}_{ds}\text{G}_{ks}\text{T}_{ks}\text{T}_k$  (SEQ ID NO: 3039), wherein

A = an adenine nucleobase,

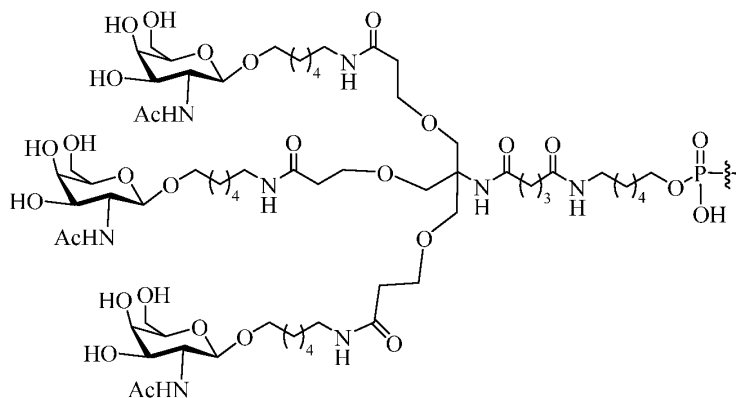
G = a guanine nucleobase,

T = a thymine nucleobase,  
 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety,  
 s = a phosphorothioate internucleoside linkage, and  
 5  
 THA-GalNAc<sub>o</sub> =



Embodiment 59. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation: THA-GalNAc-  
<sub>o</sub><sup>m</sup>C<sub>ks</sub>T<sub>ks</sub>A<sub>ds</sub>T<sub>ds</sub>T<sub>ds</sub>G<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ks</sub>T<sub>es</sub>G<sub>ks</sub>T<sub>es</sub>A<sub>k</sub> (SEQ ID NO: 3041), wherein

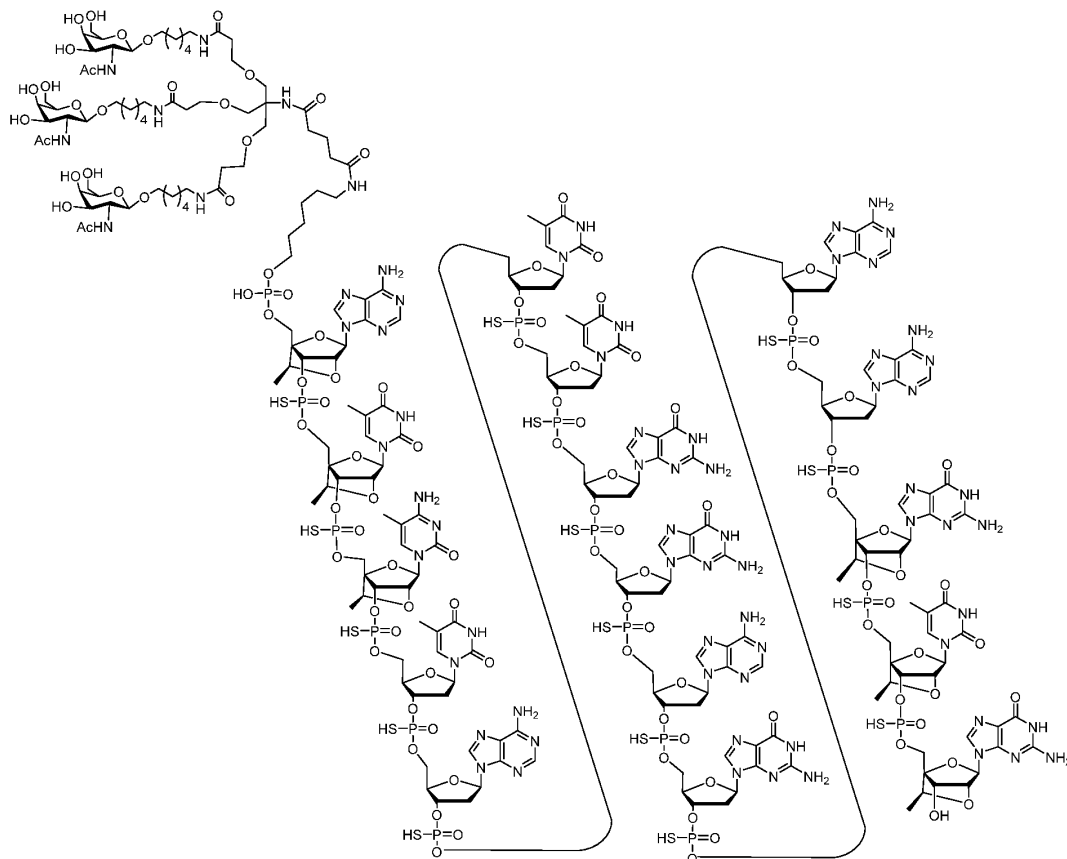
10  
 A = an adenine nucleobase,  
<sup>m</sup>C = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 e = a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> modified ribosyl sugar moiety,  
 15  
 k = a cEt sugar moiety  
 d = a 2'-β-D-deoxyribosyl sugar moiety  
 s = a phosphorothioate internucleoside linkage, and  
 THA-GalNAc<sub>o</sub> =



Embodiment 60. The oligomeric compound of any of embodiments 1 to 59, wherein the oligomeric compound comprises a terminal group.

Embodiment 61. The oligomeric compound of embodiment 60, wherein the terminal group is an abasic sugar moiety.

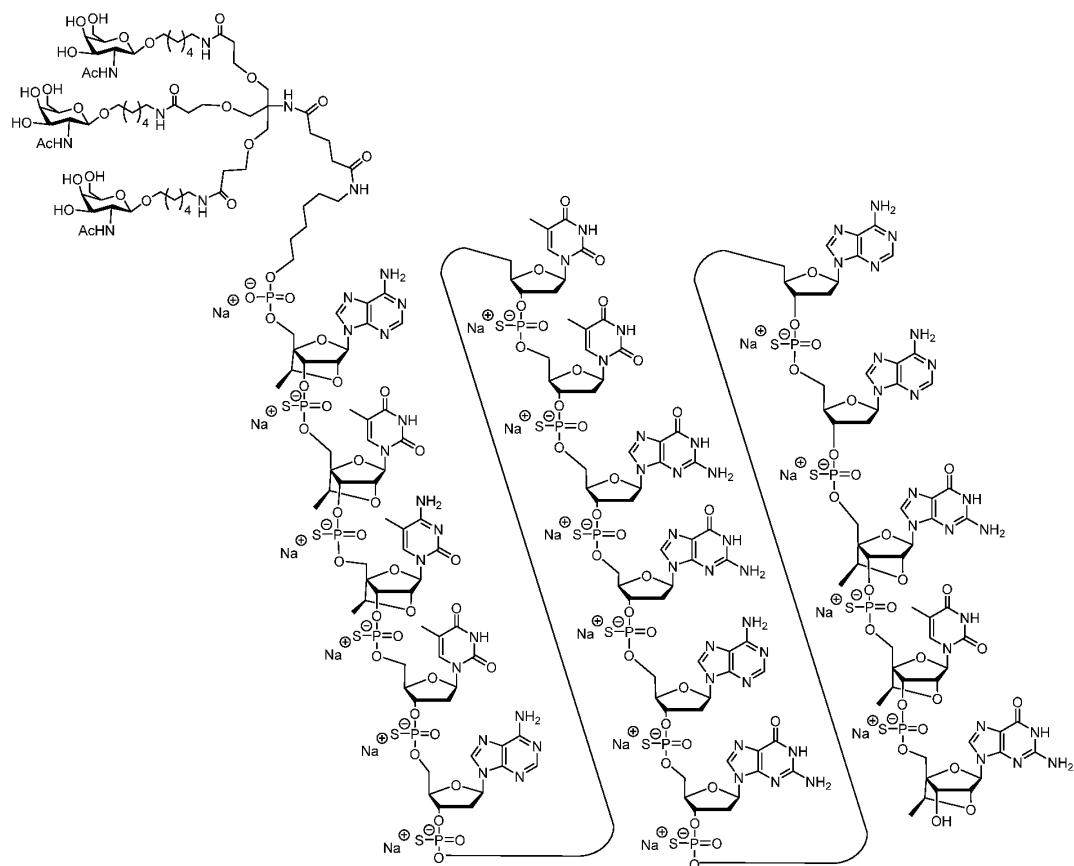
5 Embodiment 62. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3037), or a salt thereof.

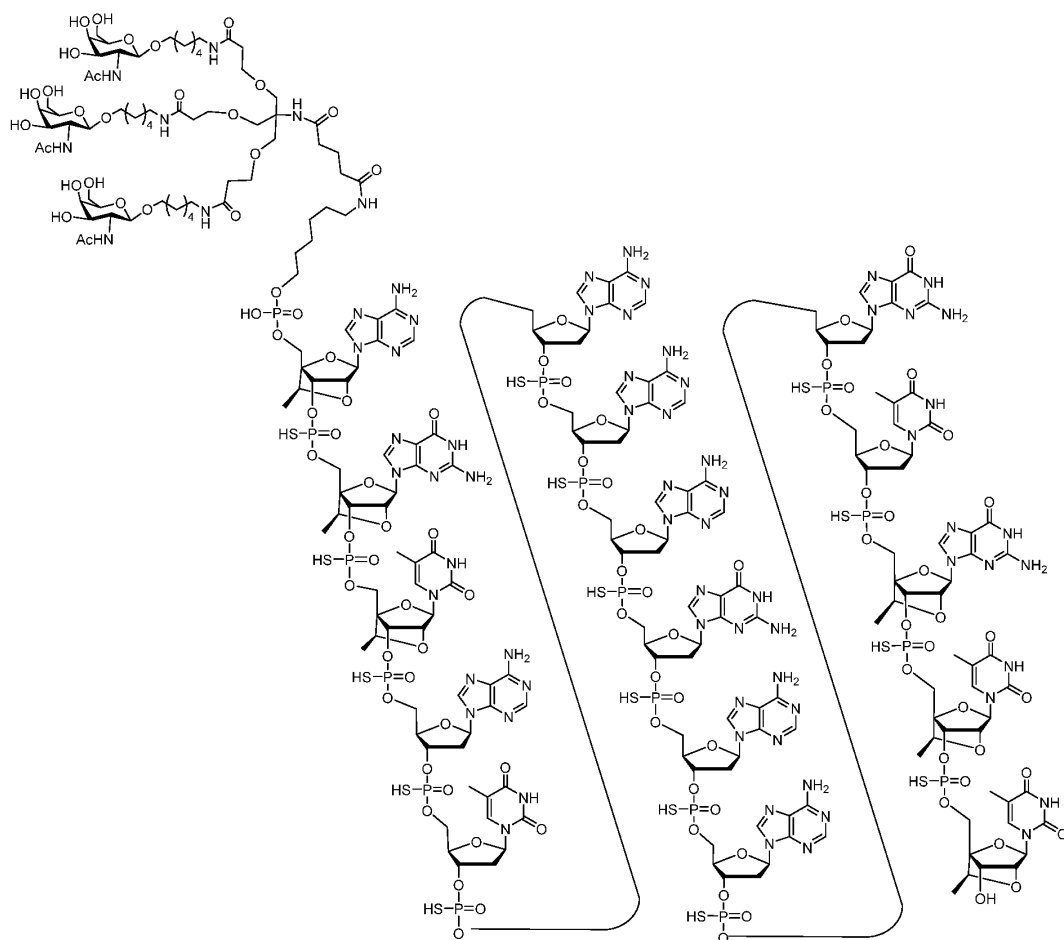
Embodiment 63. The oligomeric compound of embodiment 62, which is the sodium salt or the potassium salt.

Embodiment 64. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3037).

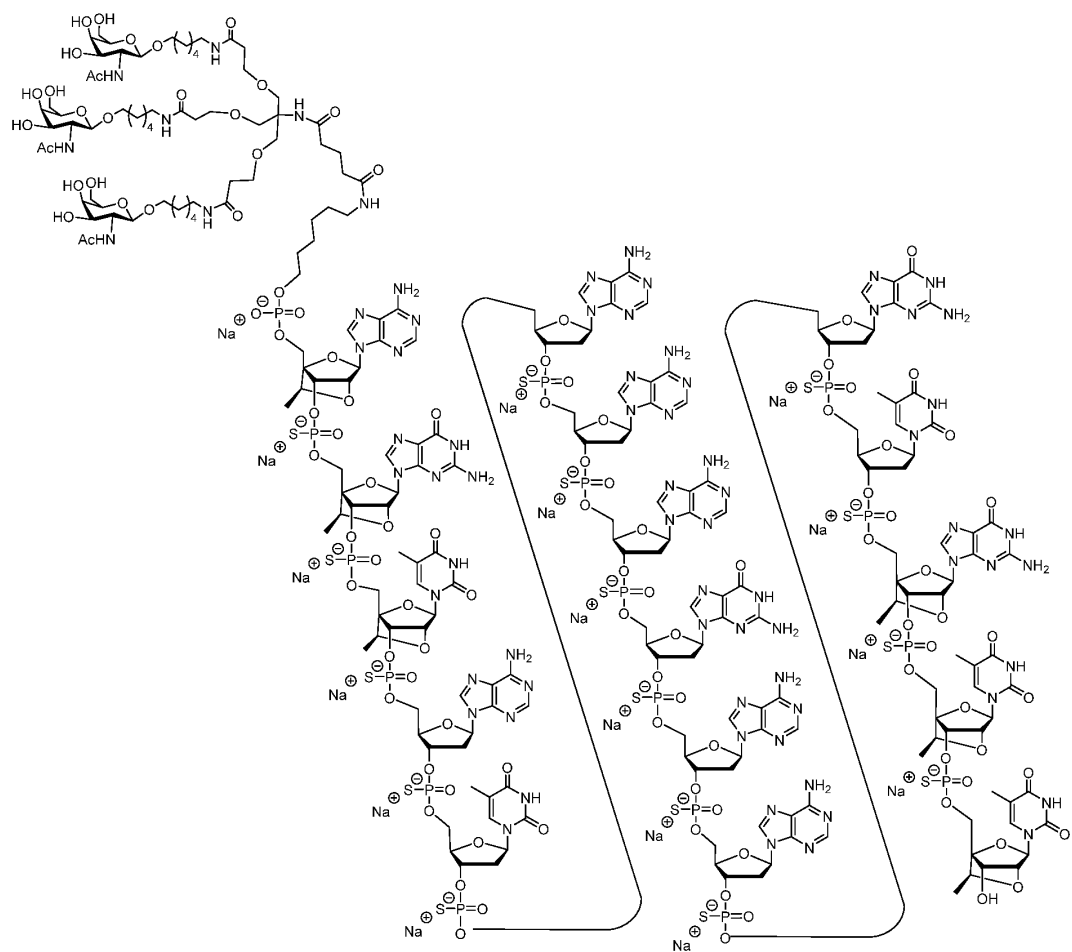
Embodiment 65. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3039), or a salt thereof.

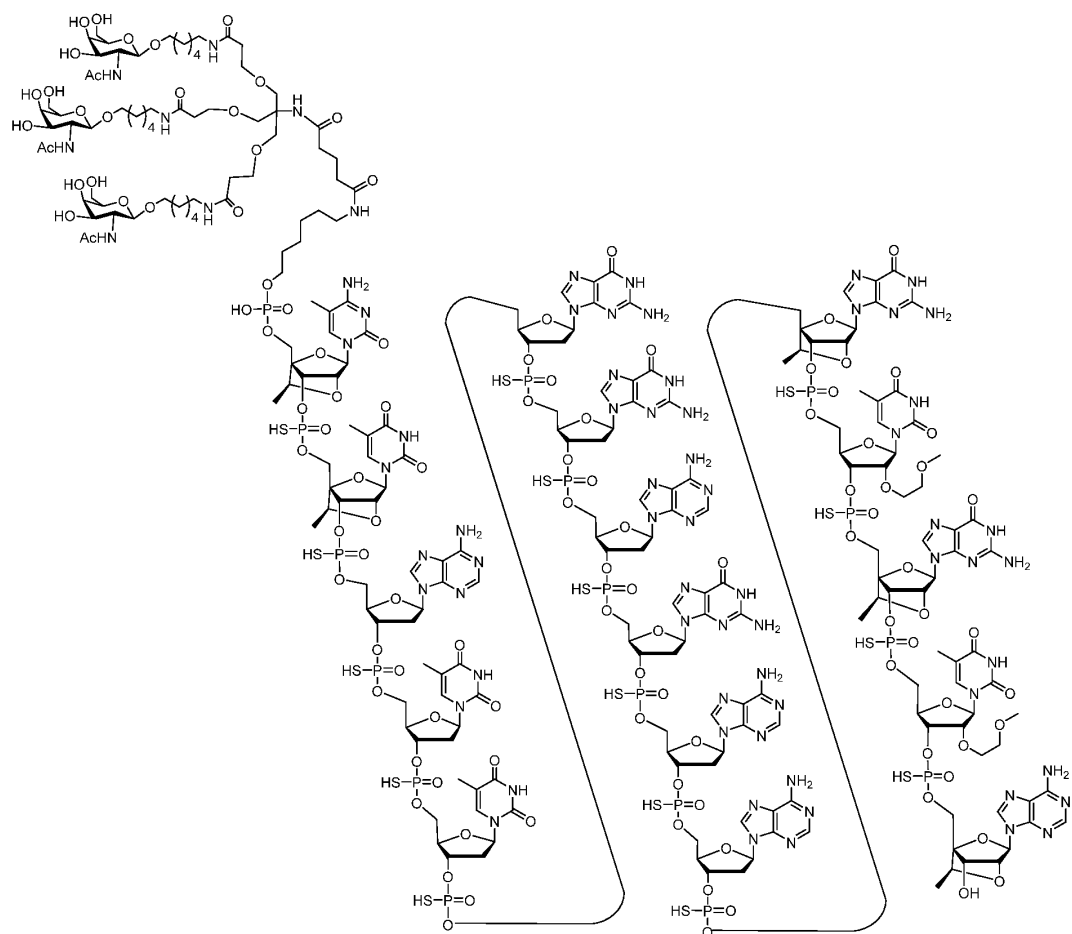
Embodiment 66. The oligomeric compound of embodiment 65, which is the sodium salt or the potassium salt.

Embodiment 67. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3039).

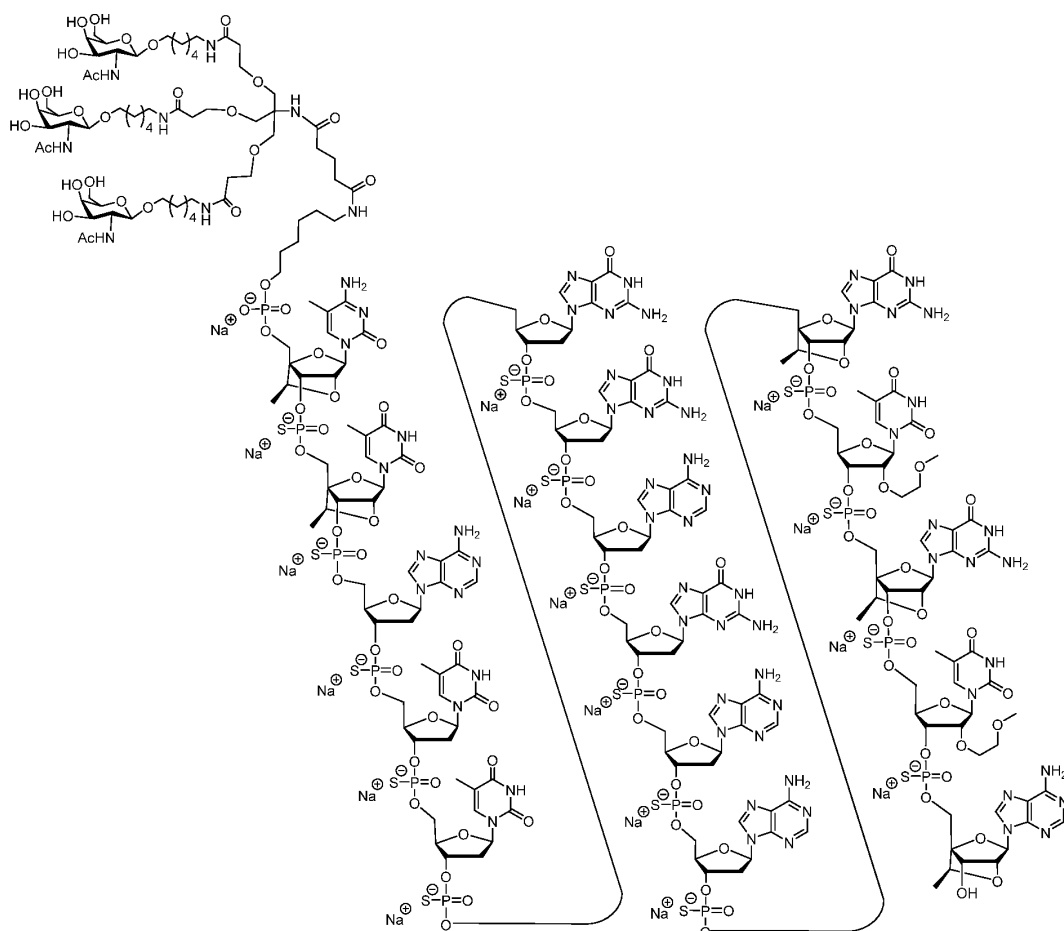
Embodiment 68. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3041), or a salt thereof.

Embodiment 69. The oligomeric compound of embodiment 68, which is the sodium salt or the potassium salt.

Embodiment 70. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3041).

Embodiment 71. A chirally enriched population of oligomeric compounds of any of embodiments 1-70, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

Embodiment 72. The chirally enriched population of embodiment 71, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*Sp*) or (*Rp*) configuration.

Embodiment 73. The chirally enriched population of embodiment 71, wherein the population is enriched for modified oligonucleotides having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage.

Embodiment 74. The chirally enriched population of embodiment 71, wherein the population is enriched for modified oligonucleotides having the (*Rp*) configuration at one particular phosphorothioate internucleoside linkage and the (*Sp*) configuration at each of the remaining phosphorothioate internucleoside linkages.

Embodiment 75. The chirally enriched population of embodiment 71, wherein the population is enriched for modified oligonucleotides having at least 3 contiguous phosphorothioate internucleoside linkages in the *Sp*, *Sp*, and *Rp* configurations, in the 5' to 3' direction.

5 Embodiment 76. A population of oligomeric compounds comprising modified oligonucleotides of any of embodiments 1-70 wherein all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

Embodiment 77. An oligomeric duplex, comprising a first oligomeric compound and a second oligomeric compound comprising a second modified oligonucleotide, wherein the first oligomeric compound is an oligomeric compound of any of embodiments 1-70.

10 Embodiment 78. The oligomeric duplex of embodiment 77, wherein the second oligomeric compound comprises a second modified oligonucleotide consisting of 8 to 80 linked nucleosides, and wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

15 Embodiment 79. The oligomeric duplex of embodiment 77 or 78, wherein the modified oligonucleotide of the first oligomeric compound comprises a 5'-stabilized phosphate group.

Embodiment 80. The oligomeric duplex of embodiment 79, wherein the stabilized phosphate group comprises a cyclopropyl phosphonate or a vinyl phosphonate.

Embodiment 81. The oligomeric duplex of any of embodiments 77-80, wherein the modified oligonucleotide of the first oligomeric compound comprises a glycol nucleic acid (GNA) sugar surrogate.

20 Embodiment 82. The oligomeric duplex of any of embodiments 77-80, wherein the modified oligonucleotide of the first oligomeric compound comprises a 2'-NMA sugar moiety.

Embodiment 83. The oligomeric duplex of any of embodiments 77-82, wherein at least one nucleoside of the second modified oligonucleotide comprises a modified sugar moiety.

25 Embodiment 84. The oligomeric duplex of embodiment 83, wherein the modified sugar moiety of the second modified oligonucleotide comprises a bicyclic sugar moiety.

Embodiment 85. The oligomeric duplex of embodiment 84, wherein the bicyclic sugar moiety of the second modified oligonucleotide comprises a 2'-4' bridge selected from -O-CH<sub>2</sub>-; and -O-CH(CH<sub>3</sub>)-.

Embodiment 86. The oligomeric duplex of embodiment 83, wherein the modified sugar moiety of the second modified oligonucleotide comprises a non-bicyclic modified sugar moiety.

30 Embodiment 87. The oligomeric duplex of embodiment 86, wherein the non-bicyclic modified sugar moiety of the second modified oligonucleotide is a 2'-MOE sugar moiety, a 2'-F sugar moiety, or 2'-OMe sugar moiety.

Embodiment 88. The oligomeric duplex of any of embodiments 77-87, wherein at least one nucleoside of the second modified oligonucleotide comprises a sugar surrogate.

35 Embodiment 89. The oligomeric duplex of any of embodiments 77-88, wherein at least one internucleoside linkage of the second modified oligonucleotide is a modified internucleoside linkage.

Embodiment 90. The oligomeric duplex of embodiment 89, wherein at least one modified internucleoside linkage of the second modified oligonucleotide is a phosphorothioate internucleoside linkage.

Embodiment 91. The oligomeric duplex of embodiment 89 or 90, wherein at least one modified internucleoside linkage of the second modified oligonucleotide is a mesyl phosphoramidate internucleoside linkage.

Embodiment 92. The oligomeric duplex of any of embodiments 77-91, wherein at least one internucleoside linkage of the second modified oligonucleotide is a phosphodiester internucleoside linkage.

Embodiment 93. The oligomeric duplex of any of embodiments 77-90 or 92, wherein each internucleoside linkage of the second modified oligonucleotide is independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

Embodiment 94. The oligomeric duplex of any of embodiments 77-92, wherein each internucleoside linkage of the second modified oligonucleotide is independently selected from a phosphodiester internucleoside linkage, a phosphorothioate internucleoside linkage, or a mesyl phosphoramidate internucleoside linkage.

Embodiment 95. The oligomeric duplex of any of embodiments 77-94, wherein the second modified oligonucleotide comprises at least one modified nucleobase.

Embodiment 96. The oligomeric duplex of embodiment 95, wherein the modified nucleobase of the second modified oligonucleotide is 5-methylcytosine.

Embodiment 97. The oligomeric duplex of any of embodiments 77-96, wherein the second modified oligonucleotide comprises a conjugate group.

Embodiment 98. The oligomeric duplex of embodiment 97, wherein the conjugate group comprises a conjugate linker and a conjugate moiety.

Embodiment 99. The oligomeric duplex of embodiment 97 or 98, wherein the conjugate group is attached to the second modified oligonucleotide at the 5'-end of the second modified oligonucleotide.

Embodiment 100. The oligomeric duplex of embodiment 97 or 98, wherein the conjugate group is attached to the second modified oligonucleotide at the 3'-end of the modified oligonucleotide.

Embodiment 101. The oligomeric duplex of any of embodiments 97-100, wherein the conjugate group comprises N-acetyl galactosamine.

Embodiment 102. The oligomeric duplex of any of embodiments 97-101, wherein the second modified oligonucleotide comprises a terminal group.

Embodiment 103. The oligomeric duplex of embodiment 102, wherein the terminal group is an abasic sugar moiety.

Embodiment 104. The oligomeric duplex of any of embodiments 77-103, wherein the second modified oligonucleotide consists of 10 to 25, 10 to 30, 10 to 50, 12 to 20, 12 to 25, 12 to 30, 12 to 50, 13 to 20, 13 to 25, 13 to 30, 13 to 50, 14 to 20, 14 to 25, 14 to 30, 14 to 50, 15 to 20, 15 to 25, 15 to 30, 15 to 50, 16 to 18, 16 to 20, 16 to 25, 16 to 30, 16 to 50, 17 to 20, 17 to 25, 17 to 30, 17 to 50, 18 to 20, 18 to 25, 18 to 30, 18 to 50, 19 to 20, 19 to 25, 19 to 30, 19 to 50, 20 to 25, 20 to 30, 20 to 50, 21 to 25, 21 to 30, 21 to 50, 22 to 25, 22 to 30, 22 to 50, 23 to 25, 23 to 30, or 23 to 50 linked nucleosides.

Embodiment 105. An antisense agent comprising an antisense compound, wherein the antisense compound is the oligomeric compound of any of embodiments 1-70.

Embodiment 106. The antisense agent of embodiment 105, wherein the antisense agent is the oligomeric duplex of any of embodiments 77-104.

Embodiment 107. The antisense agent of embodiment 105 or 106, wherein the antisense agent is:

- i. an RNase H agent capable of reducing the amount of PSD3 nucleic acid through the activation of RNase H; or

- ii. an RNAi agent capable of reducing the amount of PSD3 nucleic acid through the activation of RISC/Ago2.

Embodiment 108. The antisense agent of any of embodiments 105-107, wherein the conjugate group is a cell-targeting moiety.

5        Embodiment 109. A pharmaceutical composition comprising the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, or the antisense agent of any of embodiments 105-108, and a pharmaceutically acceptable diluent or carrier.

Embodiment 110. The pharmaceutical composition of embodiment 109, wherein the pharmaceutically acceptable diluent is water or phosphate-buffered saline.

10        Embodiment 111. The pharmaceutical composition of embodiment 110, wherein the pharmaceutical composition consists essentially of the oligomeric compound, the modified oligonucleotide, the oligomeric duplex, or the antisense agent, and water or phosphate-buffered saline.

Embodiment 112. A method comprising administering to a subject the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111.

Embodiment 113. A method of treating a disease associated with PSD3 comprising administering to a subject having a disease associated with PSD3 a therapeutically effective amount of the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111; thereby treating the disease associated with PSD3.

Embodiment 114. The method of embodiment 113, wherein the disease associated with PSD3 is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

Embodiment 115. The method of embodiment 114, wherein administering the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111 reduces liver damage, steatosis, liver fibrosis, liver inflammation, liver scarring or cirrhosis, liver failure, liver enlargement, elevated transaminases, or hepatic fat accumulation in the subject.

Embodiment 116. A method of reducing expression of PSD3 in a cell comprising contacting the cell with the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111.

Embodiment 117. The method of embodiment 116, wherein the cell is a liver cell.

Embodiment 118. Use of the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111 for treating a disease associated with PSD3.

Embodiment 119. Use of the oligomeric compound of any of embodiments 1-70, the population of any of embodiments 71-76, the oligomeric duplex of any of embodiments 77-104, the antisense agent of any of embodiments 105-108, or the pharmaceutical composition of any of embodiments 109-111 in the manufacture of a medicament for treating a disease associated with PSD3.

5 Embodiment 120. The use of embodiment 118 or 119, wherein the disease associated with PSD3 is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

#### 10 *Certain Oligomeric Duplexes*

Certain embodiments are directed to oligomeric duplexes comprising a first oligomeric compound and a second oligomeric compound.

15 In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 8 to 80 linked nucleosides, wherein the nucleobase sequence of the first modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 82205-82220, 181927-181942, 184997-185012, 217663-217678, 218081-218096, 218085-218100, 222016-222031, 222028-222043, 222044-222059, 244765-244780, 285152-285167, 285254-285269, 288678-288693, 288680-288695, 288681-288696, 291274-291289, 330574-330589, 344743-344758, or 463909-463924 of SEQ ID NO: 1; and

20 a second oligomeric compound comprising a second modified oligonucleotide consisting of 8 to 80 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 8 to 80 linked nucleosides wherein the nucleobase sequence of the first modified oligonucleotide comprises at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 contiguous nucleobases of the nucleobase sequence of any of SEQ ID NOs 20-3034, wherein each thymine is replaced by uracil; and

30 a second oligomeric compound comprising a second modified oligonucleotide consisting of 8 to 80 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

35 In certain embodiments, the first oligomeric compound is an antisense compound. In certain embodiments, the first modified oligonucleotide is an antisense oligonucleotide. In certain embodiments, the second oligomeric compound is a sense compound. In certain embodiments, the second modified oligonucleotide is a sense oligonucleotide.

In certain embodiments, an oligomeric duplex comprises:

a first oligomeric compound comprising a first modified oligonucleotide consisting of 16 to 80 linked nucleosides wherein the nucleobase sequence of the first modified oligonucleotide comprises the nucleobase sequence of any of SEQ ID NOs 20-3034, wherein each thymine is replaced by uracil; and

5 a second oligomeric compound comprising a second modified oligonucleotide consisting of 16 to 80 linked nucleosides wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 16 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

10 In certain embodiments, the first oligomeric compound is an antisense compound. In certain embodiments, the first modified oligonucleotide is an antisense oligonucleotide. In certain embodiments, the second oligomeric compound is a sense compound. In certain embodiments, the second modified oligonucleotide is a sense oligonucleotide.

In any of the oligomeric duplexes described herein, at least one nucleoside of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a modified sugar moiety. Examples of suitable modified sugar moieties include, but are not limited to, a bicyclic sugar moiety, such as a 2'-4' bridge selected from -O-CH<sub>2</sub>-; and -O-CH(CH<sub>3</sub>)-, and a non-bicyclic sugar moiety, such as a 2'-MOE sugar moiety, a 2'-F sugar moiety, a 2'-OMe sugar moiety, or a 2'-NMA sugar moiety. In certain embodiments, at least 80%, at least 90%, or 100% of the nucleosides of the first modified oligonucleotide and/or the second modified oligonucleotide comprises a modified sugar moiety selected from 2'-F and 2'-OMe.

20 In any of the oligomeric duplexes described herein, at least one nucleoside of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a sugar surrogate. Examples of suitable sugar surrogates include, but are not limited to, morpholino, peptide nucleic acid (PNA), glycol nucleic acid (GNA), and unlocked nucleic acid (UNA). In certain embodiments, at least one nucleoside of the first modified oligonucleotide comprises a sugar surrogate, which can be a GNA.

25 In any of the oligomeric duplexes described herein, at least one internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a modified internucleoside linkage. In certain embodiments, the modified internucleoside linkage is a phosphorothioate internucleoside linkage. In certain embodiments, at least one of the first, second, or third internucleoside linkages from the 5' end and/or the 3' end of the first modified oligonucleotide comprises a phosphorothioate linkage. In certain embodiments, at least one of the first, second, or third internucleoside linkages from the 5' end and/or the 3' end of the second modified oligonucleotide comprises a phosphorothioate linkage.

In any of the oligomeric duplexes described herein, at least one internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can comprise a phosphodiester internucleoside linkage.

35 In any of the oligomeric duplexes described herein, each internucleoside linkage of the first modified oligonucleotide and/or the second modified oligonucleotide can be independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

In any of the oligomeric duplexes described herein, at least one nucleobase of the first modified oligonucleotide and/or the second modified oligonucleotide can be modified nucleobase. In certain embodiments, the modified nucleobase is 5-methylcytosine.

In any of the oligomeric duplexes described herein, the first modified oligonucleotide can comprise a stabilized phosphate group attached to the 5' position of the 5'-most nucleoside. In certain embodiments, the stabilized phosphate group comprises a cyclopropyl phosphonate or an (*E*)-vinyl phosphonate.

In any of the oligomeric duplexes described herein, the first modified oligonucleotide can comprise a conjugate group. In certain embodiments, the conjugate group comprises a conjugate linker and a conjugate moiety. In certain embodiments, the conjugate group is attached to the first modified oligonucleotide at the 5'-end of the first modified oligonucleotide. In certain embodiments, the conjugate group is attached to the first modified oligonucleotide at the 3'-end of the modified oligonucleotide. In certain embodiments, the conjugate group comprises N-acetyl galactosamine. In certain embodiments, the conjugate group comprises a cell-targeting moiety having an affinity for transferrin receptor (TfR), also known as TfR1 and CD71. In certain embodiments, the conjugate group comprises an anti-TfR1 antibody or fragment thereof. In certain embodiments, the conjugate group comprises a protein or peptide capable of binding TfR1. In certain embodiments, the conjugate group comprises an aptamer capable of binding TfR1. In certain embodiments, conjugate groups may be selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, C5 alkyl, C22 alkenyl, C20 alkenyl, C16 alkenyl, C10 alkenyl, C21 alkenyl, C19 alkenyl, C18 alkenyl, C15 alkenyl, C14 alkenyl, C13 alkenyl, C12 alkenyl, C11 alkenyl, C9 alkenyl, C8 alkenyl, C7 alkenyl, C6 alkenyl, or C5 alkenyl. In certain embodiments, conjugate groups may be selected from any of C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, and C5 alkyl, where the alkyl chain has one or more unsaturated bonds.

In any of the oligomeric duplexes described herein, the second modified oligonucleotide can comprise a conjugate group. In certain embodiments, the conjugate group comprises a conjugate linker and a conjugate moiety. In certain embodiments, the conjugate group is attached to the second modified oligonucleotide at the 5'-end of the second modified oligonucleotide. In certain embodiments, the conjugate group is attached to the second modified oligonucleotide at the 3'-end of the modified oligonucleotide. In certain embodiments, the conjugate group comprises N-acetyl galactosamine. In certain embodiments, the conjugate group comprises a cell-targeting moiety having an affinity for transferrin receptor (TfR), also known as TfR1 and CD71. In certain embodiments, the conjugate group comprises an anti-TfR1 antibody or fragment thereof. In certain embodiments, the conjugate group comprises a protein or peptide capable of binding TfR1. In certain embodiments, the conjugate group comprises an aptamer capable of binding TfR1. In certain embodiments, conjugate groups may be selected from any of a C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, C5 alkyl, C22 alkenyl, C20 alkenyl, C16 alkenyl, C10 alkenyl, C21 alkenyl, C19 alkenyl, C18 alkenyl, C15 alkenyl, C14 alkenyl, C13 alkenyl, C12 alkenyl, C11 alkenyl, C9 alkenyl, C8 alkenyl, C7 alkenyl, C6 alkenyl, or C5 alkenyl. In certain embodiments, conjugate groups may be selected from any of C22 alkyl, C20 alkyl, C16 alkyl, C10 alkyl, C21 alkyl, C19 alkyl, C18 alkyl, C15 alkyl, C14 alkyl, C13 alkyl, C12 alkyl, C11 alkyl, C9 alkyl, C8 alkyl, C7 alkyl, C6 alkyl, and C5 alkyl, where the alkyl chain has one or more unsaturated bonds.

In certain embodiments, an antisense agent comprises an antisense compound, which comprises an oligomeric compound or an oligomeric duplex described herein. In certain embodiments, an antisense agent, which can comprise an oligomeric compound or an oligomeric duplex described herein, is an RNAi agent capable of reducing the amount of PSD3 nucleic acid through the activation of RISC/Ago2.

Certain embodiments provide an oligomeric agent comprising two or more oligomeric duplexes. In certain embodiments, an oligomeric agent comprises two or more of any of the oligomeric duplexes described herein. In certain embodiments, an oligomeric agent comprises two or more of the same oligomeric duplex, which can be any of the oligomeric duplexes described herein. In certain embodiments, the two or more oligomeric duplexes are linked together.

5 In certain embodiments, the two or more oligomeric duplexes are covalently linked together. In certain embodiments, the second modified oligonucleotides of two or more oligomeric duplexes are covalently linked together. In certain embodiments, the second modified oligonucleotides of two or more oligomeric duplexes are covalently linked together at their 3' ends. In certain embodiments, the two or more oligomeric duplexes are covalently linked together by a glycol linker, such as a tetraethylene glycol linker. Certain such compounds are described in, e.g., Alterman, et al., *Nature*

10 *Biotech.*, 37:844-894, 2019.

## I. Certain Oligonucleotides

In certain embodiments, provided herein are oligomeric compounds comprising oligonucleotides, which consist of linked nucleosides. Oligonucleotides may be unmodified oligonucleotides (RNA or DNA) or may be modified

15 oligonucleotides. Modified oligonucleotides comprise at least one modification relative to unmodified RNA or DNA. That is, modified oligonucleotides comprise at least one modified nucleoside (comprising a modified sugar moiety and/or a modified nucleobase) and/or at least one modified internucleoside linkage. Certain modified nucleosides and modified internucleoside linkages suitable for use in modified oligonucleotides are described below.

### 20 A. Certain Modified Nucleosides

Modified nucleosides comprise a modified sugar moiety or a modified nucleobase or both a modified sugar moiety and a modified nucleobase. In certain embodiments, modified nucleosides comprising the following modified sugar moieties and/or the following modified nucleobases may be incorporated into modified oligonucleotides.

#### 1. Certain Sugar Moieties

25 In certain embodiments, modified 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 sugar moieties comprising a furanosyl ring

30 with one or more substituent groups none of which bridges two atoms of the furanosyl ring to form a bicyclic structure. Such non bridging substituents may be at any position of the furanosyl, including but not limited to substituents at the 2', 3', 4', and/or 5' positions. In certain embodiments one or more non-bridging 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<sub>3</sub> ("OMe" or "O-methyl"), and 2'-O(CH<sub>2</sub>)<sub>2</sub>OCH<sub>3</sub> ("MOE" or "O-methoxyethyl"). In

35 certain embodiments, 2'-substituent groups are selected from among: halo, allyl, amino, azido, SH, CN, OCN, CF<sub>3</sub>, OCF<sub>3</sub>, O-C<sub>1</sub>-C<sub>10</sub> alkoxy, O-C<sub>1</sub>-C<sub>10</sub> substituted alkoxy, O-C<sub>1</sub>-C<sub>10</sub> alkyl, O-C<sub>1</sub>-C<sub>10</sub> substituted alkyl, S-alkyl, N(R<sub>m</sub>)-alkyl, O-alkenyl, S-alkenyl, N(R<sub>m</sub>)-alkenyl, O-alkynyl, S-alkynyl, N(R<sub>m</sub>)-alkynyl, O-alkylenyl-O-alkyl, alkynyl, alkaryl, aralkyl, O-alkaryl, O-aralkyl, O(CH<sub>2</sub>)<sub>2</sub>SCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>2</sub>ON(R<sub>m</sub>)(R<sub>n</sub>) or OCH<sub>2</sub>C(=O)-N(R<sub>m</sub>)(R<sub>n</sub>), where each R<sub>m</sub> and R<sub>n</sub> is, independently, H, an amino protecting group, or substituted or unsubstituted C<sub>1</sub>-C<sub>10</sub> alkyl, -O(CH<sub>2</sub>)<sub>2</sub>ON(CH<sub>3</sub>)<sub>2</sub>

("DMAOE"), 2'-OCH<sub>2</sub>OCH<sub>2</sub>N(CH<sub>2</sub>)<sub>2</sub> ("DMAEOE"), 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<sub>2</sub>), thiol, thioalkoxy, thioalkyl, halogen, alkyl, aryl, alkenyl and alkynyl.

- 5 In certain embodiments, non-bicyclic modified sugar moieties comprise a substituent group at the 3'-position. Examples of substituent groups suitable for the 3'-position of modified sugar moieties include but are not limited to alkoxy (e.g., methoxy), alkyl (e.g., methyl, ethyl). In certain embodiments, non-bicyclic modified sugar moieties comprise a substituent group at the 4'-position. 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.
- 10 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, ethyl, and 5'-methoxy. In certain embodiments, non-bicyclic modified sugar moieties 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 non-bicyclic modified nucleoside comprises a sugar moiety comprising
- 15 a non-bridging 2'-substituent group selected from: F, NH<sub>2</sub>, N<sub>3</sub>, OCF<sub>3</sub>, OCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>3</sub>NH<sub>2</sub>, CH<sub>2</sub>CH=CH<sub>2</sub>, OCH<sub>2</sub>CH=CH<sub>2</sub>, OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>2</sub>SCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>2</sub>ON(R<sub>m</sub>)(R<sub>n</sub>), O(CH<sub>2</sub>)<sub>2</sub>O(CH<sub>2</sub>)<sub>2</sub>N(CH<sub>3</sub>)<sub>2</sub>, and N-substituted acetamide (OCH<sub>2</sub>C(=O)-N(R<sub>m</sub>)(R<sub>n</sub>)), where each R<sub>m</sub> and R<sub>n</sub> is, independently, H, an amino protecting group, or substituted or unsubstituted C<sub>1</sub>-C<sub>10</sub> alkyl.

- In certain embodiments, a 2'-substituted nucleoside non-bicyclic modified nucleoside comprises a sugar moiety
- 20 comprising a non-bridging 2'-substituent group selected from: F, OCF<sub>3</sub>, OCH<sub>3</sub>, OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>2</sub>SCH<sub>3</sub>, O(CH<sub>2</sub>)<sub>2</sub>ON(CH<sub>3</sub>)<sub>2</sub>, O(CH<sub>2</sub>)<sub>2</sub>O(CH<sub>2</sub>)<sub>2</sub>N(CH<sub>3</sub>)<sub>2</sub>, O(CH<sub>2</sub>)<sub>2</sub>ON(CH<sub>3</sub>)<sub>2</sub> ("DMAOE"), OCH<sub>2</sub>OCH<sub>2</sub>N(CH<sub>2</sub>)<sub>2</sub> ("DMAEOE") and OCH<sub>2</sub>C(=O)-N(H)CH<sub>3</sub> ("NMA").

In certain embodiments, a 2'-substituted non-bicyclic modified nucleoside comprises a sugar moiety comprising a non-bridging 2'-substituent group selected from: F, OCH<sub>3</sub>, and OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub>.

- 25 In certain embodiments, modified furanosyl sugar moieties and nucleosides incorporating such modified furanosyl sugar moieties are further defined by isomeric configuration. For example, a 2'-deoxyfuranosyl sugar moiety may be in seven isomeric configurations other than the naturally occurring β-D-deoxyribose configuration. Such modified sugar moieties are described in, e.g., WO 2019/157531, incorporated by reference herein. A 2'-modified sugar moiety has an additional stereocenter at the 2'-position relative to a 2'-deoxyfuranosyl sugar moiety; therefore, such sugar
- 30 moieties have a total of sixteen possible isomeric configurations. 2'-modified sugar moieties described herein are in the β-D-ribose isomeric configuration unless otherwise specified.

- In naturally occurring nucleic acids, sugars are linked to one another 3' to 5'. In certain embodiments, oligonucleotides include one or more nucleoside or sugar moiety linked at an alternative position, for example at the 2' or inverted 5' to 3'. For example, where the linkage is at the 2' position, the 2'-substituent groups may instead be at the
- 35 3'-position.

Certain modified sugar moieties comprise a substituent that bridges two atoms of the furanosyl ring to form a second ring, resulting in a bicyclic sugar moiety. Nucleosides comprising such bicyclic sugar moieties have been referred to as bicyclic nucleosides (BNAs), locked nucleosides, or conformationally restricted nucleotides (CRN). Certain such compounds are described in US Patent Publication No. 2013/0190383; and PCT publication WO 2013/036868. 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<sub>2</sub>-2', 4'-(CH<sub>2</sub>)<sub>2</sub>-2', 4'-(CH<sub>2</sub>)<sub>3</sub>-2', 4'-CH<sub>2</sub>-O-2' ("LNA"), 4'-CH<sub>2</sub>-S-2', 4'-(CH<sub>2</sub>)<sub>2</sub>-O-2' ("ENA"), 4'-CH(CH<sub>3</sub>)-O-2' (referred to as "constrained ethyl" or "cEt" when in the *S* configuration), 4'-CH<sub>2</sub>-O-CH<sub>2</sub>-2', 4'-CH<sub>2</sub>-N(R)-2', 4'-CH(CH<sub>2</sub>OCH<sub>3</sub>)-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<sub>3</sub>)(CH<sub>3</sub>)-O-2' and analogs thereof (*see, e.g.*, Seth et al., U.S. 8,278,283), 4'-CH<sub>2</sub>-N(OCH<sub>3</sub>)-2' and analogs thereof (*see, e.g.*, Prakash et al., U.S. 8,278,425), 4'-CH<sub>2</sub>-O-N(CH<sub>3</sub>)-2' (*see, e.g.*, Allerson et al., U.S. 7,696,345 and Allerson et al., U.S. 8,124,745), 4'-CH<sub>2</sub>-C(H)(CH<sub>3</sub>)-2' (*see, e.g.*, Zhou, *et al.*, *J. Org. Chem.*, 2009, 74, 118-134), 4'-CH<sub>2</sub>-C(=CH<sub>3</sub>)-2' and analogs thereof (*see, e.g.*, Seth et al., U.S. 8,278,426), 4'-C(R<sub>a</sub>R<sub>b</sub>)-N(R)-O-2', 4'-C(R<sub>a</sub>R<sub>b</sub>)-O-N(R)-2', 4'-CH<sub>2</sub>-O-N(R)-2', and 4'-CH<sub>2</sub>-N(R)-O-2', wherein each R, R<sub>a</sub>, and R<sub>b</sub> is, independently, H, a protecting group, or C<sub>1</sub>-C<sub>12</sub> 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<sub>a</sub>)(R<sub>b</sub>)]<sub>n</sub>-, -[C(R<sub>a</sub>)(R<sub>b</sub>)]<sub>n</sub>-O-, C(R<sub>a</sub>)=C(R<sub>b</sub>)-, C(R<sub>a</sub>)=N-, C(=NRA)-, -C(=O)-, -C(=S)-, -O-, -Si(R<sub>a</sub>)<sub>2</sub>-, -S(=O)<sub>x</sub>-, and N(R<sub>a</sub>)-;

wherein:

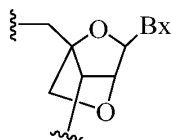
x is 0, 1, or 2;

n is 1, 2, 3, or 4;

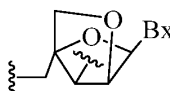
each R<sub>a</sub> and R<sub>b</sub> is, independently, H, a protecting group, hydroxyl, C<sub>1</sub>-C<sub>12</sub> alkyl, substituted C<sub>1</sub>-C<sub>12</sub> alkyl, C<sub>2</sub>-C<sub>12</sub> alkenyl, substituted C<sub>2</sub>-C<sub>12</sub> alkenyl, C<sub>2</sub>-C<sub>12</sub> alkynyl, substituted C<sub>2</sub>-C<sub>12</sub> alkynyl, C<sub>5</sub>-C<sub>20</sub> aryl, substituted C<sub>5</sub>-C<sub>20</sub> aryl, heterocycle radical, substituted heterocycle radical, heteroaryl, substituted heteroaryl, C<sub>5</sub>-C<sub>7</sub> alicyclic radical, substituted C<sub>5</sub>-C<sub>7</sub> alicyclic radical, halogen, OJ<sub>1</sub>, NJ<sub>1</sub>J<sub>2</sub>, SJ<sub>1</sub>, N<sub>3</sub>, COOJ<sub>1</sub>, acyl (C(=O)-H), substituted acyl, CN, sulfonyl (S(=O)<sub>2</sub>-J<sub>1</sub>), or sulfoxyl (S(=O)-J<sub>1</sub>); and each J<sub>1</sub> and J<sub>2</sub> is, independently, H, C<sub>1</sub>-C<sub>12</sub> alkyl, substituted C<sub>1</sub>-C<sub>12</sub> alkyl, C<sub>2</sub>-C<sub>12</sub> alkenyl, substituted C<sub>2</sub>-C<sub>12</sub> alkenyl, C<sub>2</sub>-C<sub>12</sub> alkynyl, substituted C<sub>2</sub>-C<sub>12</sub> alkynyl, C<sub>5</sub>-C<sub>20</sub> aryl, substituted C<sub>5</sub>-C<sub>20</sub> aryl, acyl (C(=O)-H), substituted acyl, a heterocycle radical, a substituted heterocycle radical, C<sub>1</sub>-C<sub>12</sub> aminoalkyl, substituted C<sub>1</sub>-C<sub>12</sub> 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, Alback 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; Wahlestedt et al., *Proc. Natl. Acad. Sci. U. S. A.*, 2000, 97, 5633-5638; 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.*, 2007, 129, 8362-8379; Elayadi et al., *Curr. Opinion Inven. Drugs*, 2001, 2, 558-561; Braasch et al., *Chem. Biol.*, 2001, 8, 1-7; Orum et al., *Curr. Opinion Mol. Ther.*, 2001, 3, 239-243; Wengel et al., 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; 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  $\alpha$ -L configuration or in the  $\beta$ -D configuration.



LNA ( $\beta$ -D-configuration)  
bridge = 4'-CH<sub>2</sub>-O-2'



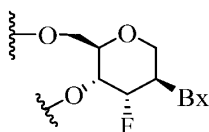
$\alpha$ -L-LNA ( $\alpha$ -L-configuration)  
bridge = 4'-CH<sub>2</sub>-O-2'

- 5  $\alpha$ -L-methyleneoxy (4'-CH<sub>2</sub>-O-2') or  $\alpha$ -L-LNA bicyclic nucleosides have been incorporated into oligonucleotides that showed antisense activity (Frieden et al., *Nucleic Acids Research*, 2003, 21, 6365-6372). The addition of locked nucleic acids to siRNAs has been shown to increase siRNA stability in serum, and to reduce off-target effects (Elmen, J. et al., (2005) *Nucleic Acids Research* 33(1):439-447; Mook, OR. et al., (2007) *Mal Cane Ther* 6(3):833-843; Grunweller, A. et al., (2003) *Nucleic Acids Research* 31(12):3185-3193). Herein, general descriptions of bicyclic
- 10 nucleosides include both isomeric configurations. When the positions of specific bicyclic nucleosides (*e.g.*, LNA or cEt) are identified in exemplified embodiments herein, they are in the  $\beta$ -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).

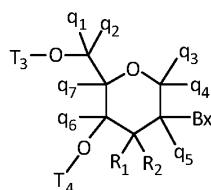
- 15 In certain embodiments, modified sugar moieties are sugar surrogates. In certain such embodiments, the oxygen atom of the sugar moiety is replaced, *e.g.*, with a sulfur, carbon or nitrogen atom. In certain such embodiments, such modified sugar moieties also comprise bridging and/or non-bridging 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.

- 20 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

- 25 ("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<sub>3</sub> and T<sub>4</sub> are each, independently, an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide or one of T<sub>3</sub> and T<sub>4</sub> is an internucleoside linking group linking the modified THP nucleoside to the remainder of an oligonucleotide and the other of T<sub>3</sub> and T<sub>4</sub> is H, a hydroxyl protecting group, a linked conjugate group, or a 5' or 3'-terminal group;

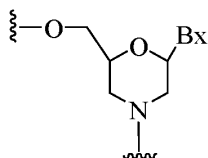
q<sub>1</sub>, q<sub>2</sub>, q<sub>3</sub>, q<sub>4</sub>, q<sub>5</sub>, q<sub>6</sub> and q<sub>7</sub> are each, independently, H, C<sub>1</sub>-C<sub>6</sub> alkyl, substituted C<sub>1</sub>-C<sub>6</sub> alkyl, C<sub>2</sub>-C<sub>6</sub> alkenyl, substituted C<sub>2</sub>-C<sub>6</sub> alkenyl, C<sub>2</sub>-C<sub>6</sub> alkynyl, or substituted C<sub>2</sub>-C<sub>6</sub> alkynyl; and

each of R<sub>1</sub> and R<sub>2</sub> is independently selected from among: hydrogen, halogen, substituted or unsubstituted alkoxy, NJ<sub>1</sub>J<sub>2</sub>, SJ<sub>1</sub>, N<sub>3</sub>, OC(=X)J<sub>1</sub>, OC(=X)NJ<sub>1</sub>J<sub>2</sub>, NJ<sub>3</sub>C(=X)NJ<sub>1</sub>J<sub>2</sub>, and CN, wherein X is O, S or NJ<sub>1</sub>, and each J<sub>1</sub>, J<sub>2</sub>, and J<sub>3</sub> is, independently, H or C<sub>1</sub>-C<sub>6</sub> alkyl.

In certain embodiments, modified THP nucleosides are provided wherein q<sub>1</sub>, q<sub>2</sub>, q<sub>3</sub>, q<sub>4</sub>, q<sub>5</sub>, q<sub>6</sub> and q<sub>7</sub> are each H.

In certain embodiments, at least one of q<sub>1</sub>, q<sub>2</sub>, q<sub>3</sub>, q<sub>4</sub>, q<sub>5</sub>, q<sub>6</sub> and q<sub>7</sub> is other than H. In certain embodiments, at least one of q<sub>1</sub>, q<sub>2</sub>, q<sub>3</sub>, q<sub>4</sub>, q<sub>5</sub>, q<sub>6</sub> and q<sub>7</sub> is methyl. In certain embodiments, modified THP nucleosides are provided wherein one of R<sub>1</sub> and R<sub>2</sub> is F. In certain embodiments, R<sub>1</sub> is F and R<sub>2</sub> is H, in certain embodiments, R<sub>1</sub> is methoxy and R<sub>2</sub> is H, and in certain embodiments, R<sub>1</sub> is methoxyethoxy and R<sub>2</sub> 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:



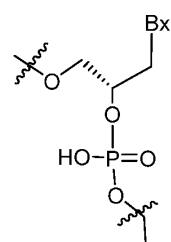
In certain embodiments, morpholinos may be modified, for example by adding or altering various substituent groups from the above morpholino structure. Such sugar surrogates are referred to herein as “modified morpholinos.”

In certain embodiments, sugar surrogates comprise acyclic moieties. 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. Representative U.S. patents that teach the preparation of PNA compounds include, but are not limited to, U.S. Patent Nos. 5,539,082; 5,714,331; and 5,719,262. Additional PNA compounds suitable for use in the oligonucleotides of the invention are described in, for example, in Nielsen *et al.*, *Science*, 1991, 254, 1497-1500.

In certain embodiments, sugar surrogates are the “unlocked” sugar structure of UNA (unlocked nucleic acid) nucleosides. UNA is an unlocked acyclic nucleic acid, wherein any of the bonds of the sugar has been removed, forming an unlocked sugar surrogate. Representative U.S. publications that teach the preparation of UNA include, but are not limited to, US Patent No. 8,314,227; and US Patent Publication Nos. 2013/0096289; 2013/0011922; and 2011/0313020, the entire contents of each of which are hereby incorporated herein by reference.

In certain embodiments, sugar surrogates are the glycerol as found in GNA (glycol nucleic acid) nucleosides as depicted below:

(S)-GNA



where Bx represents any nucleobase.

Many other bicyclic and tricyclic sugar and sugar surrogates are known in the art that can be used in modified nucleosides.

## 2. Certain Modified Nucleobases

In certain embodiments, modified oligonucleotides comprise one or more nucleosides comprising an unmodified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleosides comprising a modified nucleobase. In certain embodiments, modified oligonucleotides comprise one or more nucleosides that does not comprise a nucleobase, referred to as an abasic nucleoside. In certain embodiments, modified oligonucleotides comprise one or more inosine nucleosides (i.e., nucleosides comprising a hypoxanthine nucleobase).

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: 5-methylcytosine, 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 ( $-C\equiv C-CH_3$ ) 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

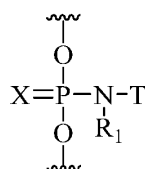
example 7-deaza-adenine, 7-deazaguanosine, 2-aminopyridine and 2-pyridone. Further nucleobases include those disclosed in Merigan et al., U.S. 3,687,808, those disclosed in *The Concise Encyclopedia Of Polymer Science And Engineering*, Kroschwitz, J.I., Ed., John Wiley & Sons, 1990, 858-859; Englisch 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, Manoharan 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., U.S. 6,166,199; and Matteucci et al., U.S. 6,005,096.

### 3. Certain Modified Internucleoside Linkages

The naturally occurring internucleoside linkage of RNA and DNA is a 3' to 5' phosphodiester linkage. In certain embodiments, nucleosides of modified oligonucleotides may be linked together using one or more modified internucleoside linkages. 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 ("O-P(=O)(OH)") (also referred to as unmodified or naturally occurring linkages), phosphotriesters, methylphosphonates, phosphoramidates, and phosphorothioates ("O-P(=S)(OH)-"), and phosphorodithioates ("O-P(=S)(SH)"). Representative non-phosphorus containing internucleoside linking groups include but are not limited to methylenemethylimino (-CH<sub>2</sub>-N(CH<sub>3</sub>)-O-CH<sub>2</sub>-), thiodiester, thionocarbamate (-O-C(=O)(NH)-S-); siloxane (-O-SiH<sub>2</sub>-O-); and N,N'-dimethylhydrazine (-CH<sub>2</sub>-N(CH<sub>3</sub>)-N(CH<sub>3</sub>)-). Modified internucleoside linkages, compared to naturally occurring phosphate linkages, can be used to alter, typically increase, nuclease resistance of the oligonucleotide. In certain embodiments, internucleoside linkages having a chiral atom can be prepared as a racemic mixture, or as separate enantiomers. Methods of preparation of phosphorous-containing and non-phosphorous-containing internucleoside linkages are well known to those skilled in the art.

In certain embodiments, a modified internucleoside linkage is any of those described in WO/2021/030778, incorporated by reference herein. In certain embodiments, a modified internucleoside linkage comprises the formula:



wherein independently for each internucleoside linking group of the modified oligonucleotide:

X is selected from O or S;

$R_1$  is selected from H, C<sub>1</sub>-C<sub>6</sub> alkyl, and substituted C<sub>1</sub>-C<sub>6</sub> alkyl; and

T is selected from SO<sub>2</sub>R<sub>2</sub>, C(=O)R<sub>3</sub>, and P(=O)R<sub>4</sub>R<sub>5</sub>, wherein:

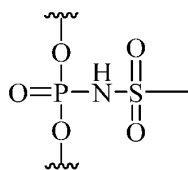
$R_2$  is selected from an aryl, a substituted aryl, a heterocycle, a substituted heterocycle, an aromatic heterocycle, a substituted aromatic heterocycle, a diazole, a substituted diazole, a C<sub>1</sub>-C<sub>6</sub> alkoxy, C<sub>1</sub>-C<sub>6</sub> alkyl, C<sub>1</sub>-C<sub>6</sub> alkenyl, C<sub>1</sub>-C<sub>6</sub> alkynyl, substituted C<sub>1</sub>-C<sub>6</sub> alkyl, substituted C<sub>1</sub>-C<sub>6</sub> alkenyl substituted C<sub>1</sub>-C<sub>6</sub> alkynyl, and a conjugate group;

$R_3$  is selected from an aryl, a substituted aryl, CH<sub>3</sub>, N(CH<sub>3</sub>)<sub>2</sub>, OCH<sub>3</sub> and a conjugate group;

$R_4$  is selected from OCH<sub>3</sub>, OH, C<sub>1</sub>-C<sub>6</sub> alkyl, substituted C<sub>1</sub>-C<sub>6</sub> alkyl and a conjugate group; and

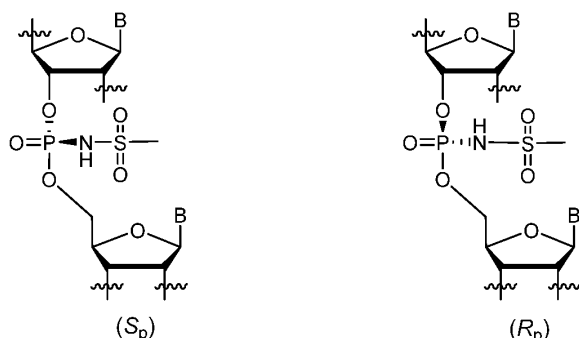
$R_5$  is selected from OCH<sub>3</sub>, OH, C<sub>1</sub>-C<sub>6</sub> alkyl, and substituted C<sub>1</sub>-C<sub>6</sub> alkyl.

In certain embodiments, a modified internucleoside linkage comprises a mesyl phosphoramidate linking group having a formula:



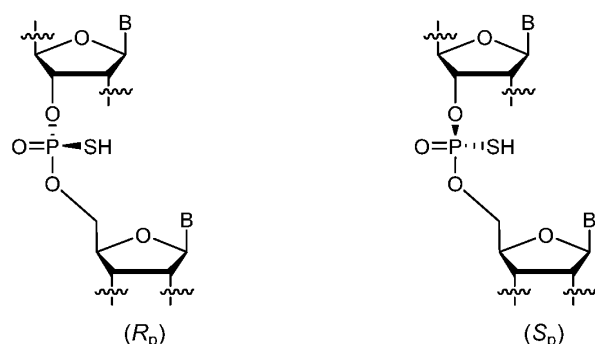
In certain embodiments, a mesyl phosphoramidate internucleoside linkage may comprise a chiral center. In certain embodiments, modified oligonucleotides comprising (*R*<sub>p</sub>) and/or (*S*<sub>p</sub>) mesyl phosphoramidates comprise one or more of the following formulas, respectively, wherein "B" indicates a nucleobase:

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Representative internucleoside linkages having a chiral center include but are not limited to alkylphosphonates, mesyl phosphoramidates, 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 or other linkages containing chiral centers in particular stereochemical configurations. In certain embodiments, populations of modified oligonucleotides comprise phosphorothioate internucleoside linkages wherein all of the phosphorothioate internucleoside linkages are stereorandom. In certain embodiments, populations of modified oligonucleotides comprise mesyl phosphoramidate internucleoside linkages wherein all of the mesyl phosphoramidate 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 or mesyl phosphoramidate linkage. Nonetheless, each individual phosphorothioate or mesyl phosphoramidate of each individual oligonucleotide molecule has a defined

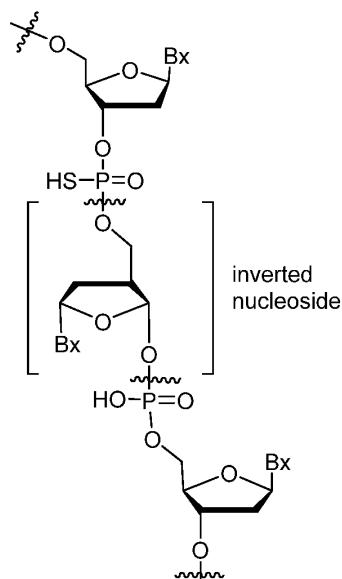
stereoconfiguration. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising one or more particular phosphorothioate or mesyl phosphoramidate internucleoside linkages in a particular, independently selected stereochemical configuration. In certain embodiments, the particular configuration of the particular phosphorothioate or mesyl phosphoramidate linkage is present in at least 65% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate or mesyl phosphoramidate linkage is present in at least 70% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate or mesyl phosphoramidate linkage is present in at least 80% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate or mesyl phosphoramidate linkage is present in at least 90% of the molecules in the population. In certain embodiments, the particular configuration of the particular phosphorothioate or mesyl phosphoramidate 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 or mesyl phosphoramidate in the (*Sp*) configuration. In certain embodiments, a population of modified oligonucleotides is enriched for modified oligonucleotides having at least one phosphorothioate or mesyl phosphoramidate in the (*Rp*) configuration. In certain embodiments, modified oligonucleotides comprising (*Rp*) and/or (*Sp*) phosphorothioates comprise one or more of the following formulas, respectively, wherein "B" indicates a nucleobase:



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<sub>2</sub>-N(CH<sub>3</sub>)-O-5'), amide-3 (3'-CH<sub>2</sub>-C(=O)-N(H)-5'), amide-4 (3'-CH<sub>2</sub>-N(H)-C(=O)-5'), formacetal (3'-O-CH<sub>2</sub>-O-5'), methoxypropyl (MOP), and thioformacetal (3'-S-CH<sub>2</sub>-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 CH<sub>2</sub> component parts.

In certain embodiments, modified oligonucleotides comprise one or more inverted nucleoside, as shown below:

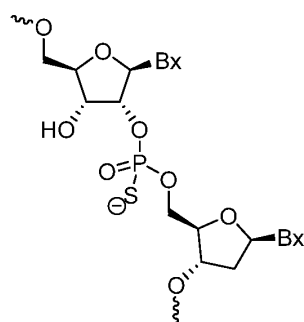


wherein each Bx independently represents any nucleobase.

In certain embodiments, an inverted nucleoside is terminal (i.e., the last nucleoside on one end of an oligonucleotide) and so only one internucleoside linkage depicted above will be present. In certain such embodiments, additional features (such as a conjugate group) may be attached to the inverted nucleoside. Such terminal inverted nucleosides can be attached to either or both ends of an oligonucleotide.

In certain embodiments, such groups lack a nucleobase and are referred to herein as inverted sugar moieties. In certain embodiments, an inverted sugar moiety is terminal (i.e., attached to the last nucleoside on one end of an oligonucleotide) and so only one internucleoside linkage above will be present. In certain such embodiments, additional features (such as a conjugate group) may be attached to the inverted sugar moiety. Such terminal inverted sugar moieties can be attached to either or both ends of an oligonucleotide.

In certain embodiments, nucleic acids can be linked 2' to 5' rather than the standard 3' to 5' linkage. Such a linkage is illustrated below.



wherein each Bx represents any nucleobase.

**B. Certain Motifs**

In certain embodiments, modified oligonucleotides comprise one or more modified nucleosides comprising a modified sugar moiety. 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 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).

**1. Certain Sugar Motifs**

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.

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*Gapmer Oligonucleotides*

In certain embodiments, modified oligonucleotides comprise or consist of a region having a gapmer motif, which is defined by two external regions or “wings” and a central or internal region or “gap.” The three regions 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 closest to the gap (the 3'-most nucleoside of the 5'-wing and the 5'-most nucleoside of the 3'-wing) differ from the sugar moiety of the neighboring gap nucleosides, thus defining the boundary between the wings and the gap (i.e., the wing/gap junction). 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 sugar motifs of the two wings are the same as one another (symmetric gapmer). In certain embodiments, the sugar motif of the 5'-wing differs from the sugar motif of the 3'-wing (asymmetric gapmer).

In certain embodiments, the wings of a gapmer comprise 1-6 nucleosides. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least one nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least two nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least three nucleosides of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least four nucleosides of each wing of a gapmer comprises a modified sugar moiety.

In certain embodiments, the gap of a gapmer comprises 7-12 nucleosides. In certain embodiments, each nucleoside of the gap of a gapmer comprises a 2'-β-D-deoxyribose sugar moiety. In certain embodiments, at least one nucleoside of the gap of a gapmer comprises a modified sugar moiety.

In certain embodiments, the gapmer is a deoxy gapmer, i.e., a gapmer that comprises a deoxy segment. In certain embodiments, the nucleosides on the gap side of each wing/gap junction comprise 2'-deoxyribose sugar moieties and the nucleosides on the wing sides of each wing/gap junction comprise modified sugar moieties. In certain embodiments,

each nucleoside of the gap comprises a 2'- $\beta$ -D-deoxyribosyl sugar moiety. In certain embodiments, each nucleoside of each wing of a gapmer comprises a modified sugar moiety. In certain embodiments, at least one nucleoside of the gap of a gapmer comprises a modified sugar moiety. In certain embodiments, one nucleoside of the gap comprises a modified sugar moiety and each remaining nucleoside of the gap comprises a 2'-deoxyribosyl sugar moiety. In certain

5 Herein, the lengths (number of nucleosides) of the three regions of a gapmer may be provided using the notation [# of nucleosides in the 5'-wing] – [# of nucleosides in the gap] – [# of nucleosides in the 3'-wing]. Thus, a 3-10-3 gapmer consists of 3 linked nucleosides in each wing and 10 linked nucleosides in the gap. Where such nomenclature is followed by a specific modification, that modification is the modification in each sugar moiety of each wing and the gap

10 nucleosides comprise 2'- $\beta$ -D-deoxyribosyl sugar moieties. Thus, a 5-10-5 MOE gapmer consists of 5 linked 2'-MOE nucleosides in the 5'-wing, 10 linked 2'- $\beta$ -D-deoxynucleosides in the gap, and 5 linked 2'-MOE nucleosides in the 3'-wing. A 3-10-3 cEt gapmer consists of 3 linked cEt nucleosides in the 5'-wing, 10 linked 2'- $\beta$ -D-deoxynucleosides in the gap, and 3 linked cEt nucleosides in the 3'-wing.

In certain embodiments, modified oligonucleotides are 5-10-5 MOE gapmers. In certain embodiments, modified

15 oligonucleotides are 3-10-3 BNA gapmers. In certain embodiments, modified oligonucleotides are 3-10-3 cEt gapmers. In certain embodiments, modified oligonucleotides are 3-10-3 LNA gapmers.

In certain embodiments, provided is an oligomeric compound having a sugar motif (5' to 3') selected from: kkkkkkkkkkkkkk, kkkdykkkkkkkkkk, kkkkkkkkkkkkkkk, and kkkkkkkkkkkkkke, wherein each "d" represents a 2'- $\beta$ -D-deoxyribosyl sugar moiety, each "k" represents a cEt modified sugar moiety, each "y" represents a 2'-O-

20 methylribosyl sugar moiety, and each "e" represents a 2'-MOE sugar moiety.

## 2. Certain Nucleobase Motifs

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

25 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-methyl cytosines. In certain embodiments, all of the cytosine nucleobases are 5-methyl cytosines and all of the other nucleobases of the modified oligonucleotide are unmodified nucleobases.

30 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

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

### 3. Certain Internucleoside Linkage Motifs

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 (Sp) phosphorothioate, and a (Rp) 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 phosphodiester internucleoside 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 (Sp) phosphorothioates, and the gap comprises at least one Sp, Sp, Rp motif. In certain embodiments, populations of modified oligonucleotides are enriched for modified oligonucleotides comprising such internucleoside linkage motifs.

### C. Certain Lengths

It is possible to increase or decrease the length of an oligonucleotide without eliminating activity. For example, in Woolf et al. (Proc. Natl. Acad. Sci. USA 89:7305-7309, 1992), a series of oligonucleotides 13-25 nucleobases in length were tested for their ability to induce cleavage of a target RNA in an oocyte injection model. Oligonucleotides 25 nucleobases in length with 8 or 11 mismatch bases near the ends of the oligonucleotides were able to direct specific cleavage of the target RNA, albeit to a lesser extent than the oligonucleotides that contained no mismatches. Similarly, target specific cleavage was achieved using 13 nucleobase oligonucleotides, including those with 1 or 3 mismatches.

In certain embodiments, oligonucleotides (including modified oligonucleotides) can have any of a variety of ranges of lengths. 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.

#### **D. Certain 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 modification 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. For example, the internucleoside linkages within the wing regions of a sugar gapmer may be the same or different from one another and may be the same or different from the internucleoside linkages of the gap region of the sugar motif. Likewise, such sugar gapmer oligonucleotides may comprise one or more modified nucleobase independent of the gapmer pattern of the sugar modifications. Unless otherwise indicated, all modifications are independent of nucleobase sequence.

#### **E. Certain Populations of Modified Oligonucleotides**

Populations of modified oligonucleotides in which all of the modified oligonucleotides of the population have the same molecular formula can be stereorandom populations or chirally enriched populations. All of the chiral centers of all of the modified oligonucleotides are stereorandom in a stereorandom population. In a chirally enriched population, at least one particular chiral center is not stereorandom in the modified oligonucleotides of the population. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for  $\beta$ -D ribosyl sugar moieties, and all of the phosphorothioate internucleoside linkages are stereorandom. In certain embodiments, the modified oligonucleotides of a chirally enriched population are enriched for both  $\beta$ -D ribosyl sugar moieties and at least one, particular phosphorothioate internucleoside linkage in a particular stereochemical configuration.

#### **F. Nucleobase Sequence**

In certain embodiments, oligonucleotides (unmodified or modified oligonucleotides) are further described by their nucleobase sequence. 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 such 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 50%, at least 60%, at least 70%, at least 80%, at least 85%, at

least 90%, at least 95%, or 100% complementary to the second oligonucleotide or nucleic acid, such as a target nucleic acid.

## II. Certain Oligomeric Compounds

5 In certain embodiments, provided herein are oligomeric compounds, which 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 which 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  
10 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  
15 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.

### 20 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.

25 In certain embodiments, conjugation of one or more carbohydrate moieties to a modified oligonucleotide can optimize one or more properties of the modified oligonucleotide. In certain embodiments, the carbohydrate moiety is attached to a modified subunit of the modified oligonucleotide. For example, the ribose sugar of one or more ribonucleotide subunits of a modified oligonucleotide can be replaced with another moiety, e.g. a non-carbohydrate (preferably cyclic) carrier to which is attached a carbohydrate ligand. A ribonucleotide subunit in which the ribose sugar  
30 of the subunit has been so replaced is referred to herein as a ribose replacement modification subunit (RRMS), which is a modified sugar moiety. A cyclic carrier may be a carbocyclic ring system, i.e., one or more ring atoms may be a heteroatom, e.g., nitrogen, oxygen, sulphur. The cyclic carrier may be a monocyclic ring system, or may contain two or more rings, e.g. fused rings. The cyclic carrier may be a fully saturated ring system, or it may contain one or more double bonds. In certain embodiments, the modified oligonucleotide is a gapmer.

35 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 acid a palmitoyl 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, 277, 923-937), a tocopherol group (Nishina et al., *Molecular Therapy Nucleic Acids*, 2015, 4, e220; 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, cholesterol, 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 oligomeric compounds, the conjugate linker is a single chemical bond (i.e., the conjugate moiety is attached directly to an oligonucleotide 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 pyrrolidine.

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 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-aminoheptanoic acid (AHEX or AHA).

5 Other conjugate linkers include but are not limited to substituted or unsubstituted C<sub>1</sub>-C<sub>10</sub> alkyl, substituted or unsubstituted C<sub>2</sub>-C<sub>10</sub> alkenyl or substituted or unsubstituted C<sub>2</sub>-C<sub>10</sub> 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.

10 In certain embodiments, conjugate linkers comprise 1-10 linker-nucleosides. In certain embodiments, conjugate linkers comprise 2-5 linker-nucleosides. In certain embodiments, conjugate linkers comprise exactly 3 linker-nucleosides. In certain embodiments, conjugate linkers comprise the TCA motif. 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.

15 In certain embodiments, a cleavable moiety is a nucleoside selected from uracil, thymine, cytosine, 4-N-benzoylcytosine, 5-methyl cytosine, 4-N-benzoyl-5-methyl cytosine, adenine, 6-N-benzoyladenine, guanine and 2-N-isobutyrylguanine. It is typically desirable for linker-nucleosides to be cleaved from the oligomeric compound after it reaches a target tissue. Accordingly, linker-nucleosides are typically linked to one another and to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are phosphodiester bonds.

20 Herein, linker-nucleosides are not considered to be part of the oligonucleotide. Accordingly, in embodiments in which an oligomeric 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 oligomeric 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.

25 For example, an oligomeric 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 an oligomeric compound is more than 30. Alternatively, an oligomeric compound may comprise a modified oligonucleotide consisting of 8-30 nucleosides and no conjugate group. The total number of contiguous linked nucleosides in such an oligomeric compound is no more than 30. Unless otherwise indicated conjugate linkers comprise

30 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.

35 In certain embodiments, it is desirable for a conjugate group to be cleaved from the oligonucleotide. For example, in certain circumstances oligomeric compounds comprising a particular conjugate moiety are better taken up by a particular cell type, but once the oligomeric compound has been taken up, it is desirable that the conjugate group be cleaved to release the unconjugated or parent oligonucleotide. Thus, certain conjugate linkers may comprise one or more cleavable moieties. In certain embodiments, a cleavable moiety is a cleavable bond. In certain embodiments, a cleavable

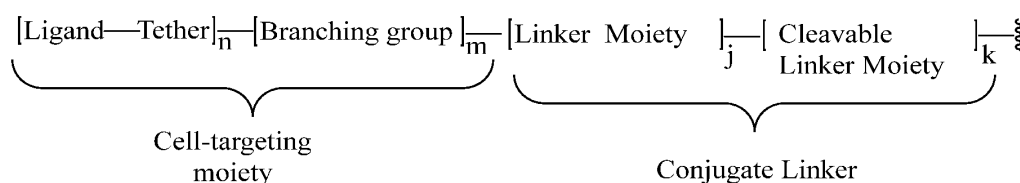
moiety is a group of atoms comprising at least one cleavable bond. In certain embodiments, a cleavable moiety comprises a group of atoms having one, two, three, four, or more than four cleavable bonds. In certain embodiments, a cleavable moiety is selectively cleaved inside a cell or subcellular compartment, 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, the one or more linker-nucleosides are linked to one another and/or to the remainder of the oligomeric compound through cleavable bonds. In certain embodiments, such cleavable bonds are unmodified phosphodiester bonds. In certain embodiments, a cleavable moiety is 2'-deoxynucleoside 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. Cell-Targeting Moieties

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



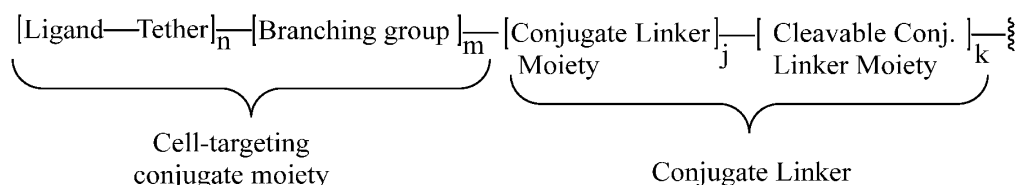
wherein n is from 1 to about 3, m is 0 when n is 1, m is 1 when n is 2 or greater, j is 1 or 0, and k is 1 or 0.

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, 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 liver cell. In certain embodiments, each ligand has an affinity for the hepatic asialoglycoprotein receptor (ASGP-R). In certain embodiments, each ligand is a carbohydrate.

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



5                    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.

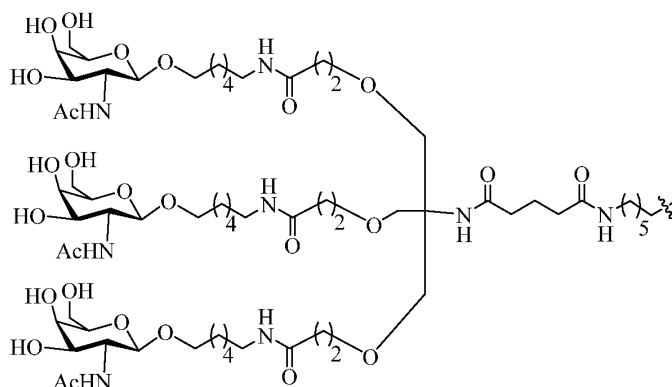
In certain embodiments, conjugate groups comprise cell-targeting moieties that have at least one tethered ligand. In certain embodiments, cell-targeting moieties comprise two tethered ligands covalently attached to a branching group. In certain embodiments, cell-targeting moieties comprise three tethered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

15                    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 liver cell. In certain embodiments, each ligand has an affinity for the hepatic asialoglycoprotein receptor (ASGP-R). In certain embodiments, each ligand is a carbohydrate. In certain embodiments, each ligand is, independently selected from galactose, N-acetyl galactosamine (GalNAc), mannose, glucose, glucosamine and fucose. In certain embodiments, each ligand is N-acetyl galactosamine (GalNAc). In certain embodiments, the cell-targeting moiety comprises 3 GalNAc ligands. In certain embodiments, the cell-targeting moiety comprises 2 GalNAc ligands. In certain

20                    In certain embodiments, the cell-targeting moiety comprises 1 GalNAc ligand.

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 Asialoglycoprotein Receptor,” *J. Med. Chem.* 2004, 47, 5798-5808). 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,  $\alpha$ -D-galactosamine,  $\beta$ -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-glycolyl- $\alpha$ -neuraminic acid. For example, thio sugars may be selected from 5-Thio- $\beta$ -D-glucopyranose, methyl 2,3,4-tri-O-acetyl-1-thio-6-O-trityl- $\alpha$ -D-glucopyranoside, 4-thio- $\beta$ -D-galactopyranose, and ethyl 3,4,6,7-tetra-O-acetyl-2-deoxy-1,5-dithio- $\alpha$ -D-glucopyranoside.

In certain embodiments, compounds comprise a conjugate group having the formula:



Representative United States patents, United States patent application publications, international patent application publications, and other publications that teach the preparation of certain of the above noted conjugate groups, compounds comprising conjugate groups, tethers, conjugate linkers, branching groups, ligands, cleavable moieties as well as other modifications include without limitation, US 5,994,517, US 6,300,319, US 6,660,720, US 6,906,182, US 7,262,177, US 7,491,805, US 8,106,022, US 7,723,509, US 2006/0148740, US 2011/0123520, WO 2013/033230 and WO 2012/037254, Biessen et al., *J. Med. Chem.* 1995, 38, 1846-1852, Lee et al., *Bioorganic & Medicinal Chemistry* 2011, 19, 2494-2500, Rensen et al., *J. Biol. Chem.* 2001, 276, 37577-37584, Rensen et al., *J. Med. Chem.* 2004, 47, 5798-5808, Slidregt et al., *J. Med. Chem.* 1999, 42, 609-618, and Valentijn et al., *Tetrahedron*, 1997, 53, 759-770.

In certain embodiments, modified oligonucleotides comprise a gapmer or fully modified sugar motif and a conjugate group comprising at least one, two, or three GalNAc ligands. In certain embodiments, compounds 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; Slidregt 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.

### **B. Certain Terminal Groups**

In certain embodiments, oligomeric compounds comprise one or more terminal groups. In certain such embodiments, oligomeric compounds comprise a stabilized 5'-phosphate. Stabilized 5'-phosphates include, but are not limited to 5'-phosphonates, including, but not limited to 5'-vinylphosphonates. In certain embodiments, terminal groups comprise one or more abasic sugar moieties and/or inverted nucleosides. In certain embodiments, terminal groups comprise one or more 2'-linked nucleosides or sugar moieties. In certain such embodiments, the 2'-linked group is an abasic sugar moiety.

### **III. Antisense Activity**

In certain embodiments, oligomeric compounds and oligomeric duplexes are capable of hybridizing to a target nucleic acid, resulting in at least one antisense activity; such oligomeric compounds and oligomeric duplexes are antisense compounds. In certain embodiments, antisense compounds have antisense activity when they reduce or inhibit the amount or activity of a target nucleic acid by 25% or more in the standard cell assay. In certain embodiments, antisense compounds selectively affect one or more target nucleic acid. Such antisense 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 significant undesired antisense activity.

In certain antisense activities, hybridization of an antisense compound to a target nucleic acid results in recruitment of a protein that cleaves the target nucleic acid. For example, certain antisense compounds 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, described herein are antisense compounds that are sufficiently "DNA-like" to elicit RNase H activity. In certain embodiments, one or more non-DNA-like nucleoside in the gap of a gapmer is tolerated.

In certain antisense activities, an antisense compound or a portion of an antisense compound is loaded into an RNA-induced silencing complex (RISC), ultimately resulting in cleavage of the target nucleic acid. For example, certain antisense compounds result in cleavage of the target nucleic acid by Argonaute. Antisense compounds that are loaded

into RISC are RNAi compounds. RNAi compounds may be double-stranded (siRNA or dsRNAi) or single-stranded (ssRNA).

In certain embodiments, hybridization of an antisense compound to a target nucleic acid does not result in recruitment of a protein that cleaves that target nucleic acid. In certain embodiments, hybridization of the antisense compound to the target nucleic acid results in alteration of splicing of the target nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in inhibition of a binding interaction between the target nucleic acid and a protein or other nucleic acid. In certain embodiments, hybridization of an antisense compound to a target nucleic acid results in alteration of translation of the target nucleic acid.

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.

#### IV. Certain Target Nucleic Acids

In certain embodiments, oligomeric compounds 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: a mature mRNA and a pre-mRNA, including intronic, exonic and untranslated regions. In certain embodiments, the target RNA is a mature mRNA. In certain embodiments, the target nucleic acid is a pre-mRNA. In certain embodiments, the target region is entirely within an intron. In certain embodiments, the target region spans an intron/exon junction. In certain embodiments, the target region is at least 50% within an intron.

##### A. Complementarity/Mismatches to the Target Nucleic Acid and Duplex Complementarity

In certain embodiments, oligonucleotides are complementary to the target nucleic acid over the entire length of the oligonucleotide. In certain embodiments, oligonucleotides are 99%, 95%, 90%, 85%, or 80% complementary to the target nucleic acid. In certain embodiments, oligonucleotides are at least 80% complementary to the target nucleic acid over the entire length of the oligonucleotide and comprise a region that is 100% or fully complementary to a target nucleic acid. In certain embodiments, the region of full complementarity is from 6 to 20, 10 to 18, or 18 to 20 nucleobases in length.

It is possible to introduce mismatch bases without eliminating activity. For example, Gautschi et al (J. Natl. Cancer Inst. 93:463-471, March 2001) demonstrated the ability of an oligonucleotide having 100% complementarity to the bcl-2 mRNA and having 3 mismatches to the bcl-xL mRNA to reduce the expression of both bcl-2 and bcl-xL in vitro and in vivo. Furthermore, this oligonucleotide demonstrated potent anti-tumor activity in vivo. Maher and Dolnick (Nuc. Acid. Res. 16:3341-3358, 1988) tested a series of tandem 14 nucleobase oligonucleotides, and 28 and 42 nucleobase oligonucleotides comprised of the sequence of two or three of the tandem oligonucleotides, respectively, for their ability to arrest translation of human DHFR in a rabbit reticulocyte assay. Each of the three 14 nucleobase oligonucleotides alone was able to inhibit translation, albeit at a more modest level than the 28 or 42 nucleobase oligonucleotides.

In certain embodiments, oligonucleotides comprise one or more mismatched nucleobases relative to the target nucleic acid. In certain 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 embodiments selectivity of the oligonucleotide is improved. In certain embodiments, the mismatch is specifically positioned within an oligonucleotide having a gapmer motif. In certain embodiments, the mismatch is at position 1, 2, 3, 4, 5, 6, 7, or 8 from the 5'-end of the gap region. In certain embodiments, the mismatch is at position 9, 8, 7, 6, 5, 4, 3, 2, 1 from the 3'-end of the gap region. In certain embodiments, the mismatch is at position 1, 2, 3, or 4 from the 5'-end of the wing region. In certain embodiments, the mismatch is at position 4, 3, 2, or 1 from the 3'-end of the wing region.

## 10 **B. PSD3**

In certain embodiments, oligomeric agents or oligomeric compounds comprise or consist of an oligonucleotide comprising a region that is complementary to a target nucleic acid, wherein the target nucleic acid is PSD3. In certain embodiments, PSD3 nucleic acid has the sequence set forth in SEQ ID NO: 1 (GENBANK Accession No. NC\_000008.11, truncated from nucleosides 18524001 to 19090000) or SEQ ID NO: 2 (GENBANK Accession No. NM\_015310.3). In certain embodiments, contacting a cell with an oligomeric compound complementary to SEQ ID NOs: 1 or 2 reduces the amount of PSD3 RNA, and in certain embodiments reduces the amount of PSD3 protein. In certain embodiments, the oligomeric compound consists of a modified oligonucleotide. In certain embodiments, the oligomeric compound comprises or consists of a modified oligonucleotide and a conjugate group.

## 20 **C. Certain Target Nucleic Acids in Certain Tissues**

In certain embodiments, oligomeric compounds comprise or consist of an oligonucleotide comprising a region that is complementary to a target nucleic acid, wherein the target nucleic acid is expressed in a pharmacologically relevant tissue. In certain embodiments, the pharmacologically relevant tissues are the liver cells and tissues.

## 25 **V. Certain Methods, Uses, and Indications**

Certain embodiments provided herein relate to methods of inhibiting PSD3 expression, which can be useful for treating a disease associated with PSD3 in a subject, by administration of an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex, any of which comprising a modified oligonucleotide having a nucleobase sequence complementary to a PSD3 nucleic acid.

30 Examples of diseases associated with PSD3 treatable with the oligomeric agents, oligomeric compounds, modified oligonucleotides, oligomeric duplexes, and methods provided herein include liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

35 In certain embodiments, a method comprises administering to a subject an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex, any of which having a nucleobase sequence complementary to a PSD3 nucleic acid. In certain embodiments, the subject has liver disease, fatty liver disease (FLD), nonalcoholic

fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

5 In certain embodiments, a method of treating liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis in a subject comprises administering to the subject a therapeutically effective amount of an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex, any of which having a nucleobase sequence complementary to a PSD3 nucleic acid, thereby treating the subject. In certain embodiments, 10 administering the therapeutically effective amount of the oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex reduces liver damage, steatosis, liver fibrosis, liver inflammation, liver scarring or cirrhosis, liver failure, liver enlargement, elevated transaminases, or hepatic fat accumulation in the subject.

In certain embodiments, a method of inhibiting expression of PSD3 nucleic acid, such as RNA, in a subject having a disease associated with PSD3 comprises administering to the subject an oligomeric agent, oligomeric compound, 15 modified oligonucleotide, or oligomeric duplex, any of which having a nucleobase sequence complementary to a PSD3 nucleic acid, thereby inhibiting expression of PSD3 nucleic acid in the subject. In certain embodiments, administering the oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex inhibits expression of PSD3 in the liver. In certain embodiments, the subject has liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, 20 alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

In certain embodiments, a method of inhibiting expression of PSD3 nucleic acid in a cell comprises contacting the cell with an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex, any of which having a nucleobase sequence complementary to a PSD3 nucleic acid, thereby inhibiting expression of PSD3 nucleic acid 25 in the cell. In certain embodiments, the cell is a liver cell. In certain embodiments, the cell is in a subject having liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

Certain embodiments are drawn to an oligomeric agent, oligomeric compound, modified oligonucleotide, or 30 oligomeric duplex, any of which having a nucleobase sequence complementary to a PSD3 nucleic acid, for use in treating a disease associated with PSD3. In certain embodiments, the disease is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis. In certain embodiments, an oligomeric agent, oligomeric 35 compound, modified oligonucleotide, or oligomeric duplex is for use in reducing liver damage, steatosis, liver fibrosis, liver inflammation, liver scarring or cirrhosis, liver failure, liver enlargement, elevated transaminases, or hepatic fat accumulation associated with liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease,

alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

Certain embodiments are drawn to an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex, any of which comprising a modified oligonucleotide having a nucleobase sequence complementary to a PSD3 nucleic acid, for the manufacture or preparation of a medicament for treating a disease associated with PSD3. In certain embodiments, the disease is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis. In certain embodiments, an oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex is for the manufacture or preparation of a medicament for reducing liver damage, steatosis, liver fibrosis, liver inflammation, liver scarring or cirrhosis, liver failure, liver enlargement, elevated transaminases, or hepatic fat accumulation associated with liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.

In any of the methods or uses described herein, the oligomeric agent, oligomeric compound, modified oligonucleotide, or oligomeric duplex can be any described herein.

## **VI. Certain Pharmaceutical Compositions**

In certain embodiments, described herein are pharmaceutical compositions comprising one or more oligomeric compounds. In certain embodiments, the one or more oligomeric compounds each consists of a modified oligonucleotide. In certain embodiments, the pharmaceutical composition comprises a pharmaceutically acceptable diluent or carrier. In certain embodiments, the pharmaceutically acceptable diluent is water or saline. In certain embodiments, a pharmaceutical composition comprises or consists of a sterile saline solution and one or more oligomeric compound. In certain embodiments, the sterile saline is pharmaceutical grade saline. In certain embodiments, a pharmaceutical composition comprises or consists of one or more oligomeric compound and sterile water. In certain embodiments, the sterile water is pharmaceutical grade water, e.g., water for injection. In certain embodiments, the saline is phosphate-buffered saline (PBS). In certain embodiments, the PBS is sterile PBS.

In certain embodiments, pharmaceutical compositions comprise one or more oligomeric compound and one or more excipients. In certain embodiments, excipients are selected from water, salt solutions, alcohol, polyethylene glycols, gelatin, lactose, amylase, magnesium stearate, talc, silicic acid, viscous paraffin, hydroxymethylcellulose and polyvinylpyrrolidone.

In certain embodiments, oligomeric compounds may be admixed with pharmaceutically acceptable active and/or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of pharmaceutical compositions depend on a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.

In certain embodiments, pharmaceutical compositions comprising an oligomeric compound encompass any pharmaceutically acceptable salts of the oligomeric compound, esters of the oligomeric compound, or salts of such esters. In certain embodiments, pharmaceutical compositions comprising oligomeric compounds comprising one or more

oligonucleotide, upon administration to an animal, including a human, are capable of providing (directly or indirectly) the biologically active metabolite or residue thereof. Accordingly, for example, the disclosure is also drawn to pharmaceutically acceptable salts of oligomeric 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. In certain embodiments, prodrugs comprise one or more conjugate group attached to an oligonucleotide, wherein the conjugate group is cleaved by endogenous nucleases within the body.

Lipid moieties have been used in nucleic acid therapies in a variety of methods. In certain such methods, the nucleic acid, such as an oligomeric compound, is introduced into preformed liposomes or lipoplexes made of mixtures of cationic lipids and neutral lipids. In certain methods, DNA complexes with mono- or poly-cationic lipids are formed without the presence of a neutral lipid. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to a particular cell or tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to fat tissue. In certain embodiments, a lipid moiety is selected to increase distribution of a pharmaceutical agent to muscle tissue.

In certain embodiments, pharmaceutical compositions comprise a delivery system. Examples of delivery systems include, but are not limited to, liposomes and emulsions. Certain delivery systems are useful for preparing certain pharmaceutical compositions including those comprising hydrophobic compounds. In certain embodiments, certain organic solvents such as dimethylsulfoxide are used.

In certain embodiments, pharmaceutical compositions comprise one or more tissue-specific delivery molecules designed to deliver the one or more pharmaceutical agents of the present invention to specific tissues or cell types. For example, in certain embodiments, pharmaceutical compositions include liposomes coated with a tissue-specific antibody.

In certain embodiments, pharmaceutical compositions comprise a co-solvent system. Certain of such co-solvent systems comprise, for example, benzyl alcohol, a nonpolar surfactant, a water-miscible organic polymer, and an aqueous phase. In certain embodiments, such co-solvent systems are used for hydrophobic compounds. A non-limiting example of such a co-solvent system is the VPD co-solvent system, which is a solution of absolute ethanol comprising 3% w/v benzyl alcohol, 8% w/v of the nonpolar surfactant Polysorbate 80™ and 65% w/v polyethylene glycol 300. The proportions of such co-solvent systems may be varied considerably without significantly altering their solubility and toxicity characteristics. Furthermore, the identity of co-solvent components may be varied: for example, other surfactants may be used instead of Polysorbate 80™; the fraction size of polyethylene glycol may be varied; other biocompatible polymers may replace polyethylene glycol, e.g., polyvinyl pyrrolidone; and other sugars or polysaccharides may substitute for dextrose.

In certain embodiments, a pharmaceutical composition is prepared for administration by injection (e.g., intravenous, subcutaneous, etc.). In certain of such embodiments, a pharmaceutical composition comprises a carrier and is formulated in aqueous solution, such as water or physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiological saline buffer. In certain embodiments, other ingredients are included (e.g., ingredients that aid in solubility or serve as preservatives). In certain embodiments, injectable suspensions are prepared using appropriate liquid carriers, suspending agents and the like. Certain pharmaceutical compositions for injection are presented in unit dosage form, e.g., in ampoules or in multi-dose containers. Certain pharmaceutical compositions for injection are suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Certain solvents suitable for use in pharmaceutical compositions for injection

include, but are not limited to, lipophilic solvents and fatty oils, such as sesame oil, synthetic fatty acid esters, such as ethyl oleate or triglycerides, and liposomes.

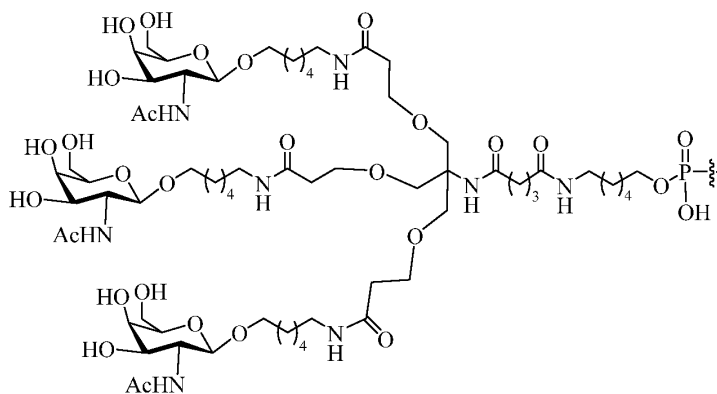
Under certain conditions, certain compounds disclosed herein act as acids. Although such compounds may be drawn or described in protonated (free acid) form, or ionized and in association with a cation (salt) form, aqueous solutions of such compounds exist in equilibrium among such forms. For example, a phosphate linkage of an oligonucleotide in aqueous solution exists in equilibrium among free acid, anion and salt forms. Unless otherwise indicated, compounds described herein are intended to include all such forms. Moreover, certain oligonucleotides have several such linkages, each of which is in equilibrium. Thus, oligonucleotides in solution exist in an ensemble of forms at multiple positions all at equilibrium. The term "oligonucleotide" is intended to include all such forms. Drawn structures necessarily depict a single form. Nevertheless, unless otherwise indicated, such drawings are likewise intended to include corresponding forms. Herein, a structure depicting the free acid of a compound followed by the term "or a salt thereof" expressly includes all such forms that may be fully or partially protonated/de-protonated/in association with a cation. In certain instances, one or more specific cation is identified.

In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with sodium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in aqueous solution with potassium. In certain embodiments, modified oligonucleotides or oligomeric compounds are in PBS. In certain embodiments, modified oligonucleotides or oligomeric compounds are in water. In certain such embodiments, the pH of the solution is adjusted with NaOH and/or HCl to achieve a desired pH.

## VII. Certain Compositions

### Compound No. 1436573

In certain embodiments, Compound No. 1436573 is characterized as a 3-10-3 cEt gapmer conjugated at the 5'-end to a conjugate group. Compound 1436573 has a sequence (from 5' to 3') of ATCTATTGGAGAAGTG (SEQ ID NO: 3037), wherein nucleosides 1-3 and 14-16 are cEt sugar moieties (from 5' to 3'), and each of nucleosides 4-13 are 2'-β-D-deoxyribose sugar moieties, and wherein each internucleoside linkage is a phosphorothioate internucleoside linkage. Compound No. 1436573 has a 5'-tris(hexamethylamino)-(THA)-C<sub>6</sub>GalNAc<sub>3</sub> endcap, represented by the structure below, wherein the phosphate group is attached at the 5'-oxygen atom of the 5'-nucleoside:



In certain embodiments, Compound No. 1436573 is represented by the following chemical notation: THA-GalNAc<sub>-o</sub>A<sub>ks</sub>T<sub>ks</sub><sup>m</sup>C<sub>ks</sub>T<sub>ds</sub>A<sub>ds</sub>T<sub>ds</sub>T<sub>ds</sub>G<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ks</sub>T<sub>ks</sub>G<sub>k</sub> (SEQ ID NO: 3037), wherein:

A = an adenine nucleobase,

<sup>m</sup>C = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

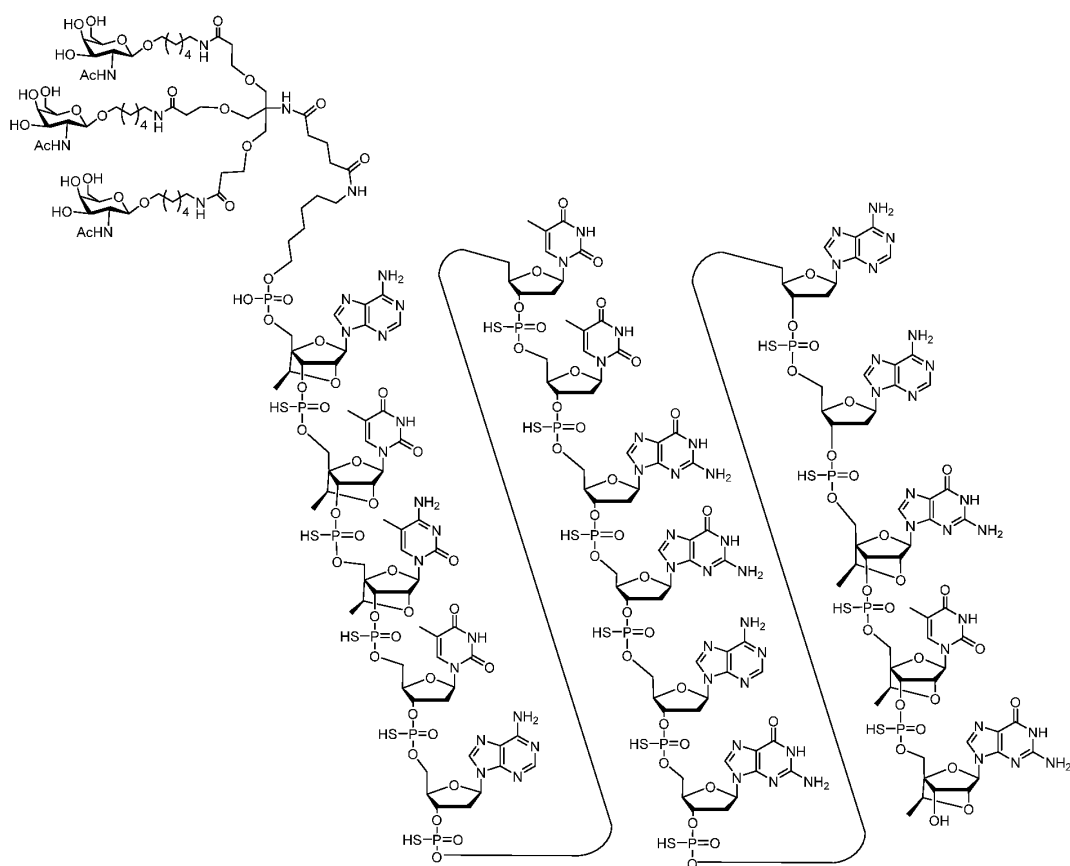
T = a thymine nucleobase,

k = a cEt modified sugar moiety,

d = a 2'-β-D-deoxyribose sugar moiety, and

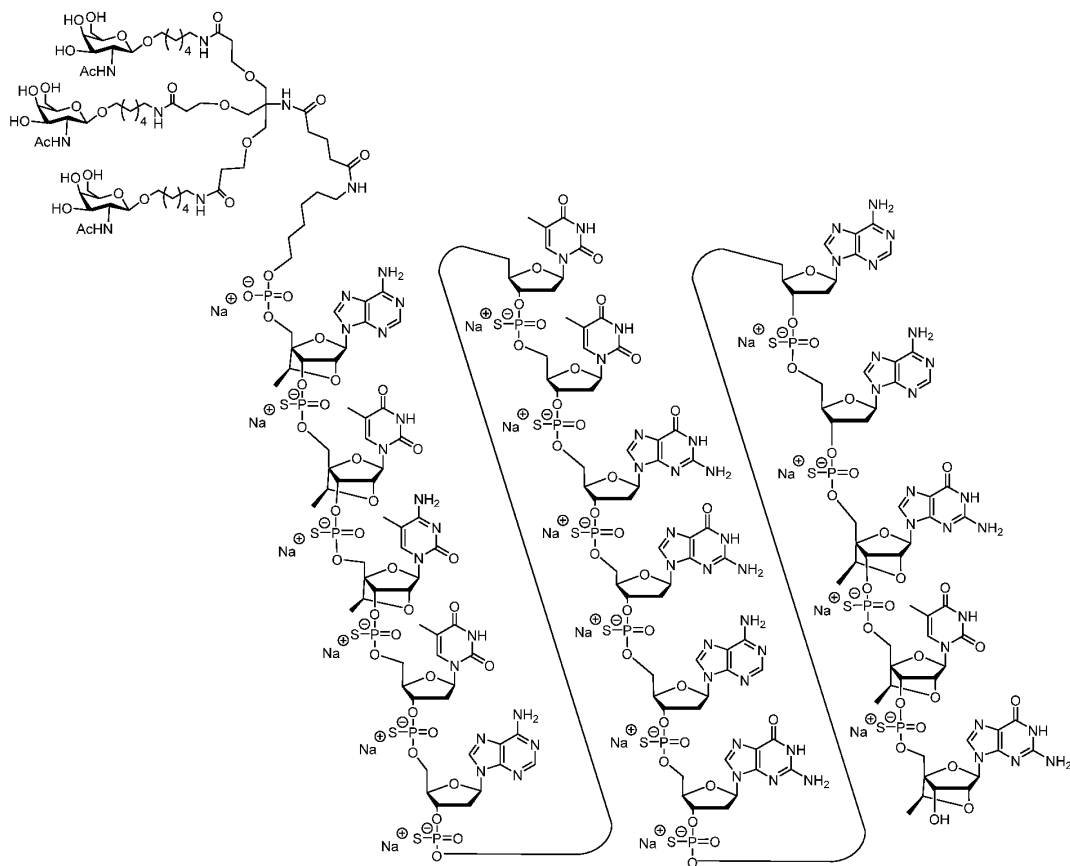
s = a phosphorothioate internucleoside linkage.

In certain embodiments, Compound No. 1436573 is represented by the following chemical structure:



(SEQ ID NO: 3037) or a salt thereof.

In certain embodiments, the sodium salt of Compound No. 1436573 is represented by the following chemical structure:

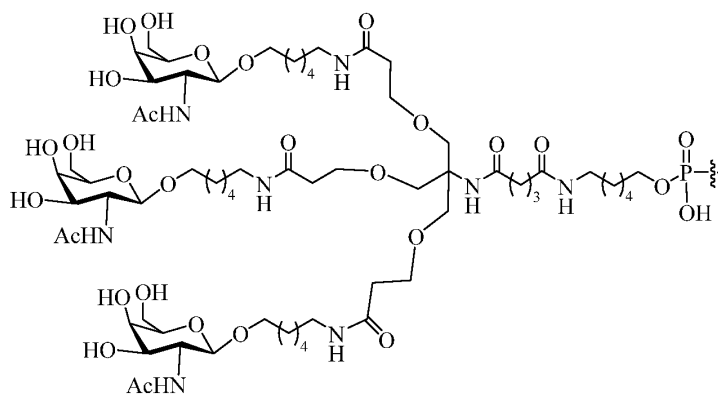


(SEQ ID NO: 3037).

5 In certain embodiments, Compound No. 1436573 is in anionic form.

#### Compound No. 1454987

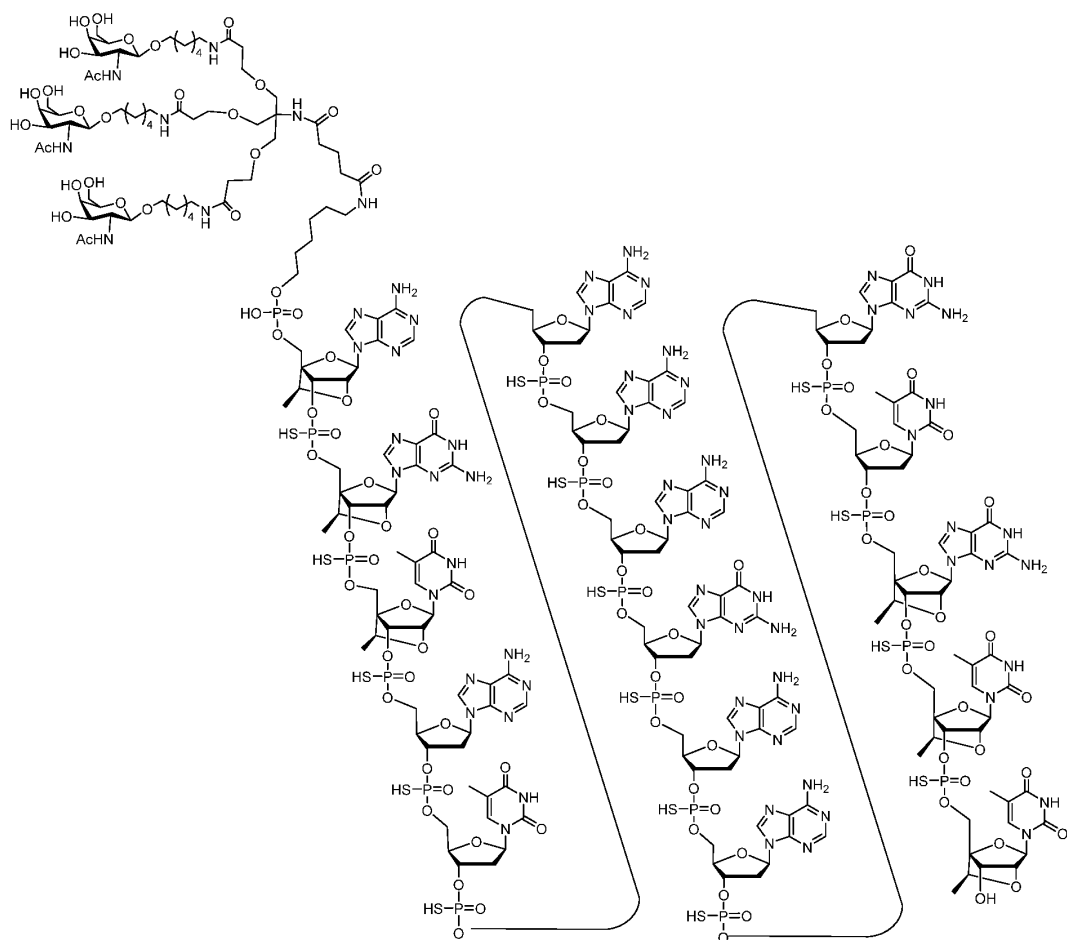
In certain embodiments, Compound No. 1454987 is characterized as a 3-10-3 cEt gapmer conjugated at the 5'-end to a conjugate group. Compound 1454987 has a sequence (from 5' to 3') of AGTATAAAGAAGTGTT (SEQ ID NO: 3039), wherein nucleosides 1-3 and 14-16 are cEt sugar moieties (from 5' to 3'), and each of nucleosides 4-13 are 2'-β-D-deoxyribosyl sugar moieties, and wherein each internucleoside linkage is a phosphorothioate internucleoside linkage. Compound No. 1454987 has a 5'-tris(hexamino)-(THA)-C<sub>6</sub>GalNAc<sub>3</sub> endcap, represented by the structure below, wherein the phosphate group is attached at the 5'-oxygen atom of the 5'-nucleoside:



In certain embodiments, Compound No. 1454987 is represented by the following chemical notation: THA-GalNAc-<sub>o</sub>A<sub>ks</sub>G<sub>ks</sub>T<sub>ks</sub>A<sub>ds</sub>T<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>T<sub>ds</sub>G<sub>ks</sub>T<sub>ks</sub>T<sub>k</sub> (SEQ ID NO: 3039), wherein:

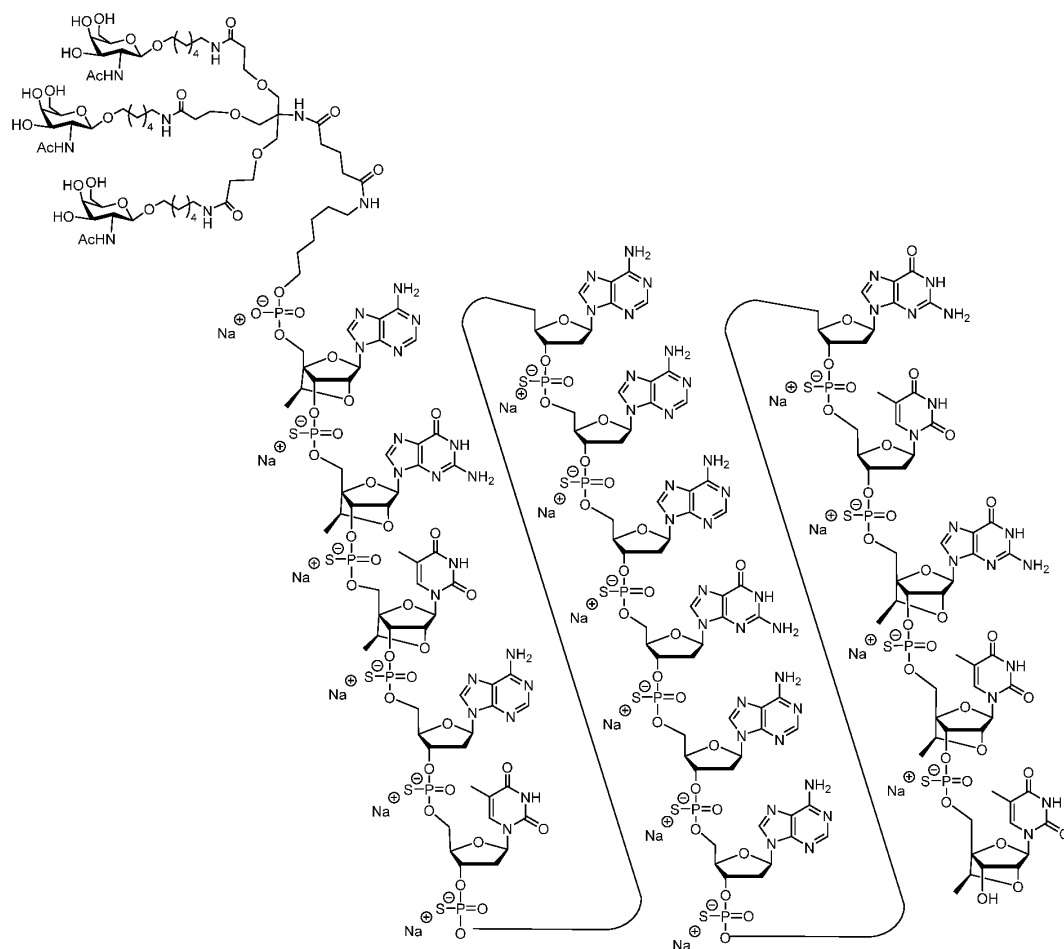
- 5      A = an adenine nucleobase,  
       G = a guanine nucleobase,  
       T = a thymine nucleobase,  
       k = a cEt modified sugar moiety,  
       d = a 2'-β-D-deoxyribose sugar moiety, and  
       s = a phosphorothioate internucleoside linkage.

In certain embodiments, Compound No. 1454987 is represented by the following chemical structure:



5 (SEQ ID NO: 3039) or a salt thereof.

In certain embodiments, the sodium salt of Compound No. 1454987 is represented by the following chemical structure:



5

(SEQ ID NO: 3039).

In certain embodiments, Compound No. 1454987 is in anionic form.

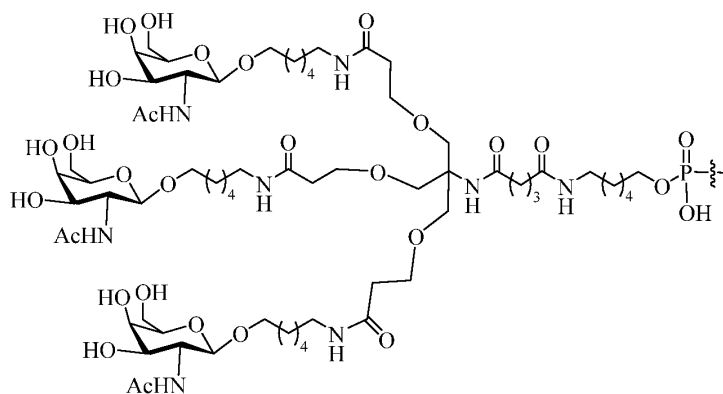
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#### Compound No. 1545962

In certain embodiments, Compound No. 1545962 is characterized as a 2-9-5 MOE/cEt mixed wing gapmer conjugated at the 5'-end to a conjugate group. Compound 1545962 has a sequence (from 5' to 3') of CTATTGGAGAAGTGTA (SEQ ID NO: 3041), wherein nucleosides 1-2 have sugar modifications of k-k (from 5' to 3'), wherein nucleosides 12-16 have sugar modifications of k-e-k-e-k, wherein each 'e' represents a 2'- MOE sugar moiety, and each 'k' refers to a cEt sugar moiety; and each of nucleosides 3-11 are 2'-β-D-deoxynucleosides; wherein

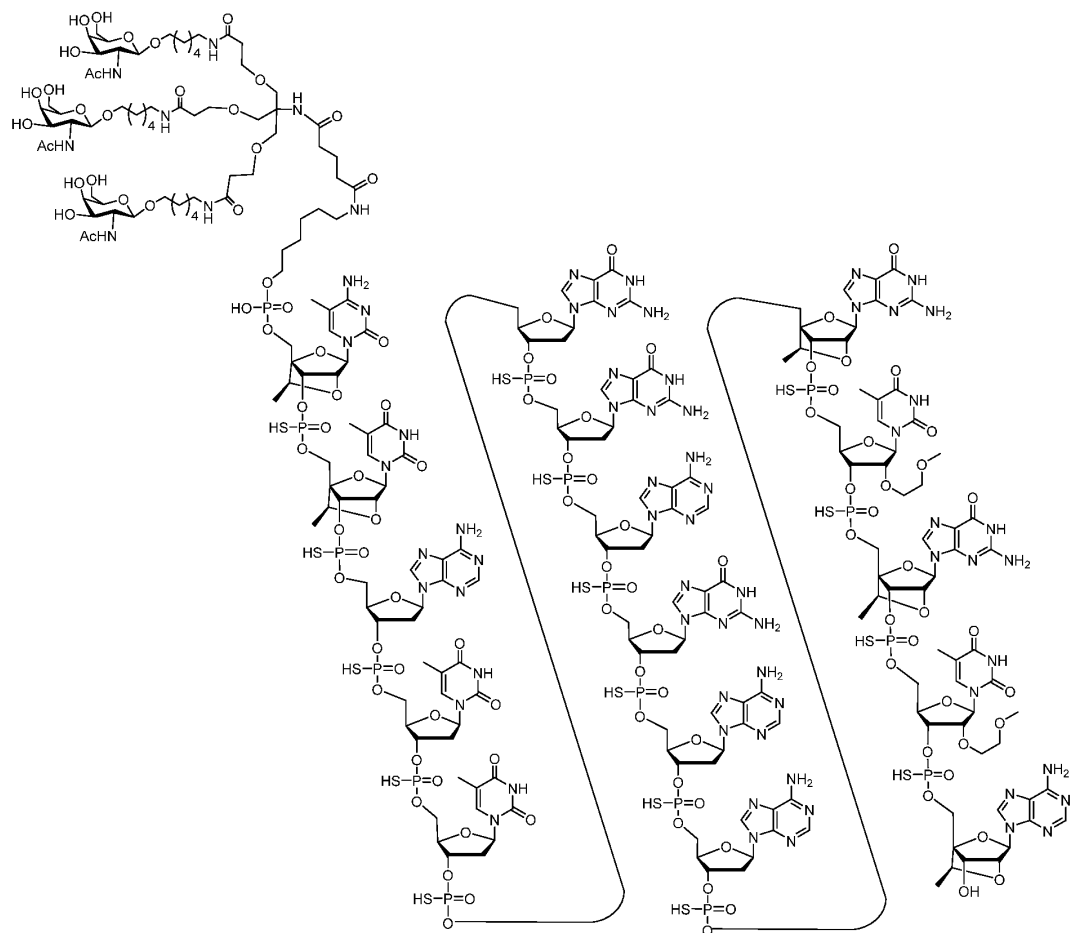
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the internucleoside linkages between nucleosides 1 to 16 are phosphorothioate internucleoside linkages, and wherein each cytosine is a 5-methylcytosine. Compound No. 1545962 has a 5'-trishexylamino-(THA)-C<sub>6</sub>GalNAc<sub>3</sub> endcap, represented by the structure below, wherein the phosphate group is attached at the 5'-oxygen atom of the 5'-nucleoside:



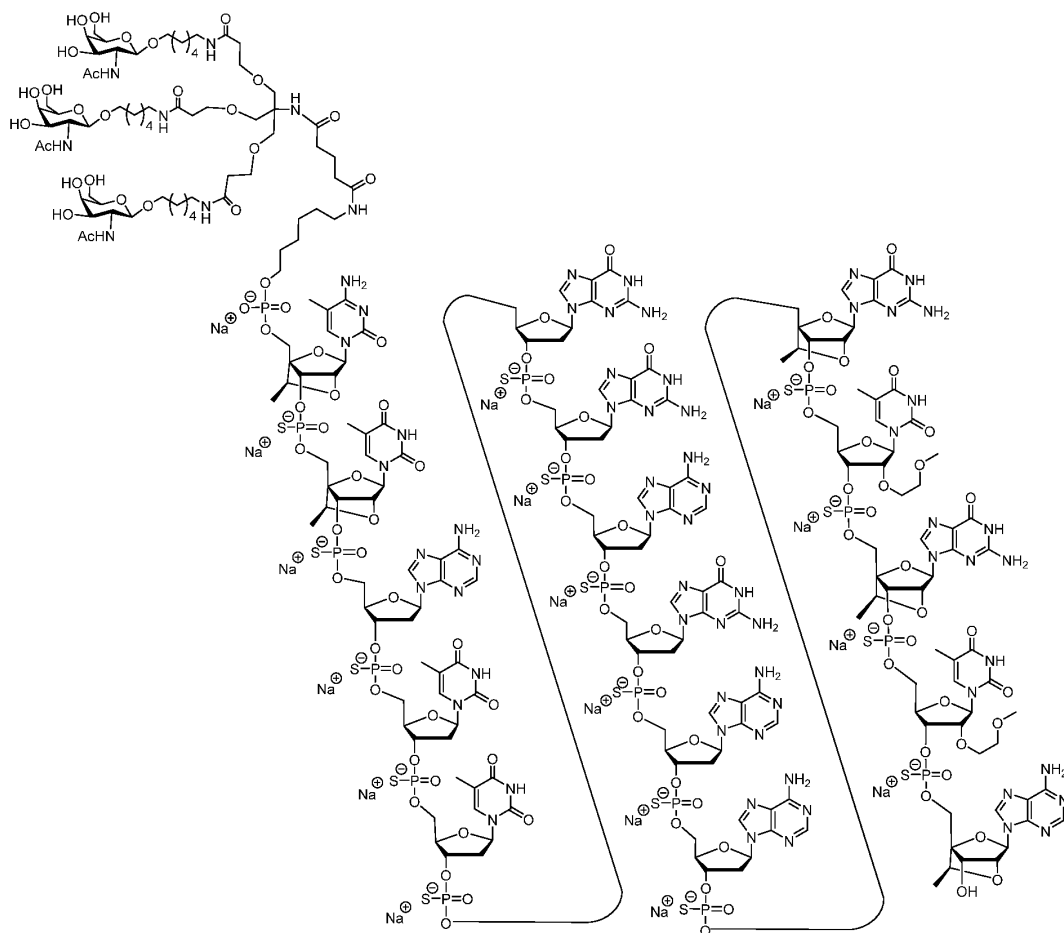
- 5 In certain embodiments, Compound No. 1545962 is represented by the following chemical notation: THA-C<sub>6</sub>-GalNAc<sub>3</sub>-<sup>m</sup>C<sub>ks</sub>T<sub>ks</sub>A<sub>ds</sub>T<sub>ds</sub>T<sub>ds</sub>G<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>G<sub>ks</sub>T<sub>es</sub>G<sub>ks</sub>T<sub>es</sub>A<sub>k</sub> (SEQ ID NO: 3041), wherein:
- A = an adenine nucleobase,
- <sup>m</sup>C = a 5-methylcytosine nucleobase,
- G = a guanine nucleobase,
- 10 T = a thymine nucleobase,
- e = a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> modified ribosyl sugar moiety,
- k = a cEt sugar moiety,
- d = a 2'-β-D-deoxyribsyl sugar moiety, and
- s = a phosphorothioate internucleoside linkage.

In certain embodiments, Compound No. 1545962 is represented by the following chemical structure:



(SEQ ID NO: 3041) or a salt thereof.

In certain embodiments, the sodium salt of Compound No. 1545962 is represented by the following chemical structure:



5 (SEQ ID NO: 3041).

In certain embodiments, Compound No. 1545962 is in anionic form.

#### Nonlimiting disclosure and incorporation by reference

Each of the literature and patent publications listed herein is incorporated by reference in its entirety.

10 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, GenBank accession numbers, ENSEMBL identifiers, and the like recited in the present application is incorporated herein by reference in its entirety.

15 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 base could be described as a DNA having a modified sugar (2'-OH in place of one 2'-H of DNA) or as an RNA having a modified base (thymine (methylated uracil) in place of an uracil of RNA). 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 natural 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 oligomeric compound having the nucleobase sequence "ATCGATCG" encompasses any oligomeric compounds 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 oligomeric compounds having other modified nucleobases, such as "AT<sup>m</sup>CGAUCG," wherein <sup>m</sup>C indicates a cytosine base comprising a methyl group at the 5-position.

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  $\alpha$  or  $\beta$  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, unless specified otherwise. Likewise, tautomeric forms of the compounds herein are also included unless otherwise indicated. Unless otherwise indicated, compounds described herein are intended to include corresponding salt forms.

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 <sup>1</sup>H hydrogen atoms. Isotopic substitutions encompassed by the compounds herein include but are not limited to: <sup>2</sup>H or <sup>3</sup>H in place of <sup>1</sup>H, <sup>13</sup>C or <sup>14</sup>C in place of <sup>12</sup>C, <sup>15</sup>N in place of <sup>14</sup>N, <sup>17</sup>O or <sup>18</sup>O in place of <sup>16</sup>O, and <sup>33</sup>S, <sup>34</sup>S, <sup>35</sup>S, or <sup>36</sup>S in place of <sup>32</sup>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.

## EXAMPLES

The following examples illustrate certain embodiments of the present disclosure and are not limiting. Moreover, where specific embodiments are provided, the inventors have contemplated generic application of those specific embodiments. For example, disclosure of an oligonucleotide having a particular motif provides reasonable support for additional oligonucleotides having the same or similar motif. And, for example, where a particular high-affinity modification appears at a particular position, other high-affinity modifications at the same position are considered suitable, unless otherwise indicated.

**Example 1: Effect of modified oligonucleotides on human PSD3 RNA *in vitro*, single dose**

Modified oligonucleotides complementary to a human PSD3 nucleic acid were designed and tested for their single dose effects on PSD3 RNA *in vitro*. The modified oligonucleotides were tested in a series of experiments that had the same culture conditions.

5 “Start site” indicates the 5’-most nucleoside to which the modified oligonucleotide is complementary in the target nucleic acid sequence. “Stop site” indicates the 3’-most nucleoside to which the modified oligonucleotide is complementary in the target nucleic acid sequence. Each modified oligonucleotide listed in the table below is 100% complementary to SEQ ID NO: 1 (the complement of GENBANK Accession No. NC\_000008.11, truncated from nucleosides 18524001 to 19090000), to SEQ ID NO: 2 (GENBANK Accession No. NM\_015310.3), or to both. “N/A”  
10 indicates that the modified oligonucleotide is not 100% complementary to that particular target nucleic acid sequence.

Cultured A431 cells were treated with modified oligonucleotide at a concentration of 2,000 nM by free uptake at a density of 10,000 cells per well. After a treatment period of approximately 48 hours, total RNA was isolated from the cells, and PSD3 RNA levels were measured by quantitative real-time RT-PCR. PSD3 RNA levels were measured by either human primer-probe set RTS41429 (forward sequence GCAAAACACCTTGGCAAGA, designated herein as SEQ ID  
15 NO: 3; reverse sequence CTCGTTCTTGAGTTTCTCCCA, designated herein as SEQ ID NO: 4; probe sequence ACCTGAGTGACTGATCCAGCGTCA, designated herein as SEQ ID NO: 5) or human primer-probe set RTS41435 (forward sequence CTTGGCTCGGAAAATTCATGC, designated herein as SEQ ID NO: 6; reverse sequence TCATCCTTTTGCAAGTAAAGAACT, designated herein as SEQ ID NO: 7; probe sequence AGGTTTTCATCCTCGTTTTCCTCTTGG, designated herein as SEQ ID NO: 8) as indicated in the tables below.  
20 PSD3 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of PSD3 RNA is presented in the table below as percent PSD3 RNA relative to the amount in untreated control cells (% UTC). The values marked with a “†” indicate that the modified oligonucleotide is complementary to the amplicon region of the primer probe set. Additional assays may be used to measure the potency and efficacy of the modified oligonucleotides complementary to the amplicon region. Each separate experiment described in this example is identified by an Assay Identification letter  
25 in the table column labeled “AID”.

The modified oligonucleotides in the Table 1 and Table 2 below are 3-10-3 cEt modified oligonucleotides with uniform phosphorothioate internucleoside linkages. The modified oligonucleotides are 16 nucleosides in length, wherein the central gap segment consists of ten 2’-β-D-deoxynucleosides, and wherein the 5’ and 3’ wing segments each consist of three cEt nucleosides. The sugar motif for the modified oligonucleotides is (from 5’ to 3’): kkkddddd kkk; wherein each “d” represents a 2’-β-D-deoxyribose sugar moiety, and each “k” represents a cEt modified sugar moiety.  
30 The internucleoside linkage motif for the modified oligonucleotides is (from 5’ to 3’): sssssssssss; wherein each “s” represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine.

**Table 1.** Reduction of PSD3 RNA by 3-10-3 cEt modified oligonucleotides with uniform phosphorothioate internucleoside linkages

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3') | PSD3 (% UTC) RTS41429 | AID | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|---------------------|-----------------------|-----|-----------|
| 1173382      | 217279                  | 217294                 | 245                     | 260                    | GGAGTAAAGTGCTTCC    | 71                    | A   | 20        |
| 1173386      | 217661                  | 217676                 | 627                     | 642                    | GTTTACGACTGGCAG     | 32                    | A   | 21        |
| 1173390      | 217983                  | 217998                 | 949                     | 964                    | GCTTCGATCACATCCC    | 29                    | A   | 22        |
| 1173393      | 221996                  | 222011                 | 1406                    | 1421                   | CGTCGGTGGAGTCCTC    | 37                    | A   | 23        |
| 1173397      | 222143                  | 222158                 | 1553                    | 1568                   | CTTCTTTAATGCGCTG    | 35                    | A   | 24        |
| 1173401      | 285407                  | 285422                 | 1941                    | 1956                   | GCAACTAGTTTGCTAA    | 76†                   | A   | 25        |
| 1173405      | 290677                  | 290692                 | 2156                    | 2171                   | CGGTATTAAGAAGCAT    | 8                     | A   | 26        |
| 1173409      | 457220                  | 457235                 | 2345                    | 2360                   | CAGTACTTTCTGAGGG    | 72                    | A   | 27        |
| 1173413      | 457351                  | 457366                 | 2476                    | 2491                   | ATGAATTTTCCGAGCC    | 61                    | A   | 28        |
| 1173417      | 554091                  | 554106                 | 3080                    | 3095                   | CGTACTCAGTAGCTC     | 73                    | A   | 29        |
| 1173421      | 554181                  | 554196                 | 3170                    | 3185                   | TACGCTTGACTTTGGC    | 63                    | A   | 30        |
| 1173425      | 554454                  | 554469                 | 3443                    | 3458                   | AGCTATCAAGTTGCAA    | 98                    | A   | 31        |
| 1173429      | 554584                  | 554599                 | 3573                    | 3588                   | AAGTTTAAACAGTTGAT   | 71                    | A   | 32        |
| 1173433      | 554765                  | 554780                 | 3754                    | 3769                   | GCAACTAGATTCCCAG    | 81                    | A   | 33        |
| 1173437      | 554857                  | 554872                 | 3846                    | 3861                   | CCTACGATCTTCACGC    | 56                    | A   | 34        |
| 1173441      | 554906                  | 554921                 | 3895                    | 3910                   | ATGGAATCAGCACTTC    | 69                    | A   | 35        |
| 1173445      | 555119                  | 555134                 | 4108                    | 4123                   | GGATATCAACGATAGA    | 67                    | A   | 36        |
| 1173449      | 555900                  | 555915                 | 4889                    | 4904                   | ACATACCACTTAGACA    | 69                    | A   | 37        |
| 1173453      | 556170                  | 556185                 | 5159                    | 5174                   | ATCTGATACATGGGCC    | 84                    | A   | 38        |
| 1173457      | 556308                  | 556323                 | 5297                    | 5312                   | TCTAGGTACCTCTCTC    | 54                    | A   | 39        |
| 1173461      | 556451                  | 556466                 | 5440                    | 5455                   | GCAAGGTACCATTCAA    | 68                    | A   | 40        |
| 1173465      | 556533                  | 556548                 | 5522                    | 5537                   | CTCATATGACACGGAC    | 53                    | A   | 41        |
| 1173469      | 556613                  | 556628                 | 5602                    | 5617                   | TATACTGAAGCTTCAA    | 86                    | A   | 42        |
| 1173473      | 556823                  | 556838                 | 5812                    | 5827                   | TAGGCAAATCAGTGAC    | 60                    | A   | 43        |
| 1173477      | 557563                  | 557578                 | 6552                    | 6567                   | TAGGATAACAGTTGGA    | 35                    | A   | 44        |
| 1173481      | 557814                  | 557829                 | 6803                    | 6818                   | ATCTTTACATGATAGA    | 110                   | A   | 45        |
| 1173485      | 558246                  | 558261                 | 7235                    | 7250                   | CTCATAAACTAGACTT    | 67                    | A   | 46        |
| 1173489      | 558506                  | 558521                 | 7495                    | 7510                   | TGCTATCAATAATCTA    | 73                    | A   | 47        |
| 1173493      | 558869                  | 558884                 | 7858                    | 7873                   | GCCTGTAAGAATAGTC    | 74                    | A   | 48        |
| 1173497      | 559241                  | 559256                 | 8230                    | 8245                   | GTATTGCACACAGTAC    | 74                    | A   | 49        |
| 1173501      | 559603                  | 559618                 | 8592                    | 8607                   | TAGGATACAGTACCCA    | 77                    | A   | 50        |
| 1173504      | 559757                  | 559772                 | 8746                    | 8761                   | GCAGTAAGCTCAAACA    | 81                    | A   | 51        |
| 1173508      | 559950                  | 559965                 | 8939                    | 8954                   | GCTGAAGTTAGTCTCC    | 68                    | A   | 52        |
| 1173512      | 560232                  | 560247                 | 9221                    | 9236                   | AAATGGTTAAGGCCCA    | 54                    | A   | 53        |
| 1173516      | 560515                  | 560530                 | 9504                    | 9519                   | CTCCTTATACACCTAA    | 73                    | A   | 54        |
| 1173520      | 561028                  | 561043                 | 10017                   | 10032                  | CAGTCGGAGCTCTCTT    | 78                    | A   | 55        |
| 1173524      | 561147                  | 561162                 | 10136                   | 10151                  | CTATTCCTAAGAGCTT    | 75                    | A   | 56        |
| 1173528      | 561251                  | 561266                 | 10240                   | 10255                  | CTTATTTATGGCGACC    | 60                    | A   | 57        |

|         |        |        |       |       |                   |    |   |    |
|---------|--------|--------|-------|-------|-------------------|----|---|----|
| 1173532 | 561506 | 561521 | 10495 | 10510 | GCAGGGTCACGCTATC  | 67 | A | 58 |
| 1173536 | 561837 | 561852 | 10826 | 10841 | AATGGGTTCCCTAAAGC | 88 | A | 59 |
| 1173540 | 561914 | 561929 | 10903 | 10918 | TACAAATTATCGCCTT  | 61 | A | 60 |
| 1173544 | 561993 | 562008 | 10982 | 10997 | ATTAGTTTGAGCCACA  | 67 | A | 61 |
| 1173548 | 562164 | 562179 | 11153 | 11168 | CTTACCCAAAACTGCT  | 77 | A | 62 |
| 1173552 | 562224 | 562239 | 11213 | 11228 | CCAGAATCTGGTAGGT  | 98 | A | 63 |
| 1173556 | 562559 | 562574 | 11548 | 11563 | AATTTTGTGCGGTAA   | 72 | A | 64 |
| 1173560 | 19133  | 19148  | N/A   | N/A   | GATAATCAATCTAGGT  | 99 | A | 65 |
| 1173564 | 48336  | 48351  | N/A   | N/A   | AGTCAATATGTATCAG  | 93 | A | 66 |
| 1173568 | 66240  | 66255  | N/A   | N/A   | AGACATTGCAGCTCTA  | 63 | A | 67 |
|         | 280858 | 280873 |       |       |                   |    |   |    |
| 1173572 | 109978 | 109993 | N/A   | N/A   | ATACACTGATCTATGT  | 65 | A | 68 |
|         | 110004 | 110019 |       |       |                   |    |   |    |
| 1173576 | 127690 | 127705 | N/A   | N/A   | AGACTAAAGTTATCAA  | 77 | A | 69 |
| 1173580 | 135804 | 135819 | N/A   | N/A   | AATATTAACACGGCAC  | 55 | A | 70 |
| 1173584 | 146122 | 146137 | N/A   | N/A   | GAAATTATGGCACCCCT | 62 | A | 71 |
| 1173588 | 188558 | 188573 | N/A   | N/A   | GTATTATTGATAGGCG  | 33 | A | 72 |
| 1173592 | 212148 | 212163 | N/A   | N/A   | GCTAGATGCCTATCTT  | 75 | A | 73 |
|         | 212460 | 212475 |       |       |                   |    |   |    |
| 1173596 | 234350 | 234365 | N/A   | N/A   | GACACAATGGCCAGTT  | 68 | A | 74 |
|         | 237553 | 237568 |       |       |                   |    |   |    |
| 1173600 | 261641 | 261656 | N/A   | N/A   | CTTATTAGTAATGGGA  | 43 | A | 75 |
| 1173604 | 275472 | 275487 | N/A   | N/A   | TATACTAAGTTGCTGC  | 43 | A | 76 |
| 1173608 | 308838 | 308853 | N/A   | N/A   | CTTATTAACCCCAGTT  | 56 | A | 77 |
| 1173612 | 332820 | 332835 | N/A   | N/A   | CTGGGATCTGGACGCG  | 76 | A | 78 |
|         | 338098 | 338113 |       |       |                   |    |   |    |
| 1173616 | 332895 | 332910 | N/A   | N/A   | GATCTGTAACACTCA   | 44 | A | 79 |
|         | 338173 | 338188 |       |       |                   |    |   |    |
| 1173620 | 332972 | 332987 | N/A   | N/A   | TTATCCCATGCCGTAC  | 57 | A | 80 |
|         | 338250 | 338265 |       |       |                   |    |   |    |
| 1173624 | 333037 | 333052 | N/A   | N/A   | CTGCTAGCCACTTAAC  | 59 | A | 81 |
|         | 338315 | 338330 |       |       |                   |    |   |    |
| 1173628 | 333074 | 333089 | N/A   | N/A   | CCCAGTCAGAACAACT  | 58 | A | 82 |
|         | 338352 | 338367 |       |       |                   |    |   |    |
| 1173632 | 333132 | 333147 | N/A   | N/A   | CGCCACCACTAGTCAC  | 56 | A | 83 |
|         | 338410 | 338425 |       |       |                   |    |   |    |
| 1173636 | 333234 | 333249 | N/A   | N/A   | CCAGAAGCCTAAACCG  | 49 | A | 84 |
|         | 338512 | 338527 |       |       |                   |    |   |    |
| 1173640 | 333331 | 333346 | N/A   | N/A   | CATCACCAGAGGAAGT  | 68 | A | 85 |
|         | 338609 | 338624 |       |       |                   |    |   |    |
| 1173644 | 333408 | 333423 | N/A   | N/A   | CTGAAACGATCCTTAC  | 57 | A | 86 |
|         | 338686 | 338701 |       |       |                   |    |   |    |
| 1173648 | 353309 | 353324 | N/A   | N/A   | ACGGAAATAATGGTGC  | 51 | A | 87 |

|         |        |        |      |      |                  |     |   |     |
|---------|--------|--------|------|------|------------------|-----|---|-----|
|         | 354724 | 354739 |      |      |                  |     |   |     |
| 1173652 | 353463 | 353478 | N/A  | N/A  | AATCCTACATTCAGTA | 56  | A | 88  |
|         | 354883 | 354898 |      |      |                  |     |   |     |
| 1173656 | 387074 | 387089 | N/A  | N/A  | AGCTATAGGTACTCTT | 64  | A | 89  |
|         | 387392 | 387407 |      |      |                  |     |   |     |
| 1173660 | 396082 | 396097 | N/A  | N/A  | TATATTAGATGGTGCA | 71  | A | 90  |
| 1173664 | 411102 | 411117 | N/A  | N/A  | TAATTTATGCATCCCT | 70  | A | 91  |
| 1173668 | 447633 | 447648 | N/A  | N/A  | ATTATAATGTACGAGT | 63  | A | 92  |
| 1173672 | 468126 | 468141 | N/A  | N/A  | TTAATTATAGTGTCGC | 57  | A | 93  |
| 1173676 | 499668 | 499683 | N/A  | N/A  | GATAGTAAATCAAACG | 101 | A | 94  |
| 1173680 | 508432 | 508447 | N/A  | N/A  | GTATATCACAAGCTCT | 56  | A | 95  |
| 1173684 | 534266 | 534281 | N/A  | N/A  | TAATTTATCAACCCCC | 87  | A | 96  |
| 1173688 | 539595 | 539610 | N/A  | N/A  | ATTATTAAGTGGACTC | 55  | A | 97  |
| 1173383 | 217280 | 217295 | 246  | 261  | GGGAGTAAAGTGCTTC | 55  | B | 98  |
| 1173387 | 217781 | 217796 | 747  | 762  | AGCGCGGTGAGATCTT | 46  | B | 99  |
| 1173391 | 218082 | 218097 | 1048 | 1063 | TATAGGATGCTGGGTC | 30  | B | 100 |
| 1173394 | 222075 | 222090 | 1485 | 1500 | GAGTATAATGTCTCCA | 51  | B | 101 |
| 1173398 | 222193 | 222208 | 1603 | 1618 | CAGGATATCCTGATGT | 87  | B | 102 |
| 1173402 | 285409 | 285424 | 1943 | 1958 | CTGCAACTAGTTTGCT | 94† | B | 103 |
| 1173406 | 290679 | 290694 | 2158 | 2173 | ATCGGTATTAAGAAGC | 21  | B | 104 |
| 1173410 | 457274 | 457289 | 2399 | 2414 | TAGTACTTCCAATACG | 69  | B | 105 |
| 1173414 | 514794 | 514809 | 2663 | 2678 | CATAGTCCGTGGCCTT | 61  | B | 106 |
| 1173418 | 554142 | 554157 | 3131 | 3146 | TCAGCGAAGGACTCGA | 60  | B | 107 |
| 1173422 | 554210 | 554225 | 3199 | 3214 | AGGTCGGTGATCCTTC | 84  | B | 108 |
| 1173426 | 554461 | 554476 | 3450 | 3465 | GTGCATTAGCTATCAA | 82  | B | 109 |
| 1173430 | 554671 | 554686 | 3660 | 3675 | TATATTAAGTCCAGCT | 80  | B | 110 |
| 1173434 | 554766 | 554781 | 3755 | 3770 | AGCAACTAGATTCCCA | 76  | B | 111 |
| 1173438 | 554859 | 554874 | 3848 | 3863 | ATCCTACGATCTTCAC | 60  | B | 112 |
| 1173442 | 554975 | 554990 | 3964 | 3979 | GGGTATCAATCTTTCC | 104 | B | 113 |
| 1173446 | 555691 | 555706 | 4680 | 4695 | TAGGGATTACAGAGTT | 63  | B | 114 |
| 1173450 | 556110 | 556125 | 5099 | 5114 | CTTAGTTACTGCCTTT | 63  | B | 115 |
| 1173454 | 556224 | 556239 | 5213 | 5228 | GACAGATAACTTGCTT | 54  | B | 116 |
| 1173458 | 556392 | 556407 | 5381 | 5396 | TAGATATAGACTGTGG | 59  | B | 117 |
| 1173462 | 556488 | 556503 | 5477 | 5492 | GTATTTCAACACTACT | 90  | B | 118 |
| 1173466 | 556544 | 556559 | 5533 | 5548 | AATATTAGTGACTCAT | 58  | B | 119 |
| 1173470 | 556614 | 556629 | 5603 | 5618 | GTATACTGAAGCTTCA | 92  | B | 120 |
| 1173474 | 556950 | 556965 | 5939 | 5954 | TGAATTGGGCAACAGG | 60  | B | 121 |
| 1173478 | 557565 | 557580 | 6554 | 6569 | ATTAGGATAACAGTTG | 36  | B | 122 |
| 1173482 | 557932 | 557947 | 6921 | 6936 | GTTAGTAAGACAATGG | 54  | B | 123 |
| 1173486 | 558453 | 558468 | 7442 | 7457 | TGCTATAAGACTGGTG | 57  | B | 124 |
| 1173490 | 558513 | 558528 | 7502 | 7517 | TCTCTATTGCTATCAA | 53  | B | 125 |
| 1173494 | 558972 | 558987 | 7961 | 7976 | GATATGCAATCTACAC | 65  | B | 126 |
| 1173498 | 559324 | 559339 | 8313 | 8328 | GTTACTAAGACTGCAC | 68  | B | 127 |

|         |        |        |       |       |                  |     |   |     |
|---------|--------|--------|-------|-------|------------------|-----|---|-----|
| 1173502 | 559670 | 559685 | 8659  | 8674  | AGTTTAAACCTGGTCC | 57  | B | 128 |
| 1173505 | 559781 | 559796 | 8770  | 8785  | ACCTATTACACTCTA  | 71  | B | 129 |
| 1173509 | 559974 | 559989 | 8963  | 8978  | ACCAACACATTACTGC | 65  | B | 130 |
| 1173513 | 560423 | 560438 | 9412  | 9427  | CACTTTACTGTCCCCT | 66  | B | 131 |
| 1173517 | 560767 | 560782 | 9756  | 9771  | GATATGGATCCCCTCA | 74  | B | 132 |
| 1173521 | 561029 | 561044 | 10018 | 10033 | TCAGTCGGAGCTCTCT | 55  | B | 133 |
| 1173525 | 561179 | 561194 | 10168 | 10183 | GAATTGAAGTTAGGGT | 79  | B | 134 |
| 1173529 | 561254 | 561269 | 10243 | 10258 | AGACTTATTTATGGCG | 65  | B | 135 |
| 1173533 | 561520 | 561535 | 10509 | 10524 | GATACCTTGCCTCAGC | 77  | B | 136 |
| 1173537 | 561865 | 561880 | 10854 | 10869 | ATAAATTCTCCGCTAG | 80  | B | 137 |
| 1173541 | 561916 | 561931 | 10905 | 10920 | GATACAAATTATCGCC | 69  | B | 138 |
| 1173545 | 561996 | 562011 | 10985 | 11000 | CCAATTAGTTTGAGCC | 62  | B | 139 |
| 1173549 | 562181 | 562196 | 11170 | 11185 | TGTTATAGTACCGCCA | 60  | B | 140 |
| 1173553 | 562449 | 562464 | 11438 | 11453 | ACATATCAGATGACTC | 73  | B | 141 |
| 1173557 | 562560 | 562575 | 11549 | 11564 | AAATTTTGTGCGGTA  | 64  | B | 142 |
| 1173561 | 30111  | 30126  | N/A   | N/A   | GTCTTCTATAACCACT | 42  | B | 143 |
|         | 246101 | 246116 |       |       |                  |     |   |     |
| 1173565 | 58138  | 58153  | N/A   | N/A   | ATCTAACTCAATCTCA | 69  | B | 144 |
|         | 271496 | 271511 |       |       |                  |     |   |     |
| 1173569 | 75453  | 75468  | N/A   | N/A   | ACCGCAAATCTTTCCC | 101 | B | 145 |
| 1173573 | 110067 | 110082 | N/A   | N/A   | GAACAGTATCCTTCTA | 56  | B | 146 |
|         | 505465 | 505480 |       |       |                  |     |   |     |
| 1173577 | 128244 | 128259 | N/A   | N/A   | GTATTTAAGATTACCA | 55  | B | 147 |
| 1173581 | 141625 | 141640 | N/A   | N/A   | GGATTTAAGTCGGGTC | 48  | B | 148 |
| 1173585 | 176695 | 176710 | N/A   | N/A   | CTCGGGTTGATICTTC | 121 | B | 149 |
| 1173589 | 189828 | 189843 | N/A   | N/A   | ATTATCGAACCATCTT | 29  | B | 150 |
| 1173593 | 216180 | 216195 | N/A   | N/A   | ATTAGTAAGATCACTA | 103 | B | 151 |
| 1173597 | 235209 | 235224 | N/A   | N/A   | TACACAATTTAGCTCT | 16  | B | 152 |
|         | 235282 | 235297 |       |       |                  |     |   |     |
| 1173601 | 263009 | 263024 | N/A   | N/A   | AGTGATATGAATGGTA | 16  | B | 153 |
|         | 263050 | 263065 |       |       |                  |     |   |     |
| 1173605 | 278066 | 278081 | N/A   | N/A   | CTTATTAAGTTTGGAC | 31  | B | 154 |
| 1173609 | 314456 | 314471 | N/A   | N/A   | CATTTTAACTCGGGTA | 33  | B | 155 |
| 1173613 | 332827 | 332842 | N/A   | N/A   | ACATTAAGTGGGATCT | 49  | B | 156 |
|         | 338105 | 338120 |       |       |                  |     |   |     |
| 1173617 | 332911 | 332926 | N/A   | N/A   | TTGGGATTACTTTCCA | 83  | B | 157 |
|         | 338189 | 338204 |       |       |                  |     |   |     |
| 1173621 | 332989 | 333004 | N/A   | N/A   | CTTAGAGGAAGGTGTT | 38  | B | 158 |
|         | 338267 | 338282 |       |       |                  |     |   |     |
| 1173625 | 333044 | 333059 | N/A   | N/A   | GGGCACACTGCTAGCC | 107 | B | 159 |
|         | 338322 | 338337 |       |       |                  |     |   |     |
| 1173629 | 333081 | 333096 | N/A   | N/A   | TCCATAACCCAGTCAG | 43  | B | 160 |
|         | 338359 | 338374 |       |       |                  |     |   |     |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1173633 | 333145 | 333160 | N/A  | N/A  | GATCACCCGGAGGCGC  | 103 | B | 161 |
|         | 338423 | 338438 |      |      |                   |     |   |     |
| 1173637 | 333271 | 333286 | N/A  | N/A  | AGCGGTGACAGGGAGG  | 72  | B | 162 |
|         | 338549 | 338564 |      |      |                   |     |   |     |
| 1173641 | 333385 | 333400 | N/A  | N/A  | CCCTGTGAAGTTGTTC  | 40  | B | 163 |
|         | 338663 | 338678 |      |      |                   |     |   |     |
| 1173645 | 341270 | 341285 | N/A  | N/A  | AGTTATAATACGGCAG  | 35  | B | 164 |
| 1173649 | 353320 | 353335 | N/A  | N/A  | CATGTTGAGATACGGA  | 50  | B | 165 |
|         | 354735 | 354750 |      |      |                   |     |   |     |
| 1173653 | 367783 | 367798 | N/A  | N/A  | AGTAATATGTCAGTGG  | 61  | B | 166 |
| 1173657 | 389692 | 389707 | N/A  | N/A  | GAATTTATCATATCGG  | 48  | B | 167 |
| 1173661 | 397335 | 397350 | N/A  | N/A  | ACAGAACCTGATTGGA  | 100 | B | 168 |
| 1173665 | 430854 | 430869 | N/A  | N/A  | GTATTAATGAAGGGCA  | 74  | B | 169 |
| 1173669 | 454855 | 454870 | N/A  | N/A  | AGTTATAATAAGGTGT  | 81  | B | 170 |
| 1173673 | 480943 | 480958 | N/A  | N/A  | GTCATAATATGGATAG  | 56  | B | 171 |
|         | 480962 | 480977 |      |      |                   |     |   |     |
| 1173677 | 505147 | 505162 | N/A  | N/A  | AACGGGTATGTAGAGC  | 89  | B | 172 |
| 1173681 | 514919 | 514934 | N/A  | N/A  | GCAATAAAGTAGTGCT  | 93  | B | 173 |
| 1173685 | 536169 | 536184 | N/A  | N/A  | AATATTAGCTGTACCA  | 73  | B | 174 |
| 1173689 | 543123 | 543138 | N/A  | N/A  | ACATATAAGTTGCACA  | 63  | B | 175 |
| 1173239 | 221982 | 221997 | 1392 | 1407 | TCCGTATATCCAGGCC  | 51  | C | 176 |
| 1173384 | 217448 | 217463 | 414  | 429  | TCTGTAACACTGTCTGA | 37  | C | 177 |
| 1173388 | 217790 | 217805 | 756  | 771  | CCAGTTAACAGCGCGG  | 44  | C | 178 |
| 1173395 | 222089 | 222104 | 1499 | 1514 | AGCTATCAGGCTCTGA  | 67  | C | 179 |
| 1173399 | 222222 | 222237 | 1632 | 1647 | ATCACGATGCCACCAT  | 34  | C | 180 |
| 1173403 | 288679 | 288694 | 2074 | 2089 | TCTATTGGAGAAGTGT  | 5   | C | 181 |
| 1173407 | 290681 | 290696 | 2160 | 2175 | AGATCGGTATTAAGAA  | 56  | C | 182 |
| 1173411 | 457279 | 457294 | 2404 | 2419 | GTTAGTAGTACTTCCA  | 75  | C | 183 |
| 1173415 | 533685 | 533700 | 2924 | 2939 | GCTCGGTGGTGATCTG  | 54  | C | 184 |
| 1173419 | 554152 | 554167 | 3141 | 3156 | GTATCCGGGTTTCAGCG | 82  | C | 185 |
| 1173423 | 554322 | 554337 | 3311 | 3326 | TATATTCACGGATTAC  | 82  | C | 186 |
| 1173427 | 554490 | 554505 | 3479 | 3494 | ATCACGATCCCCTCCT  | 70  | C | 187 |
| 1173431 | 554672 | 554687 | 3661 | 3676 | GTATATTAAGTCCAGC  | 102 | C | 188 |
| 1173435 | 554774 | 554789 | 3763 | 3778 | CATATTGGAGCAACTA  | 72  | C | 189 |
| 1173439 | 554863 | 554878 | 3852 | 3867 | CTCAATCCTACGATCT  | 108 | C | 190 |
| 1173443 | 555015 | 555030 | 4004 | 4019 | GCCGATTATTGCCCCC  | 76  | C | 191 |
| 1173447 | 555740 | 555755 | 4729 | 4744 | AGTGATACTATTAGTT  | 62  | C | 192 |
| 1173451 | 556148 | 556163 | 5137 | 5152 | GTAAGTATCCTGTTTG  | 77  | C | 193 |
| 1173455 | 556243 | 556258 | 5232 | 5247 | TTAGATTATCAGGTAG  | 77  | C | 194 |
| 1173459 | 556393 | 556408 | 5382 | 5397 | ATAGATATAGACTGTG  | 59  | C | 195 |
| 1173463 | 556515 | 556530 | 5504 | 5519 | TGCTATAGTGGTGCTG  | 87  | C | 196 |
| 1173467 | 556550 | 556565 | 5539 | 5554 | GGAGTTAATATTAGTG  | 62  | C | 197 |
| 1173471 | 556713 | 556728 | 5702 | 5717 | ATGCGCTAAAGATGGA  | 83  | C | 198 |

|         |        |        |       |       |                   |     |   |     |
|---------|--------|--------|-------|-------|-------------------|-----|---|-----|
| 1173475 | 557291 | 557306 | 6280  | 6295  | TAAAGTAAGGACTCTG  | 95  | C | 199 |
| 1173479 | 557568 | 557583 | 6557  | 6572  | TAGATTAGGATAACAG  | 53  | C | 200 |
| 1173483 | 558041 | 558056 | 7030  | 7045  | AAGCTAAACTTCTGTG  | 92  | C | 201 |
| 1173487 | 558454 | 558469 | 7443  | 7458  | ATGCTATAAGACTGGT  | 97  | C | 202 |
| 1173491 | 558615 | 558630 | 7604  | 7619  | GATACTGTAGGTACAA  | 63  | C | 203 |
| 1173495 | 558975 | 558990 | 7964  | 7979  | ACTGATATGCAATCTA  | 65  | C | 204 |
| 1173499 | 559458 | 559473 | 8447  | 8462  | GTACTTAATTCTTCCG  | 98  | C | 205 |
| 1173503 | 559671 | 559686 | 8660  | 8675  | AAGTTTAAACCTGGTC  | 85  | C | 206 |
| 1173506 | 559784 | 559799 | 8773  | 8788  | GTTACCTATTTACACT  | 91  | C | 207 |
| 1173510 | 560025 | 560040 | 9014  | 9029  | TGAGACTATAGAGTTA  | 92  | C | 208 |
| 1173514 | 560424 | 560439 | 9413  | 9428  | CCACTTACTGTCCCC   | 94  | C | 209 |
| 1173518 | 560794 | 560809 | 9783  | 9798  | AATTTGGTGGTCCACA  | 75  | C | 210 |
| 1173522 | 561105 | 561120 | 10094 | 10109 | CATTTTAGTTCGGTTC  | 70  | C | 211 |
| 1173526 | 561180 | 561195 | 10169 | 10184 | GGAATTGAAGTTAGGG  | 58  | C | 212 |
| 1173530 | 561299 | 561314 | 10288 | 10303 | GTCCTTAATCGAGCCT  | 92  | C | 213 |
| 1173534 | 561751 | 561766 | 10740 | 10755 | CTGCTAAGCTAGCACT  | 100 | C | 214 |
| 1173538 | 561884 | 561899 | 10873 | 10888 | GGTAATCAAGGCTGAC  | 65  | C | 215 |
| 1173542 | 561917 | 561932 | 10906 | 10921 | AGATACAAATTATCGC  | 100 | C | 216 |
| 1173546 | 562076 | 562091 | 11065 | 11080 | GGACATATGGCACCAG  | 80  | C | 217 |
| 1173550 | 562182 | 562197 | 11171 | 11186 | GTGTTATAGTACCGCC  | 81  | C | 218 |
| 1173554 | 562456 | 562471 | 11445 | 11460 | CTTCTATACATATCAG  | 81  | C | 219 |
| 1173558 | 13885  | 13900  | N/A   | N/A   | TCAATAAAAAATACGGT | 110 | C | 220 |
| 1173562 | 32749  | 32764  | N/A   | N/A   | CTCTACTCTTGTTTCAT | 96  | C | 221 |
|         | 32788  | 32803  |       |       |                   |     |   |     |
| 1173566 | 64282  | 64297  | N/A   | N/A   | GATTTTAACTTGCGGG  | 92  | C | 222 |
| 1173570 | 82200  | 82215  | N/A   | N/A   | GATATTAGCTCATGGA  | 29  | C | 223 |
| 1173574 | 124949 | 124964 | N/A   | N/A   | ATTTTAAATGCGGCT   | 67  | C | 224 |
| 1173578 | 133199 | 133214 | N/A   | N/A   | ATTAACAAAGGATCCA  | 85  | C | 225 |
| 1173582 | 142021 | 142036 | N/A   | N/A   | GTAACATAAGAGCTGG  | 54  | C | 226 |
| 1173586 | 181272 | 181287 | N/A   | N/A   | CTATTTAATGGTTCCT  | 32  | C | 227 |
| 1173590 | 199325 | 199340 | N/A   | N/A   | GTAATTACAAGTCACC  | 112 | C | 228 |
| 1173594 | 225073 | 225088 | N/A   | N/A   | GTATTATTGACCTGGT  | 23  | C | 229 |
| 1173598 | 243314 | 243329 | N/A   | N/A   | GAAATTAAAAGACGGC  | 32  | C | 230 |
| 1173602 | 263020 | 263035 | N/A   | N/A   | GCTCATACCAAAGTGA  | 67  | C | 231 |
|         | 263102 | 263117 |       |       |                   |     |   |     |
| 1173606 | 290259 | 290274 | N/A   | N/A   | GTAAATATGAGCCTCC  | 47  | C | 232 |
| 1173610 | 316788 | 316803 | N/A   | N/A   | TGATATAAGGGTCCTA  | 65  | C | 233 |
| 1173614 | 332850 | 332865 | N/A   | N/A   | ATTCAGCCTAACAGGC  | 93  | C | 234 |
|         | 338128 | 338143 |       |       |                   |     |   |     |
| 1173618 | 332936 | 332951 | N/A   | N/A   | TAAGTTGCTTGCCAA   | 54  | C | 235 |
|         | 338214 | 338229 |       |       |                   |     |   |     |
| 1173622 | 333003 | 333018 | N/A   | N/A   | TTCTCCTAACCGCTCT  | 45  | C | 236 |
|         | 338281 | 338296 |       |       |                   |     |   |     |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1173626 | 333050 | 333065 | N/A  | N/A  | CCACACGGGCACACTG  | 49  | C | 237 |
|         | 338328 | 338343 |      |      |                   |     |   |     |
| 1173630 | 333092 | 333107 | N/A  | N/A  | GCCCAGCGACTTCCAT  | 80  | C | 238 |
|         | 338370 | 338385 |      |      |                   |     |   |     |
| 1173634 | 333150 | 333165 | N/A  | N/A  | GAAATGATCACCCGGA  | 44  | C | 239 |
|         | 338428 | 338443 |      |      |                   |     |   |     |
| 1173638 | 333294 | 333309 | N/A  | N/A  | AACAACTTCTGGAGCA  | 72  | C | 240 |
|         | 338572 | 338587 |      |      |                   |     |   |     |
| 1173642 | 333393 | 333408 | N/A  | N/A  | CAAGATCACCCCTGTGA | 111 | C | 241 |
|         | 338671 | 338686 |      |      |                   |     |   |     |
| 1173646 | 347111 | 347126 | N/A  | N/A  | GTAATTAGTTAATCTT  | 72  | C | 242 |
| 1173650 | 353385 | 353400 | N/A  | N/A  | GCTGTAGTTCAACTCC  | 47  | C | 243 |
|         | 354805 | 354820 |      |      |                   |     |   |     |
| 1173654 | 376319 | 376334 | N/A  | N/A  | GATAGTAAGGATCAGT  | 78  | C | 244 |
| 1173658 | 390453 | 390468 | N/A  | N/A  | CTTATATTGAATGAGT  | 82  | C | 245 |
| 1173662 | 398647 | 398662 | N/A  | N/A  | GCAGAACAAAGACGGC  | 84  | C | 246 |
| 1173666 | 434509 | 434524 | N/A  | N/A  | TCTGGGTTTACTTGTA  | 67  | C | 247 |
|         | 434551 | 434566 |      |      |                   |     |   |     |
| 1173670 | 462706 | 462721 | N/A  | N/A  | AGGAGTTTGTGATGC   | 55  | C | 248 |
|         | 462733 | 462748 |      |      |                   |     |   |     |
| 1173674 | 482706 | 482721 | N/A  | N/A  | GCAGAATAGTTATCTA  | 73  | C | 249 |
| 1173678 | 505610 | 505625 | N/A  | N/A  | GTAATTACAAGGCTCT  | 70  | C | 250 |
| 1173682 | 520356 | 520371 | N/A  | N/A  | CCATTTAAGTTTTCGG  | 84  | C | 251 |
| 1173686 | 536558 | 536573 | N/A  | N/A  | AATACTAAGGTTTCTC  | 71  | C | 252 |
| 1173690 | 550902 | 550917 | N/A  | N/A  | GATTTTACTGAACCAA  | 67  | C | 253 |
| 1173172 | 559744 | 559759 | 8733 | 8748 | ACAACTAAGGCCAGTG  | 79  | D | 254 |
| 1173385 | 217576 | 217591 | 542  | 557  | CCTGTAATGTTCCGGA  | 46  | D | 255 |
| 1173389 | 217982 | 217997 | 948  | 963  | CTTCGATCACATCCCC  | 46  | D | 256 |
| 1173392 | 221983 | 221998 | 1393 | 1408 | CTCCGTATATCCAGGC  | 71  | D | 257 |
| 1173396 | 222142 | 222157 | 1552 | 1567 | TTCTTTAATGCGCTGT  | 32  | D | 258 |
| 1173400 | 222271 | 222286 | 1681 | 1696 | GGAGTCGCTGGCATCA  | 69  | D | 259 |
| 1173404 | 288680 | 288695 | 2075 | 2090 | ATCTATTGGAGAAGTG  | 4   | D | 260 |
| 1173408 | 324490 | 324505 | 2213 | 2228 | GATTTGCAATGAACTC  | 39  | D | 261 |
| 1173412 | 457284 | 457299 | 2409 | 2424 | AATGGGTTAGTAGTAC  | 61  | D | 262 |
| 1173416 | 533770 | 533785 | 3009 | 3024 | TCCAGATAGTGGTCTT  | 92  | D | 263 |
| 1173420 | 554158 | 554173 | 3147 | 3162 | GGAGAAGTATCCGGGT  | 87  | D | 264 |
| 1173424 | 554364 | 554379 | 3353 | 3368 | ATTACTAATGCACCGT  | 72  | D | 265 |
| 1173428 | 554494 | 554509 | 3483 | 3498 | TGAAATCACGATCCCC  | 71  | D | 266 |
| 1173432 | 554673 | 554688 | 3662 | 3677 | CGTATATTAACCTCAG  | 65  | D | 267 |
| 1173436 | 554775 | 554790 | 3764 | 3779 | TCATATTGGAGCAACT  | 97  | D | 268 |
| 1173440 | 554886 | 554901 | 3875 | 3890 | AAGCTAATGTGCTTCC  | 135 | D | 269 |
| 1173444 | 555066 | 555081 | 4055 | 4070 | GTAACAATTCCTGCAG  | 90  | D | 270 |
| 1173448 | 555808 | 555823 | 4797 | 4812 | CATAGTACCTTCAACA  | 72  | D | 271 |

|         |        |        |       |       |                  |     |   |     |
|---------|--------|--------|-------|-------|------------------|-----|---|-----|
| 1173452 | 556169 | 556184 | 5158  | 5173  | TCTGATACATGGGCCA | 81  | D | 272 |
| 1173456 | 556244 | 556259 | 5233  | 5248  | TTTAGATTATCAGGTA | 91  | D | 273 |
| 1173460 | 556395 | 556410 | 5384  | 5399  | ACATAGATATAGACTG | 62  | D | 274 |
| 1173464 | 556516 | 556531 | 5505  | 5520  | GTGCTATAGTGGTGCT | 76  | D | 275 |
| 1173468 | 556576 | 556591 | 5565  | 5580  | ATCTATTAGCCTATCC | 54  | D | 276 |
| 1173472 | 556794 | 556809 | 5783  | 5798  | AGCATAAACTCTTGGC | 82  | D | 277 |
| 1173476 | 557315 | 557330 | 6304  | 6319  | TCAGAAATGCCTACGG | 50  | D | 278 |
| 1173480 | 557746 | 557761 | 6735  | 6750  | GCAGTAAGAGGCCTCT | 79  | D | 279 |
| 1173484 | 558216 | 558231 | 7205  | 7220  | CTTAGGATGCCACTTT | 71  | D | 280 |
| 1173488 | 558499 | 558514 | 7488  | 7503  | AATAATCTATCACGGG | 57  | D | 281 |
| 1173492 | 558619 | 558634 | 7608  | 7623  | TCTGGATACTGTAGGT | 64  | D | 282 |
| 1173496 | 559046 | 559061 | 8035  | 8050  | ATGAGGTTGTACTTGC | 55  | D | 283 |
| 1173500 | 559568 | 559583 | 8557  | 8572  | TACTTTAGTGCTTGTG | 88  | D | 284 |
| 1173507 | 559907 | 559922 | 8896  | 8911  | AGCTACAAAGACACGA | 78  | D | 285 |
| 1173511 | 560128 | 560143 | 9117  | 9132  | GGAAATACTCTCGCAA | 69  | D | 286 |
| 1173515 | 560429 | 560444 | 9418  | 9433  | AGCAACCACTTTACTG | 69  | D | 287 |
| 1173519 | 560846 | 560861 | 9835  | 9850  | GCTACGGAGAGATGCT | 76  | D | 288 |
| 1173523 | 561106 | 561121 | 10095 | 10110 | GCATTTTAGTTCGGTT | 63  | D | 289 |
| 1173527 | 561250 | 561265 | 10239 | 10254 | TTATTTATGGCGACCG | 64  | D | 290 |
| 1173531 | 561369 | 561384 | 10358 | 10373 | TGTTATCACCACTCTC | 96  | D | 291 |
| 1173535 | 561788 | 561803 | 10777 | 10792 | GCCTTTACCTAACAGC | 84  | D | 292 |
| 1173539 | 561913 | 561928 | 10902 | 10917 | ACAAATTATCGCCTTT | 88  | D | 293 |
| 1173543 | 561961 | 561976 | 10950 | 10965 | TATTATAATAGGCTGG | 88  | D | 294 |
| 1173547 | 562153 | 562168 | 11142 | 11157 | CTGCTAATGCCGACAG | 76  | D | 295 |
| 1173551 | 562198 | 562213 | 11187 | 11202 | AACAGGTTTCCAGTAC | 93  | D | 296 |
| 1173555 | 562471 | 562486 | 11460 | 11475 | CTCTATATATCACAGC | 91  | D | 297 |
| 1173559 | 17940  | 17955  | N/A   | N/A   | TGCACATAACTTCACT | 123 | D | 298 |
|         | 274222 | 274237 |       |       |                  |     |   |     |
| 1173563 | 45763  | 45778  | N/A   | N/A   | CTTATTTAGGCCCTCA | 133 | D | 299 |
| 1173567 | 65073  | 65088  | N/A   | N/A   | ATAAGTAAAGTGCTG  | 97  | D | 300 |
| 1173571 | 95035  | 95050  | N/A   | N/A   | CTTTTAAAGTACCGCG | 41  | D | 301 |
| 1173575 | 126046 | 126061 | N/A   | N/A   | GTAATTTAGCCCCAGT | 50  | D | 302 |
| 1173579 | 133482 | 133497 | N/A   | N/A   | TATATTTAGTTGGTAG | 47  | D | 303 |
| 1173583 | 145334 | 145349 | N/A   | N/A   | GTAACGAATTATTACG | 641 | D | 304 |
| 1173587 | 185170 | 185185 | N/A   | N/A   | ATTAACATAAGACTGT | 53  | D | 305 |
| 1173591 | 207617 | 207632 | N/A   | N/A   | GATATTAGAGCCAGTT | 64  | D | 306 |
| 1173595 | 225892 | 225907 | N/A   | N/A   | TTAAGTAAATCTAGGC | 32  | D | 307 |
| 1173599 | 249394 | 249409 | N/A   | N/A   | ATTATTAGTATGTCCA | 18  | D | 308 |
| 1173603 | 271179 | 271194 | N/A   | N/A   | TATATTAGTGACAGTC | 19  | D | 309 |
| 1173607 | 305747 | 305762 | N/A   | N/A   | TTATTTAATATACGGT | 69  | D | 310 |
| 1173611 | 322667 | 322682 | N/A   | N/A   | GATTTTtaggttccgt | 42  | D | 311 |
| 1173615 | 332856 | 332871 | N/A   | N/A   | CATGACATTCAGCCTA | 66  | D | 312 |
|         | 338134 | 338149 |       |       |                  |     |   |     |

|         |        |        |     |     |                   |     |   |     |
|---------|--------|--------|-----|-----|-------------------|-----|---|-----|
| 1173619 | 332966 | 332981 | N/A | N/A | CATGCCGTACCTGAGA  | 57  | D | 313 |
|         | 338244 | 338259 |     |     |                   |     |   |     |
| 1173623 | 333027 | 333042 | N/A | N/A | CTTAACACACCTCATC  | 97  | D | 314 |
|         | 338305 | 338320 |     |     |                   |     |   |     |
| 1173627 | 333064 | 333079 | N/A | N/A | ACAACTAGTGCATTCC  | 43  | D | 315 |
|         | 338342 | 338357 |     |     |                   |     |   |     |
| 1173631 | 333099 | 333114 | N/A | N/A | GCTTAGAGCCCAGCGA  | 74  | D | 316 |
|         | 338377 | 338392 |     |     |                   |     |   |     |
| 1173635 | 333228 | 333243 | N/A | N/A | GCCTAAACCGAAAACC  | 100 | D | 317 |
|         | 338506 | 338521 |     |     |                   |     |   |     |
| 1173639 | 333321 | 333336 | N/A | N/A | GGAAGTTAGAACATGA  | 48  | D | 318 |
|         | 338599 | 338614 |     |     |                   |     |   |     |
| 1173643 | 333398 | 333413 | N/A | N/A | CCTTACAAGATCACCC  | 68  | D | 319 |
|         | 338676 | 338691 |     |     |                   |     |   |     |
| 1173647 | 353230 | 353245 | N/A | N/A | CATAGAAGTAATCTTC  | 80  | D | 320 |
|         | 354645 | 354660 |     |     |                   |     |   |     |
| 1173651 | 353457 | 353472 | N/A | N/A | ACATTCAAGTAAGAGTT | 86  | D | 321 |
|         | 354877 | 354892 |     |     |                   |     |   |     |
| 1173655 | 377931 | 377946 | N/A | N/A | ATTACGAAGTTCTCTG  | 96  | D | 322 |
| 1173659 | 394789 | 394804 | N/A | N/A | GTAATATTGAGATCAC  | 58  | D | 323 |
| 1173663 | 403696 | 403711 | N/A | N/A | GTAATATTGCAATCCC  | 77  | D | 324 |
| 1173667 | 443967 | 443982 | N/A | N/A | TTTACCAAGAGTCCAG  | 54  | D | 325 |
|         | 444361 | 444376 |     |     |                   |     |   |     |
| 1173671 | 467649 | 467664 | N/A | N/A | CAAATTACTTCTCCGA  | 69  | D | 326 |
| 1173675 | 487429 | 487444 | N/A | N/A | GTATTAGTTGGTGTG   | 80  | D | 327 |
| 1173679 | 507704 | 507719 | N/A | N/A | TTATCGATAATTCCT   | 77  | D | 328 |
| 1173683 | 524076 | 524091 | N/A | N/A | ATCGCTAAACATCCTA  | 46  | D | 329 |
| 1173687 | 539374 | 539389 | N/A | N/A | ATTAACCTAGGTGGGC  | 81  | D | 330 |
| 1173691 | 552751 | 552766 | N/A | N/A | GATAACTTACCATCCC  | 92  | D | 331 |

**Table 2.** Reduction of PSD3 RNA by 3-10-3 cEt modified oligonucleotides with uniform phosphorothioate internucleoside linkages

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3') | PSD3 (% UTC) RTS41435 | AID | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|---------------------|-----------------------|-----|-----------|
| 1173403      | 288679                  | 288694                 | 2074                    | 2089                   | TCTATTGGAGAAGTGT    | 7                     | E   | 181       |
| 1173403      | 288679                  | 288694                 | 2074                    | 2089                   | TCTATTGGAGAAGTGT    | 5                     | F   | 181       |
| 1173403      | 288679                  | 288694                 | 2074                    | 2089                   | TCTATTGGAGAAGTGT    | 3                     | G   | 181       |
| 1173403      | 288679                  | 288694                 | 2074                    | 2089                   | TCTATTGGAGAAGTGT    | 4                     | H   | 181       |
| 1173403      | 288679                  | 288694                 | 2074                    | 2089                   | TCTATTGGAGAAGTGT    | 4                     | I   | 181       |
| 1173404      | 288680                  | 288695                 | 2075                    | 2090                   | ATCTATTGGAGAAGTG    | 4                     | I   | 260       |
| 1408351      | 225893                  | 225908                 | N/A                     | N/A                    | TTTAAGTAAATCTAGG    | 61                    | I   | 332       |

|         |        |        |      |      |                   |    |   |     |
|---------|--------|--------|------|------|-------------------|----|---|-----|
| 1408352 | 225891 | 225906 | N/A  | N/A  | TAAGTAAATCTAGGCA  | 20 | I | 333 |
| 1408353 | 235212 | 235227 | N/A  | N/A  | TTATACACAATTTAGC  | 28 | I | 334 |
|         | 235285 | 235300 |      |      |                   |    |   |     |
| 1408354 | 235211 | 235226 | N/A  | N/A  | TATACACAATTTAGCT  | 37 | I | 335 |
|         | 235284 | 235299 |      |      |                   |    |   |     |
| 1408355 | 217985 | 218000 | 951  | 966  | CTGCTTCGATCACATC  | 16 | I | 336 |
| 1408356 | 235210 | 235225 | N/A  | N/A  | ATACACAATTTAGCTC  | 7  | I | 337 |
|         | 235283 | 235298 |      |      |                   |    |   |     |
| 1408357 | 235281 | 235296 | N/A  | N/A  | ACACAATTTAGCTCTG  | 4  | I | 338 |
| 1408358 | 235280 | 235295 | N/A  | N/A  | CACAATTTAGCTCTGT  | 21 | I | 339 |
| 1408359 | 235279 | 235294 | N/A  | N/A  | ACAATTTAGCTCTGTT  | 49 | I | 340 |
| 1408360 | 235208 | 235223 | N/A  | N/A  | ACACAATTTAGCTCTA  | 4  | I | 341 |
| 1408361 | 235207 | 235222 | N/A  | N/A  | CACAATTTAGCTCTAT  | 7  | I | 342 |
| 1408362 | 235206 | 235221 | N/A  | N/A  | ACAATTTAGCTCTATT  | 18 | I | 343 |
| 1408363 | 243317 | 243332 | N/A  | N/A  | GCAGAAATTTAAAAGAC | 27 | I | 344 |
| 1408364 | 243316 | 243331 | N/A  | N/A  | CAGAAATTTAAAAGACG | 51 | I | 345 |
| 1408365 | 217666 | 217681 | 632  | 647  | TCTGTGTTTTACGACT  | 8  | I | 346 |
| 1408366 | 222147 | 222162 | 1557 | 1572 | CCACCTTCTTTAATGC  | 11 | I | 347 |
| 1408368 | 222137 | 222152 | 1547 | 1562 | TAATGCGCTGTTGTAT  | 11 | I | 348 |
| 1408369 | 288684 | 288699 | 2079 | 2094 | AAATATCTATTGGAGA  | 30 | I | 349 |
| 1408370 | 288674 | 288689 | 2069 | 2084 | TGGAGAAGTGTATTAA  | 5  | I | 350 |
| 1408371 | 288685 | 288700 | 2080 | 2095 | AAAATATCTATTGGAG  | 14 | I | 351 |
| 1408372 | 288675 | 288690 | 2070 | 2085 | TTGGAGAAGTGTATTA  | 6  | I | 352 |
| 1408373 | 290672 | 290687 | 2151 | 2166 | TTAAGAAGCATTATTG  | 80 | I | 353 |
| 1408374 | 290684 | 290699 | 2163 | 2178 | TGTAGATCGGTATTAA  | 26 | I | 354 |
| 1408375 | 82205  | 82220  | N/A  | N/A  | TTTCAGATATTAGCTC  | 6  | I | 355 |
| 1408376 | 82195  | 82210  | N/A  | N/A  | TAGCTCATGGAAAGCA  | 70 | I | 356 |
| 1408377 | 181277 | 181292 | N/A  | N/A  | ATCTTCTATTTAATGG  | 36 | I | 357 |
| 1408378 | 217656 | 217671 | 622  | 637  | ACGACTGGCAGTGTCC  | 36 | I | 358 |
| 1408379 | 188563 | 188578 | N/A  | N/A  | CAAGGGTATTATTGAT  | 46 | I | 359 |
| 1408380 | 188553 | 188568 | N/A  | N/A  | ATTGATAGGCGAGAAC  | 53 | I | 360 |
| 1408381 | 189833 | 189848 | N/A  | N/A  | CTAAAATTATCGAACC  | 64 | I | 361 |
| 1408382 | 189823 | 189838 | N/A  | N/A  | CGAACCATCTTTTGCT  | 70 | I | 362 |
| 1408383 | 225078 | 225093 | N/A  | N/A  | CGTGTGTATTATTGAC  | 6  | I | 363 |
| 1408384 | 225068 | 225083 | N/A  | N/A  | ATTGACCTGGTAAATT  | 66 | I | 364 |
| 1408385 | 217988 | 218003 | 954  | 969  | GAGCTGCTTCGATCAC  | 19 | I | 365 |
| 1408386 | 225897 | 225912 | N/A  | N/A  | AGGATTTAAGTAAATC  | 95 | I | 366 |
| 1408387 | 225887 | 225902 | N/A  | N/A  | TAAATCTAGGCAATAG  | 61 | I | 367 |
| 1408388 | 235277 | 235292 | N/A  | N/A  | AATTTAGCTCTGTAA   | 41 | I | 368 |
| 1408389 | 235204 | 235219 | N/A  | N/A  | AATTTAGCTCTATTAA  | 70 | I | 369 |
| 1408390 | 243319 | 243334 | N/A  | N/A  | GTGCAGAAATTTAAAAG | 58 | I | 370 |
| 1408391 | 243309 | 243324 | N/A  | N/A  | TAAAAGACGGCCTCTG  | 46 | I | 371 |
| 1408392 | 249399 | 249414 | N/A  | N/A  | TAGGTATTATTAGTAT  | 29 | I | 372 |
| 1408393 | 249389 | 249404 | N/A  | N/A  | TAGTATGTCCACCTGG  | 22 | I | 373 |
| 1408394 | 263014 | 263029 | N/A  | N/A  | ACCAAAGTGATATGAA  | 12 | I | 374 |

|         |        |        |      |      |                  |     |   |     |
|---------|--------|--------|------|------|------------------|-----|---|-----|
|         | 263055 | 263070 |      |      |                  |     |   |     |
| 1408395 | 263045 | 263060 | N/A  | N/A  | TATGAATGGTATGATA | 62  | I | 375 |
| 1408396 | 263004 | 263019 | N/A  | N/A  | TATGAATGGTATGATG | 55  | I | 376 |
| 1408397 | 271184 | 271199 | N/A  | N/A  | AATCTTATATTAGTGA | 62  | I | 377 |
| 1408398 | 271174 | 271189 | N/A  | N/A  | TAGTGACAGTCAGAAC | 39  | I | 378 |
| 1408399 | 217978 | 217993 | 944  | 959  | GATCACATCCCCCTGG | 73  | I | 379 |
| 1408405 | 218087 | 218102 | 1053 | 1068 | AAATCTATAGGATGCT | 12  | I | 380 |
| 1408411 | 218077 | 218092 | 1043 | 1058 | GATGCTGGGTCTCTCT | 14  | I | 381 |
| 1411079 | 88242  | 88257  | N/A  | N/A  | TCAGAGAAGGAAGGTA | 26  | I | 382 |
| 1411093 | 88246  | 88261  | N/A  | N/A  | GGGCTCAGAGAAGGAA | 87  | I | 383 |
| 1411096 | 88245  | 88260  | N/A  | N/A  | GGCTCAGAGAAGGAAG | 68  | I | 384 |
| 1411181 | 88238  | 88253  | N/A  | N/A  | AGAAGGAAGGTATTCA | 88  | I | 385 |
| 1411183 | 94388  | 94403  | N/A  | N/A  | CAGGCTGCTATTAAAG | 68  | I | 386 |
| 1411191 | 94382  | 94397  | N/A  | N/A  | GCTATTAAAGACATGC | 73  | I | 387 |
| 1411214 | 94389  | 94404  | N/A  | N/A  | TCAGGCTGCTATTAAA | 42  | I | 388 |
| 1411226 | 88241  | 88256  | N/A  | N/A  | CAGAGAAGGAAGGTAT | 30  | I | 389 |
| 1411227 | 94392  | 94407  | N/A  | N/A  | TTCTCAGGCTGCTATT | 66  | I | 390 |
| 1411308 | 88240  | 88255  | N/A  | N/A  | AGAGAAGGAAGGTATT | 46  | I | 391 |
| 1411346 | 88244  | 88259  | N/A  | N/A  | GCTCAGAGAAGGAAGG | 45  | I | 392 |
| 1411391 | 94386  | 94401  | N/A  | N/A  | GGCTGCTATTAAAGAC | 73  | I | 393 |
| 1411414 | 88248  | 88263  | N/A  | N/A  | CCGGGCTCAGAGAAGG | 71  | I | 394 |
| 1411416 | 94390  | 94405  | N/A  | N/A  | CTCAGGCTGCTATTAA | 56  | I | 395 |
| 1173403 | 288679 | 288694 | 2074 | 2089 | TCTATTGGAGAAGTGT | 3   | J | 181 |
| 1408263 | 271178 | 271193 | N/A  | N/A  | ATATTAGTGACAGTCA | 17  | J | 396 |
| 1408296 | 218079 | 218094 | 1045 | 1060 | AGGATGCTGGGTCTCT | 7   | J | 397 |
| 1408346 | 225071 | 225086 | N/A  | N/A  | ATTATTGACCTGGTAA | 41  | J | 398 |
| 1408572 | 217621 | 217636 | 587  | 602  | GAAGTGAAGAACTAGA | 28  | J | 399 |
| 1408578 | 290577 | 290592 | N/A  | N/A  | ACCTTATTATCACTAA | 69  | J | 400 |
| 1408584 | 290749 | 290764 | N/A  | N/A  | TAAAAGCAGAGATAAG | 86  | J | 401 |
| 1408599 | 82210  | 82225  | N/A  | N/A  | GATACTTTCAGATATT | 51  | J | 402 |
| 1408620 | 189948 | 189963 | N/A  | N/A  | CAGATATCCATTCTTC | 57  | J | 403 |
| 1408661 | 235236 | 235251 | N/A  | N/A  | CAAAATAGATTTAAGT | 113 | J | 404 |
|         | 235309 | 235324 |      |      |                  |     |   |     |
| 1408704 | 262970 | 262985 | N/A  | N/A  | ACCAATATTAATGTCA | 9   | J | 405 |
| 1408711 | 263159 | 263174 | N/A  | N/A  | ACCTTTCAAATGTACT | 47  | J | 406 |
| 1409134 | 61016  | 61031  | N/A  | N/A  | GACCATTATATATGTG | 86  | J | 407 |
| 1409143 | 522999 | 523014 | N/A  | N/A  | TAGTATACAGTCCCTA | 70  | J | 408 |
| 1409154 | 229864 | 229879 | N/A  | N/A  | CAATATTGTGTGTCTC | 12  | J | 409 |
| 1409241 | 193663 | 193678 | N/A  | N/A  | GATATATACCAAGTGG | 14  | J | 410 |
| 1409258 | 558641 | 558656 | 7630 | 7645 | GCAGAAGGCTGCCAC  | 54  | J | 411 |
| 1409277 | 206184 | 206199 | N/A  | N/A  | TATAGTTCATCGGATT | 61  | J | 412 |
| 1409286 | 300320 | 300335 | N/A  | N/A  | ACCTAACTCACTGTCA | 67  | J | 413 |
| 1409289 | 155902 | 155917 | N/A  | N/A  | AGTTATTATATGGCTG | 16  | J | 414 |
| 1409294 | 419952 | 419967 | N/A  | N/A  | GACGATAATTCTGTCA | 76  | J | 415 |
| 1409316 | 202276 | 202291 | N/A  | N/A  | GACAATACAAACCACT | 43  | J | 416 |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1409326 | 342926 | 342941 | N/A  | N/A  | GATAATGTGAAGCTTA  | 3   | J | 417 |
| 1409413 | 142097 | 142112 | N/A  | N/A  | GTAATAAAGCCTCCCA  | 51  | J | 418 |
| 1409442 | 9709   | 9724   | N/A  | N/A  | AGGTAGAAAGATTTC   | 103 | J | 419 |
| 1409453 | 288860 | 288875 | N/A  | N/A  | GACTAGAATGAAGTAA  | 44  | J | 420 |
| 1409456 | 204092 | 204107 | N/A  | N/A  | AAAGATTCTATCTCAG  | 62  | J | 421 |
| 1409478 | 274368 | 274383 | N/A  | N/A  | TCAAATCTTACGACA   | 47  | J | 422 |
| 1409495 | 222028 | 222043 | 1438 | 1453 | GTCCAAAATGGTTTCA  | 7   | J | 423 |
| 1409509 | 211638 | 211653 | N/A  | N/A  | ACATACCAGATCATGT  | 91  | J | 424 |
| 1409513 | 198418 | 198433 | N/A  | N/A  | CCTAGAAAAGTCATCT  | 64  | J | 425 |
| 1409530 | 226629 | 226644 | N/A  | N/A  | TCTAATTTTGAGCCA   | 51  | J | 426 |
| 1409565 | 267539 | 267554 | N/A  | N/A  | GACAAACATACTCTTA  | 21  | J | 427 |
| 1409614 | 458772 | 458787 | N/A  | N/A  | ATGTATGAAGAAGGGT  | 6   | J | 428 |
| 1409683 | 537898 | 537913 | N/A  | N/A  | ACATTAGGTGGGCTGG  | 34  | J | 429 |
| 1409690 | 259410 | 259425 | N/A  | N/A  | GTATCAAAGTACACTT  | 32  | J | 430 |
| 1409734 | 292710 | 292725 | N/A  | N/A  | CCTGAATATGACAGAG  | 11  | J | 431 |
| 1409740 | 127337 | 127352 | N/A  | N/A  | GAAGTTTAAATACCTC  | 108 | J | 432 |
| 1409847 | 471937 | 471952 | N/A  | N/A  | ATTATTTAGAGACTTC  | 48  | J | 433 |
| 1409910 | 282175 | 282190 | N/A  | N/A  | CTTAACATTACATGGC  | 31  | J | 434 |
| 1409923 | 248800 | 248815 | N/A  | N/A  | ACTAATTGGATGGCTT  | 9   | J | 435 |
| 1409941 | 401272 | 401287 | N/A  | N/A  | TCACAAC TAGATTCAA | 16  | J | 436 |
| 1410005 | 187684 | 187699 | N/A  | N/A  | ACTGATTGAATTCTTC  | 30  | J | 437 |
| 1410031 | 251702 | 251717 | N/A  | N/A  | AATTACCTAAAGGTCA  | 64  | J | 438 |
| 1410049 | 278814 | 278829 | N/A  | N/A  | AGGGATTGAATTGTCA  | 16  | J | 439 |
| 1410085 | 452911 | 452926 | N/A  | N/A  | GCAATATATTGATTG   | 59  | J | 440 |
| 1410093 | 365698 | 365713 | N/A  | N/A  | GTAATATTAAAGCCAG  | 5   | J | 441 |
| 1410144 | 436706 | 436721 | N/A  | N/A  | CACTATAGTGTCTTCT  | 39  | J | 442 |
| 1410166 | 220197 | 220212 | N/A  | N/A  | GAACCTAGCACACTTT  | 72  | J | 443 |
| 1410193 | 508289 | 508304 | N/A  | N/A  | GATTTTAAAGAGTCCAC | 1   | J | 444 |
| 1410215 | 95573  | 95588  | N/A  | N/A  | AGCAAATCATGTGTTG  | 7   | J | 445 |
| 1410240 | 233327 | 233342 | N/A  | N/A  | CTTCTAAATAGAGTAA  | 52  | J | 446 |
| 1410246 | 180706 | 180721 | N/A  | N/A  | AAGGTTTGACCGTGGC  | 26  | J | 447 |
| 1410258 | 188939 | 188954 | N/A  | N/A  | GTGTATATAAGTTTGT  | 13  | J | 448 |
| 1410297 | 181927 | 181942 | N/A  | N/A  | GAATTGATAACAGGTA  | 4   | J | 449 |
| 1410317 | 108279 | 108294 | N/A  | N/A  | GTCTATTAACTGTGGA  | 34  | J | 450 |
| 1410322 | 308572 | 308587 | N/A  | N/A  | CCCTATTAAATGTTC   | 61  | J | 451 |
| 1410369 | 208712 | 208727 | N/A  | N/A  | ATTAAGTAGTCATCTG  | 45  | J | 452 |
| 1410384 | 388078 | 388093 | N/A  | N/A  | GAAATACTATGTTTAC  | 45  | J | 453 |
| 1410400 | 490657 | 490672 | N/A  | N/A  | ACCATATGGAGTTTCT  | 32  | J | 454 |
| 1410436 | 244765 | 244780 | N/A  | N/A  | GGTAATTTATGAGTTA  | 8   | J | 455 |
| 1410485 | 553016 | 553031 | N/A  | N/A  | GCAAATTCTGTTTTGA  | 42  | J | 456 |
| 1410531 | 215893 | 215908 | N/A  | N/A  | AAATACAGTGTACTCA  | 68  | J | 457 |
| 1410565 | 255337 | 255352 | N/A  | N/A  | GTCACATAAAGTAGGG  | 51  | J | 458 |
| 1410590 | 240211 | 240226 | N/A  | N/A  | AAGGTAACTTTTCTC   | 40  | J | 459 |
| 1411112 | 560514 | 560529 | 9503 | 9518 | TCCTTATACACCTAAG  | 14  | J | 460 |
| 1411113 | 285152 | 285167 | 1787 | 1802 | CCAAAATTTTCAGTGCT | 8   | J | 461 |

|         |        |        |       |       |                  |     |   |     |
|---------|--------|--------|-------|-------|------------------|-----|---|-----|
| 1411145 | N/A    | N/A    | 2005  | 2020  | GAAATACCTGAGTGAC | 5   | J | 462 |
| 1411146 | 557368 | 557383 | 6357  | 6372  | TTTAATTAGACACTGC | 7   | J | 463 |
| 1411173 | 556445 | 556460 | 5434  | 5449  | TACCATTCAATGTATA | 21  | J | 464 |
| 1411184 | 562018 | 562033 | 11007 | 11022 | GGTAAAGAAATGTTCC | 45  | J | 465 |
| 1411193 | 555858 | 555873 | 4847  | 4862  | TCTAATTCACTGGAAC | 74  | J | 466 |
| 1411301 | 559824 | 559839 | 8813  | 8828  | AATATACCAAACATGC | 54  | J | 467 |
| 1411361 | N/A    | N/A    | 2180  | 2195  | TTCCAATATTGTGGCC | 44  | J | 468 |
| 1411362 | 222159 | 222174 | 1569  | 1584  | TCCAAGAAGTACCAC  | 4   | J | 469 |
| 1411404 | 559425 | 559440 | 8414  | 8429  | GGACTAATTACAACAA | 10  | J | 470 |
| 1411426 | 554650 | 554665 | 3639  | 3654  | TTACTAAAACACAGT  | 97  | J | 471 |
| 1411435 | 559091 | 559106 | 8080  | 8095  | TACCACTATATATACT | 39  | J | 472 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 5   | K | 181 |
| 1408262 | 271180 | 271195 | N/A   | N/A   | TTATATTAGTGACAGT | 30  | K | 473 |
| 1408293 | 218080 | 218095 | 1046  | 1061  | TAGGATGCTGGGTCTC | 12  | K | 474 |
| 1408338 | 217658 | 217673 | 624   | 639   | TTACGACTGGCAGTGT | 10  | K | 475 |
| 1408345 | 225072 | 225087 | N/A   | N/A   | TATTATTGACCTGGTA | 17  | K | 476 |
| 1408548 | 288629 | 288644 | 2024  | 2039  | CAAGAGAGAATGCTTT | 71  | K | 477 |
| 1408566 | 290757 | 290772 | N/A   | N/A   | TTTGAACATAAAAGCA | 56  | K | 478 |
| 1408577 | 290597 | 290612 | N/A   | N/A   | GCTTTTCACTGTTGGA | 28  | K | 479 |
| 1408598 | 82240  | 82255  | N/A   | N/A   | TAATAATATCTGTACT | 87  | K | 480 |
| 1408655 | 235249 | 235264 | N/A   | N/A   | CTGAAATAGACAACAA | 19  | K | 481 |
|         | 235322 | 235337 |       |       |                  |     |   |     |
| 1408694 | 263160 | 263175 | N/A   | N/A   | TACCTTTCAAATGTAC | 90  | K | 482 |
| 1408722 | 262999 | 263014 | N/A   | N/A   | ATGGTATGATGGTTCT | 12  | K | 483 |
| 1409126 | 274734 | 274749 | N/A   | N/A   | TCCAAATTTTACCATC | 10  | K | 484 |
| 1409135 | 180803 | 180818 | N/A   | N/A   | ATTAATTTGCTTGGGT | 21  | K | 485 |
| 1409163 | 206217 | 206232 | N/A   | N/A   | GCACTAAGGGTCTTAT | 38  | K | 486 |
| 1409183 | 388404 | 388419 | N/A   | N/A   | CATTTAAGTGAAGTCT | 19  | K | 487 |
| 1409215 | 244766 | 244781 | N/A   | N/A   | AGGTAATTTATGAGTT | 9   | K | 488 |
| 1409220 | 189161 | 189176 | N/A   | N/A   | TTTACTGGACAGATGA | 28  | K | 489 |
| 1409230 | 523004 | 523019 | N/A   | N/A   | CTTACTAGTATACAGT | 66  | K | 490 |
| 1409291 | 190141 | 190156 | N/A   | N/A   | ATTTATAGACAAGGGC | 12  | K | 491 |
| 1409315 | 401303 | 401318 | N/A   | N/A   | CCACAATCATGGTGTT | 65  | K | 492 |
| 1409345 | 282374 | 282389 | N/A   | N/A   | TCAATATCAATGGCAG | 7   | K | 493 |
| 1409414 | 128224 | 128239 | N/A   | N/A   | GATATTTTATTTGTCC | 60  | K | 494 |
| 1409474 | 109177 | 109192 | N/A   | N/A   | CTATTTACACCCTTCA | 34  | K | 495 |
| 1409479 | 215894 | 215909 | N/A   | N/A   | GAAATACAGTGTACTC | 43  | K | 496 |
| 1409543 | 233376 | 233391 | N/A   | N/A   | AATATTACTCTTGACA | 25  | K | 497 |
| 1409561 | 255721 | 255736 | N/A   | N/A   | GATTACATGGCAACAC | 21  | K | 498 |
| 1409581 | 292724 | 292739 | N/A   | N/A   | ACCAAACACATGATCC | 26  | K | 499 |
| 1409618 | 289503 | 289518 | N/A   | N/A   | GAATCTAGTCTCAGTG | 40  | K | 500 |
| 1409648 | 539533 | 539548 | N/A   | N/A   | TGTAATACAGAATCTC | 14  | K | 501 |
| 1409649 | 202308 | 202323 | N/A   | N/A   | ATATTTCCAACCAGTA | 35  | K | 502 |
| 1409661 | 198422 | 198437 | N/A   | N/A   | ATGACCTAGAAAAGTC | 109 | K | 503 |
| 1409675 | 259413 | 259428 | N/A   | N/A   | CAGGTATCAAAGTACA | 15  | K | 504 |

|         |        |        |       |       |                    |    |   |     |
|---------|--------|--------|-------|-------|--------------------|----|---|-----|
| 1409699 | 308869 | 308884 | N/A   | N/A   | GCCAAAGTAATTCCAT   | 70 | K | 505 |
| 1409736 | 240215 | 240230 | N/A   | N/A   | GTCTAAGGTAAACTTT   | 33 | K | 506 |
| 1409742 | 508658 | 508673 | N/A   | N/A   | GTAATAATTAACCTACC  | 78 | K | 507 |
| 1409761 | 204094 | 204109 | N/A   | N/A   | GTAAAGATTCTATCTC   | 75 | K | 508 |
| 1409764 | 267777 | 267792 | N/A   | N/A   | GAAACTTTGGTTGAGA   | 12 | K | 509 |
| 1409806 | 226630 | 226645 | N/A   | N/A   | TTCTAATTTTGGAGCC   | 57 | K | 510 |
| 1409837 | 553189 | 553204 | N/A   | N/A   | TATCATATATGTTGCA   | 38 | K | 511 |
| 1409871 | 248880 | 248895 | N/A   | N/A   | CAAGTTTACAACCCAA   | 21 | K | 512 |
| 1409876 | 211639 | 211654 | N/A   | N/A   | TACATACCAGATCATG   | 84 | K | 513 |
| 1409898 | 62310  | 62325  | N/A   | N/A   | CTGTATTAATAGATTC   | 90 | K | 514 |
| 1409899 | 208720 | 208735 | N/A   | N/A   | GGTTATATATTAAGTA   | 58 | K | 515 |
| 1409911 | 300331 | 300346 | N/A   | N/A   | AAGATAAACACACCTA   | 73 | K | 516 |
| 1409935 | 453170 | 453185 | N/A   | N/A   | CATATAGTACACATGA   | 91 | K | 517 |
| 1409946 | 366240 | 366255 | N/A   | N/A   | ATCATATGAAAGCCAA   | 5  | K | 518 |
| 1409980 | 95593  | 95608  | N/A   | N/A   | AACCATATATGCCTCA   | 12 | K | 519 |
| 1410004 | 10808  | 10823  | N/A   | N/A   | GCAAATCACAAGATGA   | 92 | K | 520 |
| 1410071 | 181929 | 181944 | N/A   | N/A   | CAGAATTGATAACAGG   | 6  | K | 521 |
| 1410120 | 420049 | 420064 | N/A   | N/A   | ATTTATTTAGGCATCG   | 41 | K | 522 |
| 1410213 | 278988 | 279003 | N/A   | N/A   | CATTATCTATGGCATT   | 46 | K | 523 |
| 1410225 | 459483 | 459498 | N/A   | N/A   | CCAATTAAGTCAATCC   | 2  | K | 524 |
| 1410227 | 142889 | 142904 | N/A   | N/A   | GATATTCCAAAAGTCA   | 79 | K | 525 |
| 1410233 | 222039 | 222054 | 1449  | 1464  | AAAGAAGTGTGTCCA    | 4  | K | 526 |
| 1410318 | 194092 | 194107 | N/A   | N/A   | ACTTATTCATCCTAGC   | 75 | K | 527 |
| 1410332 | 437697 | 437712 | N/A   | N/A   | GAAGTTTTAAGAGTGA   | 52 | K | 528 |
| 1410335 | 187717 | 187732 | N/A   | N/A   | CTATTGAAGGTCTCTG   | 74 | K | 529 |
| 1410352 | 155904 | 155919 | N/A   | N/A   | GAAGTTATTATATGGC   | 6  | K | 530 |
| 1410363 | 251925 | 251940 | N/A   | N/A   | GTTTTAAGTTATCTCA   | 5  | K | 531 |
| 1410457 | 491509 | 491524 | N/A   | N/A   | ATGTAAAGGTGGTTCA   | 29 | K | 532 |
| 1410497 | 229865 | 229880 | N/A   | N/A   | TCAATATTGTGTGTCT   | 9  | K | 533 |
| 1410503 | 472182 | 472197 | N/A   | N/A   | ACCAATTTCAACCTGA   | 37 | K | 534 |
| 1410513 | 343144 | 343159 | N/A   | N/A   | ATTAATTTGTATCCTA   | 45 | K | 535 |
| 1410555 | 220850 | 220865 | N/A   | N/A   | TAAGATGATGCTCCTC   | 69 | K | 536 |
| 1411133 | 555893 | 555908 | 4882  | 4897  | ACTTAGACACTACCAT   | 32 | K | 537 |
| 1411155 | 559850 | 559865 | 8839  | 8854  | CTCAAACACACTCAGT   | 44 | K | 538 |
| 1411161 | 324519 | 324534 | 2242  | 2257  | GAAATCAACACCCTCA   | 60 | K | 539 |
| 1411245 | 556453 | 556468 | 5442  | 5457  | TAGCAAGGTACCATTC   | 23 | K | 540 |
| 1411249 | 560613 | 560628 | 9602  | 9617  | CTTAAGGTCTTATGTT   | 70 | K | 541 |
| 1411281 | 558667 | 558682 | 7656  | 7671  | ATGCAATGGGCCAATT   | 54 | K | 542 |
| 1411307 | 285153 | 285168 | 1788  | 1803  | TCCAAAATTTTCAAGTGC | 12 | K | 543 |
| 1411333 | 557369 | 557384 | 6358  | 6373  | GTTTAATTAGACACTG   | 10 | K | 544 |
| 1411372 | 554658 | 554673 | 3647  | 3662  | GCTAGAATTTACTAAA   | 72 | K | 545 |
| 1411386 | 222160 | 222175 | 1570  | 1585  | CTCCAAGAAGTACCA    | 10 | K | 546 |
| 1411411 | 562030 | 562045 | 11019 | 11034 | GAAAACCTTTGAAGGTA  | 23 | K | 547 |
| 1411419 | 559427 | 559442 | 8416  | 8431  | ATGGACTAATTACAAC   | 42 | K | 548 |
| 1411422 | 559095 | 559110 | 8084  | 8099  | ACAATACCACTATATA   | 15 | K | 549 |

|         |        |        |      |      |                   |    |   |     |
|---------|--------|--------|------|------|-------------------|----|---|-----|
| 1173403 | 288679 | 288694 | 2074 | 2089 | TCTATTGGAGAAGTGT  | 6  | L | 181 |
| 1408261 | 271181 | 271196 | N/A  | N/A  | CTTATATTAGTGACAG  | 13 | L | 550 |
| 1408290 | 218081 | 218096 | 1047 | 1062 | ATAGGATGCTGGGTCT  | 14 | L | 551 |
| 1408328 | 217659 | 217674 | 625  | 640  | TTTACGACTGGCAGTG  | 11 | L | 552 |
| 1408344 | 225074 | 225089 | N/A  | N/A  | TGTATTATTGACCTGG  | 7  | L | 553 |
| 1408446 | 222162 | 222177 | 1572 | 1587 | CTCTCCAAGAACTGAC  | 13 | L | 554 |
| 1408562 | 288630 | 288645 | 2025 | 2040 | ACAAGAGAGAATGCTT  | 30 | L | 555 |
| 1408565 | 290797 | 290812 | N/A  | N/A  | ATGTAGAGAATGGGAA  | 23 | L | 556 |
| 1408588 | 290609 | 290624 | N/A  | N/A  | AAGCATGAATTCGCTT  | 97 | L | 557 |
| 1408596 | 82250  | 82265  | N/A  | N/A  | ATCAACAGCATAATAA  | 90 | L | 558 |
| 1408660 | 235329 | 235344 | N/A  | N/A  | GAAATGACTGAAATAG  | 17 | L | 559 |
| 1408693 | 263190 | 263205 | N/A  | N/A  | TATTTCTAAAGCCAGA  | 35 | L | 560 |
| 1408721 | 263019 | 263034 | N/A  | N/A  | CTCATACCAAAGTGAT  | 81 | L | 561 |
|         | 263101 | 263116 |      |      |                   |    |   |     |
| 1409091 | 181930 | 181945 | N/A  | N/A  | GCAGAATTGATAACAG  | 8  | L | 562 |
| 1409155 | 259419 | 259434 | N/A  | N/A  | AGATATCAGGTATCAA  | 58 | L | 563 |
| 1409208 | 282805 | 282820 | N/A  | N/A  | CATTTACAAGTTCCCT  | 49 | L | 564 |
| 1409222 | 255724 | 255739 | N/A  | N/A  | CTTGATTACATGGCAA  | 45 | L | 565 |
| 1409234 | 204097 | 204112 | N/A  | N/A  | CCAGTAAAGATTCTAT  | 64 | L | 566 |
| 1409240 | 491544 | 491559 | N/A  | N/A  | TCATATACAATGACCA  | 20 | L | 567 |
| 1409246 | 289540 | 289555 | N/A  | N/A  | GCAATACTGAAGCTAA  | 16 | L | 568 |
| 1409253 | 143745 | 143760 | N/A  | N/A  | GAAGATTCAAGTCCTA  | 62 | L | 569 |
| 1409265 | 180806 | 180821 | N/A  | N/A  | CCTATTAATTTGCTTG  | 49 | L | 570 |
| 1409269 | 190142 | 190157 | N/A  | N/A  | AATTTATAGACAAGGG  | 20 | L | 571 |
| 1409314 | 129330 | 129345 | N/A  | N/A  | ATAACCAACAGATCCC  | 31 | L | 572 |
| 1409384 | 366332 | 366347 | N/A  | N/A  | AAGAATATGTCAGTGG  | 8  | L | 573 |
| 1409417 | 541339 | 541354 | N/A  | N/A  | GCTCAAATTTGTGTGC  | 91 | L | 574 |
| 1409462 | 215895 | 215910 | N/A  | N/A  | GGAAATACAGTGTACT  | 44 | L | 575 |
| 1409502 | 279255 | 279270 | N/A  | N/A  | GAAGAATCTCAAGGAG  | 72 | L | 576 |
| 1409517 | 460169 | 460184 | N/A  | N/A  | CAAATATATACTCTA   | 65 | L | 577 |
| 1409550 | 158168 | 158183 | N/A  | N/A  | GCACATTTATAGCATA  | 16 | L | 578 |
| 1409552 | 194130 | 194145 | N/A  | N/A  | TAAATTATACTCACCC  | 52 | L | 579 |
| 1409610 | 402245 | 402260 | N/A  | N/A  | GACTATAAATGGAAGC  | 20 | L | 580 |
| 1409625 | 343191 | 343206 | N/A  | N/A  | GTTTATACTTTCCACT  | 13 | L | 581 |
| 1409651 | 267779 | 267794 | N/A  | N/A  | CAGAACTTTGGTTGA   | 68 | L | 582 |
| 1409656 | 472185 | 472200 | N/A  | N/A  | GATACCAATTTCAACC  | 56 | L | 583 |
| 1409658 | 220871 | 220886 | N/A  | N/A  | TGGCATAAACTGGACC  | 82 | L | 584 |
| 1409709 | 206294 | 206309 | N/A  | N/A  | GTTTCATATCTTTGGAT | 56 | L | 585 |
| 1409715 | 292764 | 292779 | N/A  | N/A  | AGTATATCGCACACAT  | 50 | L | 586 |
| 1409753 | 553745 | 553760 | N/A  | N/A  | GAATCTAGAACACTCA  | 93 | L | 587 |
| 1409763 | 454955 | 454970 | N/A  | N/A  | AAGTATGGACACATGG  | 29 | L | 588 |
| 1409804 | 202309 | 202324 | N/A  | N/A  | AATATTTCCAACCAGT  | 62 | L | 589 |
| 1409818 | 274776 | 274791 | N/A  | N/A  | GATACAAGAGGCTGAA  | 24 | L | 590 |
| 1409944 | 252006 | 252021 | N/A  | N/A  | ATGATAGAGGACTGTT  | 12 | L | 591 |
| 1409953 | 556460 | 556475 | 5449 | 5464 | AATACTGTAGCAAGGT  | 11 | L | 592 |

|         |        |        |       |       |                   |     |   |     |
|---------|--------|--------|-------|-------|-------------------|-----|---|-----|
| 1409972 | 96459  | 96474  | N/A   | N/A   | GCAGATAGTAACCTCT  | 47  | L | 593 |
| 1410000 | 509969 | 509984 | N/A   | N/A   | GTCTATTAATTCATGG  | 36  | L | 594 |
| 1410021 | 208850 | 208865 | N/A   | N/A   | GCAAAGATGCTTTTCC  | 80  | L | 595 |
| 1410096 | 438094 | 438109 | N/A   | N/A   | AAAGTTTTACAGCACA  | 19  | L | 596 |
| 1410107 | 309554 | 309569 | N/A   | N/A   | TACTTAATTCCTGTCA  | 62  | L | 597 |
| 1410111 | 300426 | 300441 | N/A   | N/A   | AGTATAAAGCTATCCT  | 23  | L | 598 |
| 1410122 | 62480  | 62495  | N/A   | N/A   | AATGTATAGAGCTGTG  | 107 | L | 599 |
| 1410184 | 187718 | 187733 | N/A   | N/A   | TCTATTGAAGGTCTCT  | 58  | L | 600 |
| 1410236 | 226643 | 226658 | N/A   | N/A   | CTCTAATTATCCTTTC  | 40  | L | 601 |
| 1410254 | 249177 | 249192 | N/A   | N/A   | CATGATGATAATATTC  | 111 | L | 602 |
| 1410282 | 388406 | 388421 | N/A   | N/A   | ATCATTTAAGTGAAGT  | 46  | L | 603 |
| 1410300 | 523006 | 523021 | N/A   | N/A   | CACTTACTAGTATACA  | 51  | L | 604 |
| 1410340 | 233395 | 233410 | N/A   | N/A   | TCTATACTAAAGACTT  | 49  | L | 605 |
| 1410346 | 198427 | 198442 | N/A   | N/A   | CATGTATGACCTAGAA  | 57  | L | 606 |
| 1410373 | 189165 | 189180 | N/A   | N/A   | ATAATTTACTGGACAG  | 20  | L | 607 |
| 1410381 | 13296  | 13311  | N/A   | N/A   | GTTACTTTAAAGGTCA  | 81  | L | 608 |
| 1410391 | 229866 | 229881 | N/A   | N/A   | CTCAATATTGTGTGTC  | 12  | L | 609 |
| 1410402 | 423462 | 423477 | N/A   | N/A   | AGAACATTAAGTCCAA  | 56  | L | 610 |
| 1410501 | 211640 | 211655 | N/A   | N/A   | CTACATACCAGATCAT  | 75  | L | 611 |
| 1410523 | 244767 | 244782 | N/A   | N/A   | TAGGTAATTTATGAGT  | 24  | L | 612 |
| 1410544 | 109485 | 109500 | N/A   | N/A   | ATCTTTTAATTGGTAC  | 32  | L | 613 |
| 1410588 | 240679 | 240694 | N/A   | N/A   | GAAACTTCGGCTCACT  | 14  | L | 614 |
| 1411105 | 324520 | 324535 | 2243  | 2258  | AGAAATCAACACCCTC  | 46  | L | 615 |
| 1411157 | 285185 | 285200 | 1820  | 1835  | TACCATTACTGAGATT  | 8   | L | 616 |
| 1411192 | 222041 | 222056 | 1451  | 1466  | ATAAAGAAGTGTTGTC  | 10  | L | 617 |
| 1411287 | 559154 | 559169 | 8143  | 8158  | AGCATAAAGTCTTATT  | 88  | L | 618 |
| 1411354 | 557370 | 557385 | 6359  | 6374  | AGTTTAATTAGACACT  | 95  | L | 619 |
| 1411357 | 559928 | 559943 | 8917  | 8932  | ACAATTCAAACCTCTCT | 47  | L | 620 |
| 1411359 | 559439 | 559454 | 8428  | 8443  | GCTATATTTTTTATGG  | 71  | L | 621 |
| 1411376 | 554661 | 554676 | 3650  | 3665  | CCAGCTAGAATTTACT  | 38  | L | 622 |
| 1411400 | 558690 | 558705 | 7679  | 7694  | CTCTATGAAGACATTC  | 37  | L | 623 |
| 1411441 | 560614 | 560629 | 9603  | 9618  | TCTTAAGGTCTTATGT  | 44  | L | 624 |
| 1411448 | 555896 | 555911 | 4885  | 4900  | ACCACTTAGACACTAC  | 16  | L | 625 |
| 1411450 | 562035 | 562050 | 11024 | 11039 | GTGGAGAAAACTTTGA  | 23  | L | 626 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5   | M | 181 |
| 1408260 | 271182 | 271197 | N/A   | N/A   | TCTTATATTAGTGACA  | 35  | M | 627 |
| 1408286 | 218083 | 218098 | 1049  | 1064  | CTATAGGATGCTGGGT  | 9   | M | 628 |
| 1408319 | 217660 | 217675 | 626   | 641   | TTTTACGACTGGCAGT  | 11  | M | 629 |
| 1408343 | 225075 | 225090 | N/A   | N/A   | GTGTATTATTGACCTG  | 6   | M | 630 |
| 1408415 | 222232 | 222247 | 1642  | 1657  | AGAATAGCCCATCACG  | 9   | M | 631 |
| 1408501 | 222042 | 222057 | 1452  | 1467  | TATAAAGAAGTGTTGT  | 43  | M | 632 |
| 1408547 | 288669 | 288684 | 2064  | 2079  | AAGTGTATTAATACTC  | 82  | M | 633 |
| 1408583 | 290799 | 290814 | N/A   | N/A   | CCATGTAGAGAATGGG  | 89  | M | 634 |
| 1408595 | 82260  | 82275  | N/A   | N/A   | GAATGCTTAAATCAAC  | 87  | M | 635 |
| 1408654 | 235372 | 235387 | N/A   | N/A   | TATAGACTGCAATTC   | 24  | M | 636 |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1408691 | 249264 | 249279 | N/A  | N/A  | CTACAGCTTATCCTGC  | 55  | M | 637 |
| 1408692 | 263200 | 263215 | N/A  | N/A  | CTGAGATGAATATTTTC | 46  | M | 638 |
| 1408720 | 263029 | 263044 | N/A  | N/A  | ATAGTATCAGCTCATA  | 50  | M | 639 |
| 1409136 | 198457 | 198472 | N/A  | N/A  | CACTAGCAGTGATCTG  | 69  | M | 640 |
| 1409167 | 220975 | 220990 | N/A  | N/A  | ATTACTGGAATCCACA  | 57  | M | 641 |
| 1409182 | 541498 | 541513 | N/A  | N/A  | GATTTTGAGGCTCTCT  | 50  | M | 642 |
| 1409184 | 267814 | 267829 | N/A  | N/A  | GCTATTAGATTTACAC  | 40  | M | 643 |
| 1409194 | 97097  | 97112  | N/A  | N/A  | TTAATCACAATCTCCA  | 7   | M | 644 |
| 1409219 | 204158 | 204173 | N/A  | N/A  | ACTTTTAACAAACAGG  | 45  | M | 645 |
| 1409279 | 366439 | 366454 | N/A  | N/A  | ACATATGACAGAGTTC  | 16  | M | 646 |
| 1409330 | 274779 | 274794 | N/A  | N/A  | TGGGATACAAGAGGCT  | 32  | M | 647 |
| 1409393 | 344743 | 344758 | N/A  | N/A  | AATTTAGTATCCTTCA  | 4   | M | 648 |
| 1409420 | 391181 | 391196 | N/A  | N/A  | TAGGATTAAGGAGTTC  | 6   | M | 649 |
| 1409441 | 16857  | 16872  | N/A  | N/A  | ACAGAATGATAACCCA  | 108 | M | 650 |
| 1409459 | 259452 | 259467 | N/A  | N/A  | GAAATTATCTTCTGTC  | 90  | M | 651 |
| 1409470 | 310545 | 310560 | N/A  | N/A  | TCTAATTTAGTTCTGC  | 24  | M | 652 |
| 1409525 | 244769 | 244784 | N/A  | N/A  | TATAGGTAATTTATGA  | 95  | M | 653 |
| 1409527 | 143950 | 143965 | N/A  | N/A  | AAGTACAAATGAGTCA  | 25  | M | 654 |
| 1409541 | 209074 | 209089 | N/A  | N/A  | GTTCATACTTTACTGC  | 44  | M | 655 |
| 1409560 | 187719 | 187734 | N/A  | N/A  | TTCTATTGAAGGTCTC  | 60  | M | 656 |
| 1409598 | 189503 | 189518 | N/A  | N/A  | AAGCAATTCACCCTTC  | 73  | M | 657 |
| 1409612 | 109872 | 109887 | N/A  | N/A  | CATGATAAATGCTACT  | 64  | M | 658 |
| 1409620 | 438335 | 438350 | N/A  | N/A  | GTGTAGAAACTGCTGG  | 27  | M | 659 |
| 1409634 | 181089 | 181104 | N/A  | N/A  | ACAAATCTCAGTTCCC  | 19  | M | 660 |
| 1409641 | 190235 | 190250 | N/A  | N/A  | GCAGAAGAGTTCTTGT  | 65  | M | 661 |
| 1409643 | 558703 | 558718 | 7692 | 7707 | TTAATGACATTCTCTC  | 19  | M | 662 |
| 1409652 | 233418 | 233433 | N/A  | N/A  | ACTATTCAATACATCT  | 10  | M | 663 |
| 1409681 | 256327 | 256342 | N/A  | N/A  | GCATTTAGTTATCTAG  | 46  | M | 664 |
| 1409706 | 211659 | 211674 | N/A  | N/A  | TTGTAGATTCCTCAGG  | 64  | M | 665 |
| 1409749 | 510574 | 510589 | N/A  | N/A  | ATCTAATTACTATCCA  | 43  | M | 666 |
| 1409760 | 181961 | 181976 | N/A  | N/A  | TATATTGATGGATGTA  | 13  | M | 667 |
| 1409841 | 426279 | 426294 | N/A  | N/A  | ACATTAAGATTGCTGC  | 22  | M | 668 |
| 1409848 | 553761 | 553776 | N/A  | N/A  | CCAGATGGAACACCAT  | 40  | M | 669 |
| 1409870 | 158523 | 158538 | N/A  | N/A  | GAAAATTTGCTTAGAC  | 10  | M | 670 |
| 1409927 | 460170 | 460185 | N/A  | N/A  | TCAAACATATACTCT   | 55  | M | 671 |
| 1409928 | 252076 | 252091 | N/A  | N/A  | GATCTTGAAGATGCCA  | 40  | M | 672 |
| 1409963 | 279470 | 279485 | N/A  | N/A  | GCAATAGTATACTTTG  | 98  | M | 673 |
| 1409974 | 206447 | 206462 | N/A  | N/A  | GCAATGTAAACTTGA   | 71  | M | 674 |
| 1409979 | 456755 | 456770 | N/A  | N/A  | GCATAGAACTAGGTGT  | 73  | M | 675 |
| 1410006 | 129362 | 129377 | N/A  | N/A  | GAAGTAGTAAGTCATT  | 42  | M | 676 |
| 1410018 | 292765 | 292780 | N/A  | N/A  | AAGTATATCGCACACA  | 10  | M | 677 |
| 1410043 | 62815  | 62830  | N/A  | N/A  | CCTATTAAAGACTCTC  | 90  | M | 678 |
| 1410056 | 242135 | 242150 | N/A  | N/A  | ACAACTTAAAGTCCTC  | 12  | M | 679 |
| 1410129 | 478979 | 478994 | N/A  | N/A  | AGATTATTAGGACACA  | 5   | M | 680 |
| 1410199 | 404955 | 404970 | N/A  | N/A  | CAGATAAAGGAGGCTT  | 51  | M | 681 |

|         |        |        |       |       |                   |     |   |     |
|---------|--------|--------|-------|-------|-------------------|-----|---|-----|
| 1410337 | 194131 | 194146 | N/A   | N/A   | GTAAATTATACTCACC  | 64  | M | 682 |
| 1410338 | 525748 | 525763 | N/A   | N/A   | AATATTTAGTATTGGG  | 25  | M | 683 |
| 1410353 | 202311 | 202326 | N/A   | N/A   | CTAATATTTCCAACCA  | 42  | M | 684 |
| 1410418 | 289709 | 289724 | N/A   | N/A   | GGCTAATGGTGACAGA  | 58  | M | 685 |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 4   | M | 686 |
| 1410445 | 215920 | 215935 | N/A   | N/A   | TATCATGAAAACCCTC  | 101 | M | 687 |
| 1410489 | 226682 | 226697 | N/A   | N/A   | GACACAAAGGAACCCA  | 12  | M | 688 |
| 1410553 | 491546 | 491561 | N/A   | N/A   | GATCATATACAATGAC  | 64  | M | 689 |
| 1410554 | 282990 | 283005 | N/A   | N/A   | CCGGATTTTATACTTT  | 84  | M | 690 |
| 1410571 | 229867 | 229882 | N/A   | N/A   | TCTCAATATTGTGTGT  | 19  | M | 691 |
| 1410580 | 300427 | 300442 | N/A   | N/A   | GAGTATAAAGCTATCC  | 34  | M | 692 |
| 1411099 | 559470 | 559485 | 8459  | 8474  | ATGATATGGTGGGTAC  | 28  | M | 693 |
| 1411115 | 559158 | 559173 | 8147  | 8162  | TTCTAGCATAAAAGTCT | 49  | M | 694 |
| 1411158 | 555899 | 555914 | 4888  | 4903  | CATACCACTTAGACAC  | 21  | M | 695 |
| 1411164 | 324521 | 324536 | 2244  | 2259  | GAGAAATCAACACCCT  | 31  | M | 696 |
| 1411180 | 554670 | 554685 | 3659  | 3674  | ATATTAACCTCCAGCTA | 50  | M | 697 |
| 1411208 | 557383 | 557398 | 6372  | 6387  | AAAAGTATTGCTCAGT  | 12  | M | 698 |
| 1411209 | 556462 | 556477 | 5451  | 5466  | GAAATACTGTAGCAAG  | 11  | M | 699 |
| 1411237 | 559929 | 559944 | 8918  | 8933  | CACAATTCAAACTCTC  | 30  | M | 700 |
| 1411272 | 562045 | 562060 | 11034 | 11049 | GAAATGATTGGTGGAG  | 15  | M | 701 |
| 1411298 | 290648 | 290663 | 2127  | 2142  | AGGCAATGGACTCCAT  | 54  | M | 702 |
| 1411319 | 560615 | 560630 | 9604  | 9619  | ATCTTAAGGTCTTATG  | 18  | M | 703 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 4   | N | 181 |
| 1408283 | 218084 | 218099 | 1050  | 1065  | TCTATAGGATGCTGGG  | 16  | N | 704 |
| 1408304 | 217662 | 217677 | 628   | 643   | TGTTTTACGACTGGCA  | 4   | N | 705 |
| 1408342 | 225076 | 225091 | N/A   | N/A   | TGTGTATTATTGACCT  | 5   | N | 706 |
| 1408561 | 288670 | 288685 | 2065  | 2080  | GAAGTGTATTA AAACT | 19  | N | 707 |
| 1408594 | 82280  | 82295  | N/A   | N/A   | GTAAGCACTTAATATT  | 20  | N | 708 |
| 1408653 | 235382 | 235397 | N/A   | N/A   | ACAACTATTTTATAGA  | 77  | N | 709 |
| 1408690 | 249274 | 249289 | N/A   | N/A   | ACACCCTGAACTACAG  | 48  | N | 710 |
| 1408703 | 263030 | 263045 | N/A   | N/A   | AATAGTATCAGCTCAT  | 16  | N | 711 |
| 1408733 | 271259 | 271274 | N/A   | N/A   | GTCTTTAAAATCAGTT  | 46  | N | 712 |
| 1409093 | 480013 | 480028 | N/A   | N/A   | AGTATTAATTATCCCT  | 18  | N | 713 |
| 1409142 | 23017  | 23032  | N/A   | N/A   | GATTATAAACACCTCA  | 85  | N | 714 |
| 1409148 | 293013 | 293028 | N/A   | N/A   | GTCAAACAGACACTAA  | 56  | N | 715 |
| 1409181 | 182206 | 182221 | N/A   | N/A   | CGTGAATACAACAACA  | 76  | N | 716 |
| 1409255 | 259517 | 259532 | N/A   | N/A   | CTTTTAGTCATTTCCC  | 7   | N | 717 |
| 1409344 | 460171 | 460186 | N/A   | N/A   | CTCAAACCTATATACTC | 36  | N | 718 |
| 1409365 | 189591 | 189606 | N/A   | N/A   | CTTACAACGGTACTTA  | 36  | N | 719 |
| 1409386 | 233421 | 233436 | N/A   | N/A   | GTAACCTATTCAATACA | 84  | N | 720 |
| 1409396 | 161477 | 161492 | N/A   | N/A   | GACTATTATTCCACAC  | 7   | N | 721 |
| 1409418 | 301012 | 301027 | N/A   | N/A   | GATATTCAATGTGCTC  | 5   | N | 722 |
| 1409419 | 347109 | 347124 | N/A   | N/A   | AATTAGTTAATCTTCC  | 9   | N | 723 |
| 1409457 | 252132 | 252147 | N/A   | N/A   | TGAATTAAGAACAAGG  | 5   | N | 724 |
| 1409466 | 291133 | 291148 | N/A   | N/A   | ACTAGTAAAAGACTAG  | 89  | N | 725 |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1409497 | 541574 | 541589 | N/A  | N/A  | GCATTAGAAGAAGCAG  | 59  | N | 726 |
| 1409504 | 279471 | 279486 | N/A  | N/A  | GGCAATAGTATACTTT  | 95  | N | 727 |
| 1409515 | 310547 | 310562 | N/A  | N/A  | CCTCTAATTTAGTTCT  | 21  | N | 728 |
| 1409545 | 256329 | 256344 | N/A  | N/A  | CAGCATTTAGTTATCT  | 17  | N | 729 |
| 1409576 | 209102 | 209117 | N/A  | N/A  | ACACTAGTAGAATGTG  | 96  | N | 730 |
| 1409592 | 426280 | 426295 | N/A  | N/A  | AACATTAAGATTGCTG  | 20  | N | 731 |
| 1409597 | 560636 | 560651 | 9625 | 9640 | TAGAATATTCTGGCTC  | 17  | N | 732 |
| 1409628 | 202312 | 202327 | N/A  | N/A  | CCTAATATTTCCAACC  | 66  | N | 733 |
| 1409637 | 217188 | 217203 | N/A  | N/A  | GCATATTCACACAGAT  | 32  | N | 734 |
| 1409674 | 283006 | 283021 | N/A  | N/A  | GAATATGCCCAAACCA  | 46  | N | 735 |
| 1409758 | 112127 | 112142 | N/A  | N/A  | AAGATTTTAACTGTCG  | 55  | N | 736 |
| 1409827 | 229903 | 229918 | N/A  | N/A  | CATTTAGAGGCATTGC  | 6   | N | 737 |
| 1409845 | 63020  | 63035  | N/A  | N/A  | GCAAGAATAGTATGTT  | 106 | N | 738 |
| 1409865 | 181090 | 181105 | N/A  | N/A  | TACAAATCTCAGTTCC  | 37  | N | 739 |
| 1409884 | 456917 | 456932 | N/A  | N/A  | ACAGATTTAGTGATGA  | 34  | N | 740 |
| 1409894 | 391217 | 391232 | N/A  | N/A  | AAGTAGGTGTATTGAT  | 92  | N | 741 |
| 1409903 | 198471 | 198486 | N/A  | N/A  | CTACAGTATCCATTCA  | 37  | N | 742 |
| 1409907 | 190336 | 190351 | N/A  | N/A  | GCTAAGGGTATTGTCC  | 29  | N | 743 |
| 1409937 | 129434 | 129449 | N/A  | N/A  | ACAATAGATCACCAGC  | 79  | N | 744 |
| 1409943 | 206501 | 206516 | N/A  | N/A  | TCACAATGAATGGCCA  | 74  | N | 745 |
| 1409961 | 511378 | 511393 | N/A  | N/A  | ACTATTGAATGACTTA  | 26  | N | 746 |
| 1409970 | 97752  | 97767  | N/A  | N/A  | CTCATTAATCAAGGC   | 7   | N | 747 |
| 1409996 | 438442 | 438457 | N/A  | N/A  | ACACTATGATCAGCAA  | 29  | N | 748 |
| 1410015 | 526683 | 526698 | N/A  | N/A  | GCTATACAGGATCTTC  | 24  | N | 749 |
| 1410063 | 290654 | 290669 | 2133 | 2148 | CAGGTAAGGCAATGGA  | 3   | N | 750 |
| 1410073 | 289911 | 289926 | N/A  | N/A  | TCACAAGTTCTACATA  | 34  | N | 751 |
| 1410140 | 194646 | 194661 | N/A  | N/A  | CATCATTAAACATCTCC | 26  | N | 752 |
| 1410153 | 244778 | 244793 | N/A  | N/A  | AGCATAAATTATAGGT  | 20  | N | 753 |
| 1410179 | 227001 | 227016 | N/A  | N/A  | GATGTAATTCACCTGT  | 33  | N | 754 |
| 1410262 | 263253 | 263268 | N/A  | N/A  | AATCTAATTATGGCTA  | 35  | N | 755 |
| 1410279 | 187927 | 187942 | N/A  | N/A  | ACTTTTGAGATTCTGT  | 14  | N | 756 |
| 1410310 | 274873 | 274888 | N/A  | N/A  | GGTAATAAATGCTACA  | 70  | N | 757 |
| 1410348 | 242389 | 242404 | N/A  | N/A  | GTCAAGTAATGAGTTT  | 4   | N | 758 |
| 1410354 | 558717 | 558732 | 7706 | 7721 | GCAGATTCAAGTATTT  | 21  | N | 759 |
| 1410377 | 211664 | 211679 | N/A  | N/A  | CATATTTGTAGATTCC  | 40  | N | 760 |
| 1410382 | 220979 | 220994 | N/A  | N/A  | AGGTATTACTGGAATC  | 43  | N | 761 |
| 1410449 | 366440 | 366455 | N/A  | N/A  | GACATATGACAGAGTT  | 27  | N | 762 |
| 1410459 | 204252 | 204267 | N/A  | N/A  | CCCAAGTATATCTAGA  | 49  | N | 763 |
| 1410466 | 144612 | 144627 | N/A  | N/A  | GATACTACAACACTGG  | 88  | N | 764 |
| 1410494 | 493729 | 493744 | N/A  | N/A  | ACCAATAGGCAAGTTT  | 48  | N | 765 |
| 1410496 | 267815 | 267830 | N/A  | N/A  | AGCTATTAGATTTACA  | 79  | N | 766 |
| 1410520 | 406822 | 406837 | N/A  | N/A  | GCAAAAACACGAGTGG  | 75  | N | 767 |
| 1411083 | 556465 | 556480 | 5454 | 5469 | TCAGAAATACTGTAGC  | 11  | N | 768 |
| 1411087 | 554043 | 554058 | 3032 | 3047 | TTTCATAGCGGGTTTT  | 24  | N | 769 |
| 1411094 | 555901 | 555916 | 4890 | 4905 | AACATACCACCTTAGAC | 27  | N | 770 |

|         |        |        |       |       |                   |     |   |     |
|---------|--------|--------|-------|-------|-------------------|-----|---|-----|
| 1411102 | 557384 | 557399 | 6373  | 6388  | CAAAAGTATTGCTCAG  | 14  | N | 771 |
| 1411116 | 562047 | 562062 | 11036 | 11051 | CTGAAATGATTGGTGG  | 12  | N | 772 |
| 1411134 | 554885 | 554900 | 3874  | 3889  | AGCTAATGTGCTTCCC  | 57  | N | 773 |
| 1411169 | 559472 | 559487 | 8461  | 8476  | AAATGATATGGTGGGT  | 19  | N | 774 |
| 1411210 | 559980 | 559995 | 8969  | 8984  | GTAAC TACCAACACAT | 55  | N | 775 |
| 1411246 | 285263 | 285278 | 1898  | 1913  | CAACATCTGATCTTTT  | 60  | N | 776 |
| 1411321 | 222043 | 222058 | 1453  | 1468  | GTATAAAGAAGTGTTG  | 11  | N | 777 |
| 1411370 | 559163 | 559178 | 8152  | 8167  | GAATTTTCTAGCATAA  | 47  | N | 778 |
| 1411403 | 222233 | 222248 | 1643  | 1658  | TAGAATAGCCCATCAC  | 8   | N | 779 |
| 1411408 | 324522 | 324537 | 2245  | 2260  | GGAGAAATCAACACCC  | 90  | N | 780 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5   | O | 181 |
| 1408282 | 218085 | 218100 | 1051  | 1066  | ATCTATAGGATGCTGG  | 7   | O | 781 |
| 1408292 | 217663 | 217678 | 629   | 644   | GTGTTTTACGACTGGC  | 5   | O | 782 |
| 1408308 | 288676 | 288691 | 2071  | 2086  | ATTGGAGAAGTGTATT  | 9   | O | 783 |
| 1408575 | 290657 | 290672 | 2136  | 2151  | GCACAGGTAAGGCAAT  | 25  | O | 784 |
| 1408593 | 82320  | 82335  | N/A   | N/A   | GGACAAGGTTTTTTGG  | 21  | O | 785 |
| 1408634 | 225093 | 225108 | N/A   | N/A   | AAAAATGTGTGGAAAC  | 60  | O | 786 |
| 1408652 | 235392 | 235407 | N/A   | N/A   | AGTTTTTTGAACAACT  | 87  | O | 787 |
| 1408689 | 249284 | 249299 | N/A   | N/A   | TTTAGAGACCACACCC  | 44  | O | 788 |
| 1408719 | 263039 | 263054 | N/A   | N/A   | TGGTATGATAATAGTA  | 20  | O | 789 |
| 1408732 | 271269 | 271284 | N/A   | N/A   | AGAATGAAGAGTCTTT  | 76  | O | 790 |
| 1409172 | 190337 | 190352 | N/A   | N/A   | GGCTAAGGGTATTGTC  | 70  | O | 791 |
| 1409191 | 279497 | 279512 | N/A   | N/A   | CAGTATACTATTGCC   | 106 | O | 792 |
| 1409272 | 189649 | 189664 | N/A   | N/A   | GTTCAAGGTTTTGTGC  | 42  | O | 793 |
| 1409290 | 256433 | 256448 | N/A   | N/A   | CAAGACAAGCCAGTGG  | 46  | O | 794 |
| 1409309 | 194725 | 194740 | N/A   | N/A   | ACACATTTAACATGTC  | 68  | O | 795 |
| 1409343 | 283198 | 283213 | N/A   | N/A   | AACCATTTACTGTCTA  | 24  | O | 796 |
| 1409349 | 511747 | 511762 | N/A   | N/A   | GAAACTAAAAAGTCCC  | 81  | O | 797 |
| 1409357 | 252381 | 252396 | N/A   | N/A   | GATGATAAATGTAGAT  | 34  | O | 798 |
| 1409363 | 211762 | 211777 | N/A   | N/A   | TTCTTTAGATCATTCA  | 33  | O | 799 |
| 1409387 | 480203 | 480218 | N/A   | N/A   | TGTATATTAACCTCTA  | 49  | O | 800 |
| 1409422 | 291143 | 291158 | N/A   | N/A   | TATTATTTCAACTAGT  | 83  | O | 801 |
| 1409469 | 229905 | 229920 | N/A   | N/A   | AACATTTAGAGGCATT  | 5   | O | 802 |
| 1409496 | 541658 | 541673 | N/A   | N/A   | TGAAATTGGTTACTAG  | 35  | O | 803 |
| 1409507 | 198475 | 198490 | N/A   | N/A   | TAACCTACAGTATCCA  | 51  | O | 804 |
| 1409522 | 285360 | 285375 | N/A   | N/A   | GGTTATTGAAAGGTAA  | 72  | O | 805 |
| 1409556 | 202315 | 202330 | N/A   | N/A   | AACCCTAATATTTCCA  | 42  | O | 806 |
| 1409578 | 493799 | 493814 | N/A   | N/A   | GACAATAATTTGAGAC  | 89  | O | 807 |
| 1409613 | 181094 | 181109 | N/A   | N/A   | ACTATACAAATCTCAG  | 30  | O | 808 |
| 1409616 | 206512 | 206527 | N/A   | N/A   | GTAAATTTCTCTCACA  | 89  | O | 809 |
| 1409636 | 366671 | 366686 | N/A   | N/A   | TAGGAATGAGCTGTCA  | 4   | O | 810 |
| 1409702 | 310815 | 310830 | N/A   | N/A   | CCAAATATTGGTAGTT  | 62  | O | 811 |
| 1409744 | 526767 | 526782 | N/A   | N/A   | AATACCTTAAGCTCTC  | 73  | O | 812 |
| 1409788 | 27335  | 27350  | N/A   | N/A   | CATACTAATATGCTTT  | 87  | O | 813 |
| 1409826 | 324765 | 324780 | N/A   | N/A   | AATTTACTTACCTCAG  | 47  | O | 814 |

|         |        |        |       |       |                   |     |   |     |
|---------|--------|--------|-------|-------|-------------------|-----|---|-----|
| 1409887 | 204884 | 204899 | N/A   | N/A   | TGTCATAACTTCTGGT  | 33  | O | 815 |
| 1409917 | 244779 | 244794 | N/A   | N/A   | CAGCATAAATTATAGG  | 17  | O | 816 |
| 1409919 | 129631 | 129646 | N/A   | N/A   | TAGAATACAAGACACA  | 68  | O | 817 |
| 1409929 | 227004 | 227019 | N/A   | N/A   | GCAGATGTAATTCACC  | 15  | O | 818 |
| 1409945 | 112378 | 112393 | N/A   | N/A   | CTGATATGAGAGATGT  | 9   | O | 819 |
| 1409947 | 217219 | 217234 | N/A   | N/A   | TGTAGAAAGACAGGGC  | 83  | O | 820 |
| 1409956 | 242425 | 242440 | N/A   | N/A   | TAATCTAAGGAGCCAG  | 11  | O | 821 |
| 1409967 | 220999 | 221014 | N/A   | N/A   | CATAAGTCATCCACAT  | 80  | O | 822 |
| 1409969 | 98076  | 98091  | N/A   | N/A   | AATCATTCAACCCTCA  | 40  | O | 823 |
| 1410070 | 407487 | 407502 | N/A   | N/A   | CACATTAAGGACTTT   | 16  | O | 824 |
| 1410077 | 65031  | 65046  | N/A   | N/A   | AGTAAATTATCAATCC  | 105 | O | 825 |
| 1410083 | 164331 | 164346 | N/A   | N/A   | GTTTATTCAAGGACTA  | 17  | O | 826 |
| 1410099 | 426309 | 426324 | N/A   | N/A   | ATGAATAACACTATTC  | 99  | O | 827 |
| 1410104 | 260250 | 260265 | N/A   | N/A   | TCTAATAGGGCACTTC  | 22  | O | 828 |
| 1410113 | 182221 | 182236 | N/A   | N/A   | ACAGAGTAACAACCCC  | 10  | O | 829 |
| 1410131 | 233648 | 233663 | N/A   | N/A   | CTCATTAAGTTCTTCA  | 4   | O | 830 |
| 1410146 | 209207 | 209222 | N/A   | N/A   | CTGAATTAGTCCTACC  | 90  | O | 831 |
| 1410176 | 222044 | 222059 | 1454  | 1469  | AGTATAAAGAAGTGTT  | 6   | O | 832 |
| 1410217 | 268234 | 268249 | N/A   | N/A   | TAAACTTCTATACCCA  | 22  | O | 833 |
| 1410219 | 438491 | 438506 | N/A   | N/A   | CCATTAACATCCTTTC  | 36  | O | 834 |
| 1410269 | 188085 | 188100 | N/A   | N/A   | TCTAATGGAGAGTCCC  | 68  | O | 835 |
| 1410299 | 391218 | 391233 | N/A   | N/A   | GAAGTAGGTGTATTGA  | 68  | O | 836 |
| 1410307 | 456979 | 456994 | N/A   | N/A   | GATATTAATATCCTCT  | 71  | O | 837 |
| 1410361 | 348229 | 348244 | N/A   | N/A   | ACAATATGGGCTTCAA  | 21  | O | 838 |
| 1410450 | 263254 | 263269 | N/A   | N/A   | AAATCTAATTATGGCT  | 76  | O | 839 |
| 1410454 | 145780 | 145795 | N/A   | N/A   | CCAATTACAGATCACA  | 44  | O | 840 |
| 1410470 | 293045 | 293060 | N/A   | N/A   | ATGATTTCGATTTCATA | 87  | O | 841 |
| 1410491 | 289917 | 289932 | N/A   | N/A   | TTATTATCACAAGTTC  | 29  | O | 842 |
| 1410492 | 460809 | 460824 | N/A   | N/A   | AGGAATATAACCAGGG  | 12  | O | 843 |
| 1410507 | 301111 | 301126 | N/A   | N/A   | GATTATGTCATGCTGC  | 14  | O | 844 |
| 1410522 | 274909 | 274924 | N/A   | N/A   | AATTTAGTTTGATCAA  | 91  | O | 845 |
| 1411077 | 555909 | 555924 | 4898  | 4913  | ATCATAATAACATACC  | 17  | O | 846 |
| 1411190 | 557460 | 557475 | 6449  | 6464  | ACACATAATCCAGGGA  | 15  | O | 847 |
| 1411216 | 222234 | 222249 | 1644  | 1659  | CTAGAATAGCCCATCA  | 16  | O | 848 |
| 1411290 | 559473 | 559488 | 8462  | 8477  | TAAATGATATGGTGGG  | 18  | O | 849 |
| 1411324 | 556549 | 556564 | 5538  | 5553  | GAGTTAATATTAGTGA  | 19  | O | 850 |
| 1411363 | 554909 | 554924 | 3898  | 3913  | GAAATGGAATCAGCAC  | 74  | O | 851 |
| 1411364 | 558728 | 558743 | 7717  | 7732  | CAAAGTGCATGCAGA   | 37  | O | 852 |
| 1411383 | 554048 | 554063 | 3037  | 3052  | ATACATTTTCATAGCGG | 23  | O | 853 |
| 1411385 | 562048 | 562063 | 11037 | 11052 | ACTGAAATGATTGGTG  | 67  | O | 854 |
| 1411407 | 560637 | 560652 | 9626  | 9641  | TTAGAATATTCTGGCT  | 25  | O | 855 |
| 1411420 | 560032 | 560047 | 9021  | 9036  | AATAGTTTGAGACTAT  | 88  | O | 856 |
| 1411446 | 559219 | 559234 | 8208  | 8223  | AAAGATTACAAAGGTT  | 13  | O | 857 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5   | P | 181 |
| 1408242 | 217664 | 217679 | 630   | 645   | TGTGTTTTACGACTGG  | 6   | P | 858 |

|         |        |        |      |      |                   |     |   |     |
|---------|--------|--------|------|------|-------------------|-----|---|-----|
| 1408307 | 288677 | 288692 | 2072 | 2087 | TATTGGAGAAGTGTAT  | 15  | P | 859 |
| 1408609 | 181162 | 181177 | N/A  | N/A  | AGAAATTAGTTAAACG  | 86  | P | 860 |
| 1408629 | 189678 | 189693 | N/A  | N/A  | CATAACAGCTACATTT  | 82  | P | 861 |
| 1408633 | 225133 | 225148 | N/A  | N/A  | CGCAGATGAAATTTTA  | 6   | P | 862 |
| 1408651 | 235432 | 235447 | N/A  | N/A  | ACAAAGTAACTTTGCC  | 16  | P | 863 |
| 1408688 | 249334 | 249349 | N/A  | N/A  | AACACGGCAGGCCAGT  | 34  | P | 864 |
| 1408702 | 263040 | 263055 | N/A  | N/A  | ATGGTATGATAATAGT  | 14  | P | 865 |
| 1408731 | 271289 | 271304 | N/A  | N/A  | CCAGCAAAAAAAGGAA  | 91  | P | 866 |
| 1408821 | 218092 | 218107 | 1058 | 1073 | TCTCAAAATCTATAGG  | 24  | P | 867 |
| 1409097 | 367746 | 367761 | N/A  | N/A  | GTCTTAAGAGATTCCC  | 7   | P | 868 |
| 1409104 | 263255 | 263270 | N/A  | N/A  | AAAATCTAATTATGGC  | 101 | P | 869 |
| 1409112 | 233649 | 233664 | N/A  | N/A  | GCTCATTAAAGTTCTTC | 11  | P | 870 |
| 1409159 | 494220 | 494235 | N/A  | N/A  | AGTAAACATTGACAGG  | 11  | P | 871 |
| 1409176 | 460810 | 460825 | N/A  | N/A  | AAGGAATATAACCAGG  | 12  | P | 872 |
| 1409273 | 165660 | 165675 | N/A  | N/A  | GTCTAACACATACTTG  | 19  | P | 873 |
| 1409281 | 528193 | 528208 | N/A  | N/A  | GAAGACAGTATTGCTT  | 59  | P | 874 |
| 1409302 | 348316 | 348331 | N/A  | N/A  | GCTAAGATTATCCGTC  | 8   | P | 875 |
| 1409304 | 202574 | 202589 | N/A  | N/A  | CCAGTAACATCCATTT  | 27  | P | 876 |
| 1409551 | 274910 | 274925 | N/A  | N/A  | GAATTTAGTTTGATCA  | 52  | P | 877 |
| 1409574 | 439154 | 439169 | N/A  | N/A  | GAAACATTGAGACTCA  | 72  | P | 878 |
| 1409586 | 293104 | 293119 | N/A  | N/A  | GCATTAAGGAGAAGGT  | 18  | P | 879 |
| 1409594 | 190413 | 190428 | N/A  | N/A  | TGAATTAGAGATACTG  | 46  | P | 880 |
| 1409608 | 145781 | 145796 | N/A  | N/A  | TCCAATTACAGATCAC  | 36  | P | 881 |
| 1409653 | 68194  | 68209  | N/A  | N/A  | TTAAACTATGCAGTCC  | 100 | P | 882 |
| 1409672 | 29562  | 29577  | N/A  | N/A  | ACATATTAATGTCTCA  | 79  | P | 883 |
| 1409810 | 194966 | 194981 | N/A  | N/A  | ACATTATCTCAGAAGG  | 26  | P | 884 |
| 1409833 | 301257 | 301272 | N/A  | N/A  | CCCATATGACAATTCC  | 5   | P | 885 |
| 1409892 | 209497 | 209512 | N/A  | N/A  | AATAGTACAGGTGAGA  | 83  | P | 886 |
| 1409895 | 98134  | 98149  | N/A  | N/A  | GAATATTTACAATGCG  | 18  | P | 887 |
| 1409921 | 407648 | 407663 | N/A  | N/A  | GCCAATTTTATAGCCA  | 26  | P | 888 |
| 1409922 | 511991 | 512006 | N/A  | N/A  | TAGGTATAGAACTGGA  | 8   | P | 889 |
| 1409940 | 227249 | 227264 | N/A  | N/A  | TCAAATCGCACTTCAA  | 10  | P | 890 |
| 1409985 | 198476 | 198491 | N/A  | N/A  | CTAACCTACAGTATCC  | 66  | P | 891 |
| 1410012 | 289935 | 289950 | N/A  | N/A  | ATTTATTCTAGTACCA  | 13  | P | 892 |
| 1410034 | 268373 | 268388 | N/A  | N/A  | GCTAATTCAAACACTG  | 38  | P | 893 |
| 1410105 | 188189 | 188204 | N/A  | N/A  | GCATAGTATTCCTGGC  | 43  | P | 894 |
| 1410110 | 541767 | 541782 | N/A  | N/A  | GAATCAATGAACTCTT  | 37  | P | 895 |
| 1410123 | 182392 | 182407 | N/A  | N/A  | AGGATTAGAGCCTAGG  | 35  | P | 896 |
| 1410125 | 204973 | 204988 | N/A  | N/A  | GAATTTGAGCTCATCT  | 73  | P | 897 |
| 1410142 | 82463  | 82478  | N/A  | N/A  | AACAATGCTGATTCAG  | 4   | P | 898 |
| 1410181 | 252445 | 252460 | N/A  | N/A  | GGATTAAGTGGAGGTT  | 9   | P | 899 |
| 1410196 | 211921 | 211936 | N/A  | N/A  | GTATTACTATTACATC  | 85  | P | 900 |
| 1410211 | 290664 | 290679 | 2143 | 2158 | CATTATTGCACAGGTA  | 7   | P | 901 |
| 1410235 | 426497 | 426512 | N/A  | N/A  | CTAACATAATACTTCA  | 55  | P | 902 |
| 1410270 | 285371 | 285386 | N/A  | N/A  | AGAATAGACTTGGTTA  | 92  | P | 903 |

|         |        |        |       |       |                   |    |   |     |
|---------|--------|--------|-------|-------|-------------------|----|---|-----|
| 1410273 | 279834 | 279849 | N/A   | N/A   | CCAAATTCTGTGAACT  | 27 | P | 904 |
| 1410285 | 260440 | 260455 | N/A   | N/A   | CCACTAAATTTTCCC   | 41 | P | 905 |
| 1410294 | 242427 | 242442 | N/A   | N/A   | ACTAATCTAAGGAGCC  | 12 | P | 906 |
| 1410328 | 221001 | 221016 | N/A   | N/A   | CTCATAAGTCATCCAC  | 45 | P | 907 |
| 1410341 | 244877 | 244892 | N/A   | N/A   | AATATGGTATCTTGTC  | 6  | P | 908 |
| 1410351 | 391265 | 391280 | N/A   | N/A   | CATACAAGTAACATCC  | 10 | P | 909 |
| 1410370 | 112417 | 112432 | N/A   | N/A   | GATAGAGAGATTTGTC  | 14 | P | 910 |
| 1410379 | 256980 | 256995 | N/A   | N/A   | GAGGTTATAATTGAGC  | 10 | P | 911 |
| 1410404 | 480317 | 480332 | N/A   | N/A   | GAAGATACAACCTCACG | 23 | P | 912 |
| 1410409 | 310816 | 310831 | N/A   | N/A   | GCCAAATATTGGTAGT  | 94 | P | 913 |
| 1410479 | 129805 | 129820 | N/A   | N/A   | ATCATTTAGATGCATG  | 84 | P | 914 |
| 1410506 | 229906 | 229921 | N/A   | N/A   | GAACATTTAGAGGCAT  | 4  | P | 915 |
| 1410512 | 324766 | 324781 | N/A   | N/A   | AAATTTACTTACCTCA  | 56 | P | 916 |
| 1410521 | 291177 | 291192 | N/A   | N/A   | TTAAGTAGATGATGAG  | 7  | P | 917 |
| 1410559 | 206514 | 206529 | N/A   | N/A   | TAGTAAATTTCTCTCA  | 72 | P | 918 |
| 1410589 | 283200 | 283215 | N/A   | N/A   | ATAACCATTTACTGTC  | 38 | P | 919 |
| 1411076 | 457264 | 457279 | 2389  | 2404  | AATACGACTGATGGTC  | 11 | P | 920 |
| 1411106 | 560037 | 560052 | 9026  | 9041  | GCAAAAATAGTTTGAG  | 17 | P | 921 |
| 1411118 | 222235 | 222250 | 1645  | 1660  | ACTAGAATAGCCCATC  | 6  | P | 922 |
| 1411140 | N/A    | N/A    | 224   | 239   | GATCACTAGTATCTGG  | 30 | P | 923 |
| 1411147 | 558798 | 558813 | 7787  | 7802  | GAGACTTAAGAAAACC  | 31 | P | 924 |
| 1411148 | 559474 | 559489 | 8463  | 8478  | ATAAATGATATGGTGG  | 18 | P | 925 |
| 1411174 | 556622 | 556637 | 5611  | 5626  | CAACATGGTATACTG   | 11 | P | 926 |
| 1411199 | 554972 | 554987 | 3961  | 3976  | TATCAATCTTTCCTCA  | 35 | P | 927 |
| 1411229 | 557461 | 557476 | 6450  | 6465  | TACACATAATCCAGGG  | 17 | P | 928 |
| 1411323 | 559222 | 559237 | 8211  | 8226  | GCAAAAAGATTACAAAG | 20 | P | 929 |
| 1411338 | 554243 | 554258 | 3232  | 3247  | CTAAGTAACTTTTGC   | 28 | P | 930 |
| 1411342 | 556080 | 556095 | 5069  | 5084  | GAGAGTTAAAAGTGAG  | 19 | P | 931 |
| 1411378 | 562074 | 562089 | 11063 | 11078 | ACATATGGCACCAGGA  | 23 | P | 932 |
| 1411424 | 222045 | 222060 | 1455  | 1470  | TAGTATAAAGAAGTGT  | 23 | P | 933 |
| 1411449 | 560726 | 560741 | 9715  | 9730  | CTCAAAGTCAGACACT  | 19 | P | 934 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5  | Q | 181 |
| 1408259 | 263006 | 263021 | N/A   | N/A   | GATATGAATGGTATGA  | 3  | Q | 935 |
|         | 263047 | 263062 |       |       |                   |    |   |     |
| 1408306 | 288678 | 288693 | 2073  | 2088  | CTATTGGAGAAGTGTA  | 7  | Q | 936 |
| 1408414 | 217721 | 217736 | 687   | 702   | GAAAGAGGTATTTCTG  | 6  | Q | 937 |
| 1408608 | 181172 | 181187 | N/A   | N/A   | AATTATGTGCAGAAAT  | 70 | Q | 938 |
| 1408632 | 225143 | 225158 | N/A   | N/A   | GATGTTTTAACGCAGA  | 5  | Q | 939 |
| 1408677 | 243174 | 243189 | N/A   | N/A   | ATTATGGCAGGTTGGT  | 11 | Q | 940 |
| 1408687 | 249364 | 249379 | N/A   | N/A   | AAAACAAAGCACAGGT  | 78 | Q | 941 |
| 1408730 | 271299 | 271314 | N/A   | N/A   | CCCCCAACAACCAGCA  | 76 | Q | 942 |
| 1408792 | 218142 | 218157 | 1108  | 1123  | CACTTTGGAAGACTCT  | 17 | Q | 943 |
| 1409110 | 293105 | 293120 | N/A   | N/A   | AGCATTAAAGGAGAAGG | 13 | Q | 944 |
| 1409133 | 230055 | 230070 | N/A   | N/A   | GAACTTTTATTGCAT   | 19 | Q | 945 |
| 1409152 | 283490 | 283505 | N/A   | N/A   | AGTAAGACATGCTCAT  | 17 | Q | 946 |

|         |        |        |      |      |                  |     |   |     |
|---------|--------|--------|------|------|------------------|-----|---|-----|
| 1409160 | 541770 | 541785 | N/A  | N/A  | GAGGAATCAATGAACT | 37  | Q | 947 |
| 1409214 | 290665 | 290680 | 2144 | 2159 | GCATTATTGCACAGGT | 10  | Q | 948 |
| 1409293 | 263338 | 263353 | N/A  | N/A  | GAAGTTTGAAGAATGC | 4   | Q | 949 |
| 1409324 | 194970 | 194985 | N/A  | N/A  | ATCTACATTATCTCAG | 57  | Q | 950 |
| 1409358 | 512182 | 512197 | N/A  | N/A  | GATTATACATTCTGAG | 31  | Q | 951 |
| 1409359 | 182873 | 182888 | N/A  | N/A  | ATAGTTACAGTAATCT | 37  | Q | 952 |
| 1409362 | 439560 | 439575 | N/A  | N/A  | ACAAATAGATGCTTCA | 21  | Q | 953 |
| 1409383 | 112419 | 112434 | N/A  | N/A  | AAGATAGAGAGATTTG | 13  | Q | 954 |
| 1409389 | 82464  | 82479  | N/A  | N/A  | GAACAATGCTGATTCA | 60  | Q | 955 |
| 1409392 | 206678 | 206693 | N/A  | N/A  | ACTAAAGTAAGTTCCA | 68  | Q | 956 |
| 1409402 | 235490 | 235505 | N/A  | N/A  | CTTATTTGGAGTGGTT | 12  | Q | 957 |
| 1409524 | 202577 | 202592 | N/A  | N/A  | AAACCAGTAACATCCA | 22  | Q | 958 |
| 1409533 | 461061 | 461076 | N/A  | N/A  | GCAGATTTAAAGTCAA | 22  | Q | 959 |
| 1409544 | 280006 | 280021 | N/A  | N/A  | CCATATTCTGTAGCAT | 12  | Q | 960 |
| 1409650 | 302424 | 302439 | N/A  | N/A  | GCTAATCAAGGTATCA | 20  | Q | 961 |
| 1409664 | 480686 | 480701 | N/A  | N/A  | GAAACAGGTATGTGGG | 44  | Q | 962 |
| 1409678 | 189697 | 189712 | N/A  | N/A  | TATAGGTATCCTGCAT | 78  | Q | 963 |
| 1409705 | 257386 | 257401 | N/A  | N/A  | AGACATAATGGTCAAC | 96  | Q | 964 |
| 1409726 | 260441 | 260456 | N/A  | N/A  | CCCACTAAATTTTCC  | 55  | Q | 965 |
| 1409735 | 190439 | 190454 | N/A  | N/A  | TCCTTATGACCCCTG  | 36  | Q | 966 |
| 1409768 | 188341 | 188356 | N/A  | N/A  | CATGATAGTGATTTTC | 50  | Q | 967 |
| 1409777 | 227279 | 227294 | N/A  | N/A  | AAGTTTAAACTGGGAT | 16  | Q | 968 |
| 1409782 | 367784 | 367799 | N/A  | N/A  | GAGTAATATGTCAGTG | 11  | Q | 969 |
| 1409785 | 274912 | 274927 | N/A  | N/A  | ATGAATTTAGTTTGAT | 70  | Q | 970 |
| 1409824 | 222046 | 222061 | 1456 | 1471 | GTAGTATAAAGAAGTG | 5   | Q | 971 |
| 1409914 | 98292  | 98307  | N/A  | N/A  | ACCTTTAGACAAAGGC | 85  | Q | 972 |
| 1409993 | 310924 | 310939 | N/A  | N/A  | GCAGTAAAAATCTCCT | 57  | Q | 973 |
| 1410029 | 233963 | 233978 | N/A  | N/A  | TTAACAATTCCTTCA  | 71  | Q | 974 |
| 1410044 | 69109  | 69124  | N/A  | N/A  | AGATTTAGGATGGGAG | 107 | Q | 975 |
| 1410052 | 289995 | 290010 | N/A  | N/A  | TAGTAGGTGATTTCTG | 11  | Q | 976 |
| 1410053 | 393162 | 393177 | N/A  | N/A  | GTCTATAAAAGCCACA | 36  | Q | 977 |
| 1410064 | 31648  | 31663  | N/A  | N/A  | GATATAACAGTTCTGT | 67  | Q | 978 |
| 1410109 | 528195 | 528210 | N/A  | N/A  | ATGAAGACAGTATTGC | 22  | Q | 979 |
| 1410167 | 325799 | 325814 | N/A  | N/A  | GTTGATAAAAGCCTCA | 5   | Q | 980 |
| 1410175 | 221013 | 221028 | N/A  | N/A  | TCTATTAAGCATCTCA | 32  | Q | 981 |
| 1410191 | 350180 | 350195 | N/A  | N/A  | ACATTTGAAATTGACC | 29  | Q | 982 |
| 1410208 | 291181 | 291196 | N/A  | N/A  | TATCTTAAGTAGATGA | 89  | Q | 983 |
| 1410220 | 165801 | 165816 | N/A  | N/A  | AGTTATAGTCACTCC  | 8   | Q | 984 |
| 1410247 | 211923 | 211938 | N/A  | N/A  | CAGTATTACTATTACA | 114 | Q | 985 |
| 1410251 | 132194 | 132209 | N/A  | N/A  | GTTAATAATGAATGCA | 65  | Q | 986 |
| 1410287 | 244885 | 244900 | N/A  | N/A  | GAGGTAAAAATATGGT | 9   | Q | 987 |
| 1410305 | 252447 | 252462 | N/A  | N/A  | TGGGATTAAGTGAGG  | 35  | Q | 988 |
| 1410390 | 268500 | 268515 | N/A  | N/A  | ATTAGTTAAGACCAGT | 4   | Q | 989 |
| 1410401 | 204974 | 204989 | N/A  | N/A  | TGAATTTGAGCTCATC | 51  | Q | 990 |
| 1410437 | 149455 | 149470 | N/A  | N/A  | CCATTAACATACTCCA | 29  | Q | 991 |

|         |        |        |       |       |                   |     |   |      |
|---------|--------|--------|-------|-------|-------------------|-----|---|------|
| 1410448 | 494592 | 494607 | N/A   | N/A   | ATGGATTAAACTCCCA  | 115 | Q | 992  |
| 1410472 | 209588 | 209603 | N/A   | N/A   | ATGTTAGAAAGCTCGC  | 44  | Q | 993  |
| 1410511 | 427593 | 427608 | N/A   | N/A   | CAGCTAATGGAGTCAA  | 33  | Q | 994  |
| 1410527 | 285372 | 285387 | N/A   | N/A   | CAGAATAGACTTGGTT  | 127 | Q | 995  |
| 1410540 | 407837 | 407852 | N/A   | N/A   | CATAATTCTGGGTGAA  | 29  | Q | 996  |
| 1410582 | 198866 | 198881 | N/A   | N/A   | TCCTTAAAAACCTCCC  | 84  | Q | 997  |
| 1411080 | 560116 | 560131 | 9105  | 9120  | GCAAAACTAAGACCCT  | 34  | Q | 998  |
| 1411104 | 457265 | 457280 | 2390  | 2405  | CAATACGACTGATGGT  | 14  | Q | 999  |
| 1411131 | 555103 | 555118 | 4092  | 4107  | GATGATGGATTTCTAG  | 18  | Q | 1000 |
| 1411136 | 222236 | 222251 | 1646  | 1661  | CACTAGAATAGCCCAT  | 9   | Q | 1001 |
| 1411142 | 558841 | 558856 | 7830  | 7845  | CAATACTACAGATACA  | 56  | Q | 1002 |
| 1411230 | 562075 | 562090 | 11064 | 11079 | GACATATGGCACCAGG  | 12  | Q | 1003 |
| 1411252 | 557462 | 557477 | 6451  | 6466  | TTACACATAATCCAGG  | 14  | Q | 1004 |
| 1411305 | 556656 | 556671 | 5645  | 5660  | GAACCTTTAAAGTTGT  | 29  | Q | 1005 |
| 1411326 | 554247 | 554262 | 3236  | 3251  | GACTCTAAGTAACTTT  | 40  | Q | 1006 |
| 1411371 | 559224 | 559239 | 8213  | 8228  | CTGCAAAAGATTACACA | 26  | Q | 1007 |
| 1411395 | 217278 | 217293 | 244   | 259   | GAGTAAAGTGCTTCCT  | 7   | Q | 1008 |
| 1411406 | 560775 | 560790 | 9764  | 9779  | AAGAATGTGATATGGA  | 12  | Q | 1009 |
| 1411421 | 556083 | 556098 | 5072  | 5087  | GCAGAGAGTTAAAAGT  | 31  | Q | 1010 |
| 1411439 | 559477 | 559492 | 8466  | 8481  | TACATAAATGATATGG  | 41  | Q | 1011 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5   | R | 181  |
| 1408258 | 263007 | 263022 | N/A   | N/A   | TGATATGAATGGTATG  | 7   | R | 1012 |
|         | 263048 | 263063 |       |       |                   |     |   |      |
| 1408305 | 288681 | 288696 | 2076  | 2091  | TATCTATTGGAGAAGT  | 4   | R | 1013 |
| 1408488 | 222072 | 222087 | 1482  | 1497  | TATAATGTCTCCAGGG  | 22  | R | 1014 |
| 1408574 | 290667 | 290682 | 2146  | 2161  | AAGCATTATTGCACAG  | 13  | R | 1015 |
| 1408607 | 181182 | 181197 | N/A   | N/A   | AATACTCCATAATTAT  | 69  | R | 1016 |
| 1408619 | 188418 | 188433 | N/A   | N/A   | AGCCTAAGTCTTGATT  | 80  | R | 1017 |
| 1408628 | 189698 | 189713 | N/A   | N/A   | TTATAGGTATCCTGCA  | 58  | R | 1018 |
| 1408676 | 243184 | 243199 | N/A   | N/A   | GAAATTACAGATTATG  | 73  | R | 1019 |
| 1408686 | 249374 | 249389 | N/A   | N/A   | GCAGATGAGGAAAACA  | 69  | R | 1020 |
| 1408729 | 271319 | 271334 | N/A   | N/A   | ATAATGTCCTCTCCAT  | 40  | R | 1021 |
| 1408781 | 218162 | 218177 | 1128  | 1143  | GATGAGATGAGATGGC  | 8   | R | 1022 |
| 1409102 | 100338 | 100353 | N/A   | N/A   | CTTACATAACTTGCAT  | 50  | R | 1023 |
| 1409116 | 230797 | 230812 | N/A   | N/A   | TGTC AATGAGTAGCAG | 30  | R | 1024 |
| 1409138 | 427603 | 427618 | N/A   | N/A   | AAGAATTAGTCAGCTA  | 53  | R | 1025 |
| 1409149 | 512545 | 512560 | N/A   | N/A   | CTACTAGTTTATCCCC  | 30  | R | 1026 |
| 1409162 | 530289 | 530304 | N/A   | N/A   | GATTTAGGCTTTCCAA  | 19  | R | 1027 |
| 1409177 | 221014 | 221029 | N/A   | N/A   | ATCTATTAAGCATCTC  | 38  | R | 1028 |
| 1409248 | 205140 | 205155 | N/A   | N/A   | CAATTT CAGAGGCAGC | 36  | R | 1029 |
| 1409264 | 326728 | 326743 | N/A   | N/A   | TATATGATTATGAGGA  | 5   | R | 1030 |
| 1409274 | 289996 | 290011 | N/A   | N/A   | ATAGTAGGTGATTCT   | 11  | R | 1031 |
| 1409306 | 257387 | 257402 | N/A   | N/A   | CAGACATAATGGTCAA  | 79  | R | 1032 |
| 1409313 | 439594 | 439609 | N/A   | N/A   | AATTATCAGCAGGCTG  | 92  | R | 1033 |
| 1409364 | 393173 | 393188 | N/A   | N/A   | GTCCAATAGAAGTCTA  | 17  | R | 1034 |

|         |        |        |      |      |                   |     |   |      |
|---------|--------|--------|------|------|-------------------|-----|---|------|
| 1409366 | 69115  | 69130  | N/A  | N/A  | GTAACAAGATTTAGGA  | 96  | R | 1035 |
| 1409385 | 302930 | 302945 | N/A  | N/A  | TACTATTATTCAGGCA  | 10  | R | 1036 |
| 1409410 | 245068 | 245083 | N/A  | N/A  | TACAATGATCAGTTCA  | 6   | R | 1037 |
| 1409471 | 311381 | 311396 | N/A  | N/A  | TACTATGATGTGTTCT  | 89  | R | 1038 |
| 1409519 | 182956 | 182971 | N/A  | N/A  | ATAGTTGTACAATGTA  | 8   | R | 1039 |
| 1409534 | 82471  | 82486  | N/A  | N/A  | CTCTATTGAACAATGC  | 5   | R | 1040 |
| 1409630 | 543336 | 543351 | N/A  | N/A  | ATCTATTATCCTCAGG  | 38  | R | 1041 |
| 1409631 | 275129 | 275144 | N/A  | N/A  | ATTAGTATCAGTGTAT  | 31  | R | 1042 |
| 1409632 | 165802 | 165817 | N/A  | N/A  | AAGTTATAGTCACTTC  | 93  | R | 1043 |
| 1409677 | 31672  | 31687  | N/A  | N/A  | TAGCATTAAATGAGTTG | 100 | R | 1044 |
| 1409739 | 209589 | 209604 | N/A  | N/A  | CATGTTAGAAAGCTCG  | 79  | R | 1045 |
| 1409790 | 285373 | 285388 | N/A  | N/A  | ACAGAATAGACTTGGT  | 95  | R | 1046 |
| 1409795 | 263345 | 263360 | N/A  | N/A  | TATCTTTGAAGTTGA   | 18  | R | 1047 |
| 1409879 | 190449 | 190464 | N/A  | N/A  | GCCTTAATGGTCCTTA  | 80  | R | 1048 |
| 1409882 | 252458 | 252473 | N/A  | N/A  | TCATAGGTAACCTGGGA | 30  | R | 1049 |
| 1409883 | 112504 | 112519 | N/A  | N/A  | GCTTTATTACTAATCA  | 5   | R | 1050 |
| 1409964 | 283492 | 283507 | N/A  | N/A  | GAAGTAAGACATGCTC  | 20  | R | 1051 |
| 1409966 | 227343 | 227358 | N/A  | N/A  | TCACTAATGTCACATT  | 12  | R | 1052 |
| 1409977 | 350509 | 350524 | N/A  | N/A  | TTTATTATAGGGTTGA  | 3   | R | 1053 |
| 1409989 | 407842 | 407857 | N/A  | N/A  | ACAACCATAATTCTGG  | 37  | R | 1054 |
| 1410042 | 268501 | 268516 | N/A  | N/A  | AATTAGTTAAGACCAG  | 7   | R | 1055 |
| 1410060 | 198867 | 198882 | N/A  | N/A  | ATCCTTAAAAACCTCC  | 55  | R | 1056 |
| 1410126 | 494990 | 495005 | N/A  | N/A  | TTGTAATAGTGGTGTG  | 11  | R | 1057 |
| 1410148 | 481051 | 481066 | N/A  | N/A  | TCAAAATCTTGTCTCTG | 27  | R | 1058 |
| 1410154 | 194977 | 194992 | N/A  | N/A  | GTTACATATCTACATT  | 60  | R | 1059 |
| 1410156 | 368427 | 368442 | N/A  | N/A  | GATATTGTATAAGGTT  | 6   | R | 1060 |
| 1410186 | 291248 | 291263 | N/A  | N/A  | GCTAAAATTCTACTTC  | 50  | R | 1061 |
| 1410248 | 235491 | 235506 | N/A  | N/A  | GCTTATTTGGAGTGGT  | 6   | R | 1062 |
| 1410252 | 293136 | 293151 | N/A  | N/A  | AAGTAATGGGTGGTCA  | 43  | R | 1063 |
| 1410260 | 202578 | 202593 | N/A  | N/A  | AAAACCAGTAACATCC  | 39  | R | 1064 |
| 1410316 | 212095 | 212110 | N/A  | N/A  | GCAGTAAGTGAAATCT  | 54  | R | 1065 |
| 1410320 | 233964 | 233979 | N/A  | N/A  | GTTAACAATTCCCTTC  | 72  | R | 1066 |
| 1410374 | 280173 | 280188 | N/A  | N/A  | GCCTATAATCTACTGA  | 57  | R | 1067 |
| 1410378 | 133252 | 133267 | N/A  | N/A  | TTTACATATATCCCTC  | 46  | R | 1068 |
| 1410396 | 149998 | 150013 | N/A  | N/A  | CATGATTAAAAGTGTA  | 90  | R | 1069 |
| 1410415 | 206769 | 206784 | N/A  | N/A  | TACATTTAATGCCTAC  | 58  | R | 1070 |
| 1410421 | 461281 | 461296 | N/A  | N/A  | GCTATAAGGGTCTCAA  | 33  | R | 1071 |
| 1410427 | 217303 | 217318 | 269  | 284  | GAAATTCATTTGTGAC  | 11  | R | 1072 |
| 1410456 | 225179 | 225194 | N/A  | N/A  | AATACCTCAATGTCCA  | 6   | R | 1073 |
| 1410465 | 260563 | 260578 | N/A  | N/A  | TAGAATGGATGTCATT  | 32  | R | 1074 |
| 1410535 | 457266 | 457281 | 2391 | 2406 | CCAATACGACTGATGG  | 57  | R | 1075 |
| 1411101 | 558842 | 558857 | 7831 | 7846 | GCAATACTACAGATAC  | 26  | R | 1076 |
| 1411149 | 559515 | 559530 | 8504 | 8519 | CACGAGAGTGGTTTGA  | 66  | R | 1077 |
| 1411235 | 554288 | 554303 | 3277 | 3292 | CCCTATTTTGCTCCAT  | 14  | R | 1078 |
| 1411236 | 556093 | 556108 | 5082 | 5097 | CCCAAACAAGGCAGAG  | 34  | R | 1079 |

|         |        |        |       |       |                   |     |   |      |
|---------|--------|--------|-------|-------|-------------------|-----|---|------|
| 1411276 | 562102 | 562117 | 11091 | 11106 | CACTAATTACTTTCAC  | 35  | R | 1080 |
| 1411345 | 557522 | 557537 | 6511  | 6526  | CACAAGACCACTGCAC  | 68  | R | 1081 |
| 1411351 | 560142 | 560157 | 9131  | 9146  | AATAATTCTTAGAAGG  | 68  | R | 1082 |
| 1411355 | 217723 | 217738 | 689   | 704   | CTGAAAGAGGTATTTTC | 12  | R | 1083 |
| 1411366 | 222307 | 222322 | 1717  | 1732  | CCAGAAAGCAATCTCC  | 42  | R | 1084 |
| 1411399 | 556793 | 556808 | 5782  | 5797  | GCATAAACTCTTGGCC  | 82  | R | 1085 |
| 1411405 | 560795 | 560810 | 9784  | 9799  | CAATTTGGTGGTCCAC  | 33  | R | 1086 |
| 1411418 | 555156 | 555171 | 4145  | 4160  | CATATGTAGAGTAAGA  | 81  | R | 1087 |
| 1411425 | 559234 | 559249 | 8223  | 8238  | ACACAGTACACTGCAA  | 40  | R | 1088 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 6   | S | 181  |
| 1408253 | 249391 | 249406 | N/A   | N/A   | ATTAGTATGTCCACCT  | 22  | S | 1089 |
| 1408257 | 263008 | 263023 | N/A   | N/A   | GTGATATGAATGGTAT  | 4   | S | 1090 |
|         | 263049 | 263064 |       |       |                   |     |   |      |
| 1408303 | 288682 | 288697 | 2077  | 2092  | ATATCTATTGGAGAAG  | 14  | S | 1091 |
| 1408606 | 181192 | 181207 | N/A   | N/A   | GTACACAGCAAATACT  | 72  | S | 1092 |
| 1408618 | 188448 | 188463 | N/A   | N/A   | TTCTATCATTGCAGTT  | 55  | S | 1093 |
| 1408631 | 225183 | 225198 | N/A   | N/A   | GCTTAATACCTCAATG  | 53  | S | 1094 |
| 1408674 | 243194 | 243209 | N/A   | N/A   | CATGAAGAGGGAAATT  | 88  | S | 1095 |
| 1408728 | 271329 | 271344 | N/A   | N/A   | AATTTAGTGAATAATG  | 101 | S | 1096 |
| 1408774 | 218172 | 218187 | 1138  | 1153  | CAAACCAGCTGATGAG  | 8   | S | 1097 |
| 1408780 | 217751 | 217766 | 717   | 732   | TAAAAACTTTTCCTCCG | 7   | S | 1098 |
| 1409106 | 199112 | 199127 | N/A   | N/A   | CATTTTGAGATTCCTG  | 46  | S | 1099 |
| 1409125 | 543337 | 543352 | N/A   | N/A   | GATCTATTATCCTCAG  | 33  | S | 1100 |
| 1409132 | 328985 | 329000 | N/A   | N/A   | GAAGTATTTGCTTCC   | 57  | S | 1101 |
| 1409144 | 289997 | 290012 | N/A   | N/A   | TATAGTAGGTGATTTC  | 12  | S | 1102 |
| 1409239 | 165908 | 165923 | N/A   | N/A   | AAGTAGTTAAGGCTAC  | 77  | S | 1103 |
| 1409245 | 205217 | 205232 | N/A   | N/A   | CATACTAATGATTCAG  | 31  | S | 1104 |
| 1409247 | 512696 | 512711 | N/A   | N/A   | CCAAATTTGGTAAGGT  | 94  | S | 1105 |
| 1409303 | 206793 | 206808 | N/A   | N/A   | ACAATATCTACAAGTC  | 82  | S | 1106 |
| 1409334 | 368466 | 368481 | N/A   | N/A   | GACAATAATGCAATGT  | 74  | S | 1107 |
| 1409339 | 252459 | 252474 | N/A   | N/A   | CTCATAGGTAACGGG   | 69  | S | 1108 |
| 1409352 | 227888 | 227903 | N/A   | N/A   | GTATTTAATGAGCTCC  | 18  | S | 1109 |
| 1409353 | 408274 | 408289 | N/A   | N/A   | AATGATTAGGGTCACT  | 17  | S | 1110 |
| 1409368 | 291259 | 291274 | N/A   | N/A   | TTCGAGTAAATGCTAA  | 43  | S | 1111 |
| 1409372 | 439597 | 439612 | N/A   | N/A   | CCAAATTATCAGCAGG  | 35  | S | 1112 |
| 1409373 | 530294 | 530309 | N/A   | N/A   | CTTTAGATTTAGGCTT  | 44  | S | 1113 |
| 1409374 | 245070 | 245085 | N/A   | N/A   | GTTACAATGATCAGTT  | 11  | S | 1114 |
| 1409379 | 101776 | 101791 | N/A   | N/A   | TAAACATGTGAGTCC   | 12  | S | 1115 |
| 1409439 | 190487 | 190502 | N/A   | N/A   | CACTAACAATTCTTTC  | 82  | S | 1116 |
| 1409444 | 150062 | 150077 | N/A   | N/A   | GTAAGATAAGCATTGT  | 25  | S | 1117 |
| 1409464 | 428079 | 428094 | N/A   | N/A   | CACATTAGAGAATGTA  | 94  | S | 1118 |
| 1409483 | 231341 | 231356 | N/A   | N/A   | CTCAATGAGGTTTACA  | 50  | S | 1119 |
| 1409505 | 183359 | 183374 | N/A   | N/A   | TCAGAAGTGGTAGTAT  | 15  | S | 1120 |
| 1409582 | 481052 | 481067 | N/A   | N/A   | ATCAAAATCTTGTCTT  | 44  | S | 1121 |
| 1409633 | 113211 | 113226 | N/A   | N/A   | TCAATAAACAGTACCA  | 32  | S | 1122 |

|         |        |        |       |       |                  |     |   |      |
|---------|--------|--------|-------|-------|------------------|-----|---|------|
| 1409716 | 280374 | 280389 | N/A   | N/A   | AGTTTAACTAGGCATC | 24  | S | 1123 |
| 1409741 | 235758 | 235773 | N/A   | N/A   | AGTACAAACTGCTACA | 83  | S | 1124 |
| 1409873 | 303207 | 303222 | N/A   | N/A   | GACTAGCTGAAGTTGC | 40  | S | 1125 |
| 1409886 | 350545 | 350560 | N/A   | N/A   | TCTATAGAGAACCAGA | 97  | S | 1126 |
| 1409932 | 261566 | 261581 | N/A   | N/A   | CCACATTCAAGCTTCG | 17  | S | 1127 |
| 1409983 | 222358 | 222373 | N/A   | N/A   | CCTACAAAAACCACCA | 57  | S | 1128 |
| 1410002 | 83080  | 83095  | N/A   | N/A   | GCAGATTCAAAGAGGG | 31  | S | 1129 |
| 1410024 | 275131 | 275146 | N/A   | N/A   | GAATTAGTATCAGTGT | 10  | S | 1130 |
| 1410054 | 313760 | 313775 | N/A   | N/A   | TACTATATTGGTTACC | 34  | S | 1131 |
| 1410072 | 202625 | 202640 | N/A   | N/A   | TTTAATGGGTGATTGC | 32  | S | 1132 |
| 1410075 | 283494 | 283509 | N/A   | N/A   | TGGAAGTAAGACATGC | 12  | S | 1133 |
| 1410091 | 189699 | 189714 | N/A   | N/A   | CTTATAGGTATCCTGC | 27  | S | 1134 |
| 1410100 | 263405 | 263420 | N/A   | N/A   | TACCATCAAAGAAGGA | 31  | S | 1135 |
| 1410114 | 70523  | 70538  | N/A   | N/A   | TTCAATAAGCGGGCTG | 97  | S | 1136 |
| 1410115 | 234584 | 234599 | N/A   | N/A   | AGTCAAAATGCCCATA | 29  | S | 1137 |
| 1410119 | 393352 | 393367 | N/A   | N/A   | ATAAGTATCACAGTCA | 5   | S | 1138 |
| 1410152 | 222073 | 222088 | 1483  | 1498  | GTATAATGTCTCCAGG | 9   | S | 1139 |
| 1410192 | 209649 | 209664 | N/A   | N/A   | ATGTACTAAACACAGG | 62  | S | 1140 |
| 1410205 | 221096 | 221111 | N/A   | N/A   | AGCTATATCACTTGAA | 88  | S | 1141 |
| 1410243 | 195252 | 195267 | N/A   | N/A   | GACAATCGGAACTCCC | 30  | S | 1142 |
| 1410304 | 461282 | 461297 | N/A   | N/A   | TGCTATAAGGGTCTCA | 30  | S | 1143 |
| 1410323 | 293137 | 293152 | N/A   | N/A   | CAAGTAATGGGTGGTC | 19  | S | 1144 |
| 1410399 | 285374 | 285389 | N/A   | N/A   | AACAGAATAGACTTGG | 96  | S | 1145 |
| 1410416 | 257465 | 257480 | N/A   | N/A   | ACCAATAACATGTCAA | 96  | S | 1146 |
| 1410458 | 268502 | 268517 | N/A   | N/A   | GAATTAGTTAAGACCA | 6   | S | 1147 |
| 1410477 | 133466 | 133481 | N/A   | N/A   | TCAATTTAAGGAAAGG | 23  | S | 1148 |
| 1410484 | 212633 | 212648 | N/A   | N/A   | GTAGAAATCCAACCTC | 74  | S | 1149 |
| 1410529 | 33387  | 33402  | N/A   | N/A   | CTACATATTATGTCTG | 114 | S | 1150 |
| 1410546 | 495082 | 495097 | N/A   | N/A   | ATATTTCAATCTCAGG | 8   | S | 1151 |
| 1411119 | 559517 | 559532 | 8506  | 8521  | ACCACGAGAGTGGTTT | 98  | S | 1152 |
| 1411128 | 290671 | 290686 | 2150  | 2165  | TAAGAAGCATTATTGC | 66  | S | 1153 |
| 1411132 | 555157 | 555172 | 4146  | 4161  | ACATATGTAGAGTAAG | 64  | S | 1154 |
| 1411143 | 217313 | 217328 | 279   | 294   | CCATATTCTGGAAATT | 23  | S | 1155 |
| 1411154 | 457268 | 457283 | 2393  | 2408  | TTCCAATACGACTGAT | 36  | S | 1156 |
| 1411232 | 556795 | 556810 | 5784  | 5799  | TAGCATAAACTCTTGG | 28  | S | 1157 |
| 1411233 | 560882 | 560897 | 9871  | 9886  | AAAATGATGCACACCA | 27  | S | 1158 |
| 1411244 | 558844 | 558859 | 7833  | 7848  | CTGCAATACTACAGAT | 101 | S | 1159 |
| 1411320 | 557544 | 557559 | 6533  | 6548  | GCATAGAGGGTCTTGT | 71  | S | 1160 |
| 1411322 | 554291 | 554306 | 3280  | 3295  | AAACCCTATTTTGCTC | 50  | S | 1161 |
| 1411353 | 560145 | 560160 | 9134  | 9149  | CACAATAATTCTTAGA | 68  | S | 1162 |
| 1411374 | 556095 | 556110 | 5084  | 5099  | TACCCAAACAAGGCAG | 43  | S | 1163 |
| 1411393 | 562199 | 562214 | 11188 | 11203 | GAACAGGTTTCCAGTA | 71  | S | 1164 |
| 1411410 | 559267 | 559282 | 8256  | 8271  | CCAAATTACAGGGAGC | 31  | S | 1165 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 4   | T | 181  |
| 1408252 | 249392 | 249407 | N/A   | N/A   | TATTAGTATGTCCACC | 37  | T | 1166 |

|         |        |        |      |      |                   |    |   |      |
|---------|--------|--------|------|------|-------------------|----|---|------|
| 1408256 | 263010 | 263025 | N/A  | N/A  | AAGTGATATGAATGGT  | 3  | T | 1167 |
|         | 263051 | 263066 |      |      |                   |    |   |      |
| 1408309 | 288683 | 288698 | 2078 | 2093 | AATATCTATTGGAGAA  | 8  | T | 1168 |
| 1408314 | 290674 | 290689 | 2153 | 2168 | TATTAAGAAGCATTAT  | 90 | T | 1169 |
| 1408476 | 222092 | 222107 | 1502 | 1517 | AATAGCTATCAGGCTC  | 28 | T | 1170 |
| 1408605 | 181202 | 181217 | N/A  | N/A  | GCAATATTGGGTACAC  | 5  | T | 1171 |
| 1408617 | 188498 | 188513 | N/A  | N/A  | TGTATATCCTTTGTTC  | 34 | T | 1172 |
| 1408630 | 225223 | 225238 | N/A  | N/A  | ATTCTAACACTTGGGC  | 6  | T | 1173 |
| 1408673 | 243254 | 243269 | N/A  | N/A  | AAACCGACTGGTCTCA  | 80 | T | 1174 |
| 1408766 | 218182 | 218197 | 1148 | 1163 | TTGAATTACACAAACC  | 4  | T | 1175 |
| 1409195 | 206799 | 206814 | N/A  | N/A  | ACTACAACAATATCTA  | 69 | T | 1176 |
| 1409242 | 189700 | 189715 | N/A  | N/A  | TCTTATAGGTATCCTG  | 36 | T | 1177 |
| 1409244 | 495277 | 495292 | N/A  | N/A  | TACATAACATGACACA  | 34 | T | 1178 |
| 1409254 | 209666 | 209681 | N/A  | N/A  | AATATTGATTACCTGC  | 66 | T | 1179 |
| 1409287 | 202726 | 202741 | N/A  | N/A  | ACAAATCCTGCTTTGC  | 62 | T | 1180 |
| 1409295 | 293139 | 293154 | N/A  | N/A  | ATCAAGTAATGGGTGG  | 6  | T | 1181 |
| 1409297 | 290000 | 290015 | N/A  | N/A  | TAGTATAGTAGGTGAT  | 13 | T | 1182 |
| 1409318 | 263461 | 263476 | N/A  | N/A  | AAGATTATTCCTCAAG  | 18 | T | 1183 |
| 1409325 | 33485  | 33500  | N/A  | N/A  | GCAAATGAAGATATGT  | 93 | T | 1184 |
| 1409367 | 291270 | 291285 | N/A  | N/A  | ATTATGAAGAGTTCGA  | 22 | T | 1185 |
| 1409380 | 261665 | 261680 | N/A  | N/A  | CCATTGAAGGCTTTGT  | 18 | T | 1186 |
| 1409390 | 234665 | 234680 | N/A  | N/A  | CTAGAGAAGTTCCTCC  | 52 | T | 1187 |
| 1409416 | 252562 | 252577 | N/A  | N/A  | CATACGCCAAGCTCAA  | 26 | T | 1188 |
| 1409427 | 221246 | 221261 | N/A  | N/A  | ACAATTAATATGCAGC  | 26 | T | 1189 |
| 1409447 | 271422 | 271437 | N/A  | N/A  | GACATAAGCTGGAACA  | 36 | T | 1190 |
| 1409452 | 231724 | 231739 | N/A  | N/A  | GTCTAAAAACAACAGT  | 62 | T | 1191 |
| 1409463 | 183363 | 183378 | N/A  | N/A  | CAAATCAGAAGTGGTA  | 19 | T | 1192 |
| 1409482 | 481053 | 481068 | N/A  | N/A  | CATCAAAATCTTGTC   | 60 | T | 1193 |
| 1409492 | 303318 | 303333 | N/A  | N/A  | ATTAGTACAATCATCC  | 33 | T | 1194 |
| 1409506 | 280375 | 280390 | N/A  | N/A  | AAGTTTAACTAGGCAT  | 47 | T | 1195 |
| 1409575 | 313762 | 313777 | N/A  | N/A  | CATACTATATTGGTTA  | 59 | T | 1196 |
| 1409607 | 101811 | 101826 | N/A  | N/A  | ACTAGAAAAGCTGCTT  | 61 | T | 1197 |
| 1409662 | 283507 | 283522 | N/A  | N/A  | CTTTATCTTAACTTGG  | 25 | T | 1198 |
| 1409680 | 275133 | 275148 | N/A  | N/A  | TTGAATTAGTATCAGT  | 26 | T | 1199 |
| 1409684 | 544385 | 544400 | N/A  | N/A  | AAAAGTTTGTCACCTCA | 9  | T | 1200 |
| 1409771 | 350573 | 350588 | N/A  | N/A  | CATGTAAATACAGTGC  | 26 | T | 1201 |
| 1409805 | 222523 | 222538 | N/A  | N/A  | CAGACTAAAATGATCA  | 58 | T | 1202 |
| 1409814 | 227929 | 227944 | N/A  | N/A  | ATAACTTTTCTTTGGG  | 7  | T | 1203 |
| 1409830 | 150248 | 150263 | N/A  | N/A  | GAATTTTATCAGACTA  | 68 | T | 1204 |
| 1409850 | 166321 | 166336 | N/A  | N/A  | GTATACTATCTAGGTT  | 52 | T | 1205 |
| 1409930 | 408278 | 408293 | N/A  | N/A  | AGTCAATGATTAGGGT  | 9  | T | 1206 |
| 1409994 | 512860 | 512875 | N/A  | N/A  | TTCTAGATAGTTTGTA  | 48 | T | 1207 |
| 1410007 | 530296 | 530311 | N/A  | N/A  | AGCTTTAGATTTAGGC  | 77 | T | 1208 |
| 1410057 | 205218 | 205233 | N/A  | N/A  | ACATACTAATGATTCA  | 51 | T | 1209 |
| 1410065 | 370021 | 370036 | N/A  | N/A  | ATATTTCTCATATCGA  | 31 | T | 1210 |

|         |        |        |       |       |                   |    |   |      |
|---------|--------|--------|-------|-------|-------------------|----|---|------|
| 1410092 | 393466 | 393481 | N/A   | N/A   | TGTTAAGATACATTCC  | 13 | T | 1211 |
| 1410103 | 83460  | 83475  | N/A   | N/A   | GAATTTTCACTGCTA   | 14 | T | 1212 |
| 1410106 | 439598 | 439613 | N/A   | N/A   | CCCAAATTATCAGCAG  | 21 | T | 1213 |
| 1410177 | 134400 | 134415 | N/A   | N/A   | GTTTATGAAAATCTCC  | 42 | T | 1214 |
| 1410228 | 245085 | 245100 | N/A   | N/A   | TTTCATACAAAGCTGG  | 24 | T | 1215 |
| 1410278 | 428707 | 428722 | N/A   | N/A   | AAGAATTATGACACCA  | 26 | T | 1216 |
| 1410280 | 199260 | 199275 | N/A   | N/A   | GCTAAGCTCATTGTCT  | 63 | T | 1217 |
| 1410295 | 461352 | 461367 | N/A   | N/A   | AGTTTTAGAACATAGA  | 30 | T | 1218 |
| 1410413 | 212635 | 212650 | N/A   | N/A   | AAGTAGAAATCCAAC   | 93 | T | 1219 |
| 1410429 | 268503 | 268518 | N/A   | N/A   | TGAATTAGTTAAGACC  | 12 | T | 1220 |
| 1410432 | 285551 | 285566 | N/A   | N/A   | TAAGATTCTAGCTAGA  | 76 | T | 1221 |
| 1410462 | 257466 | 257481 | N/A   | N/A   | CACCAATAACATGTCA  | 72 | T | 1222 |
| 1410476 | 235849 | 235864 | N/A   | N/A   | TTGAAGAGCATTCTCC  | 51 | T | 1223 |
| 1410514 | 71847  | 71862  | N/A   | N/A   | GTTGAATAGATAGCCC  | 88 | T | 1224 |
| 1410548 | 190488 | 190503 | N/A   | N/A   | GCACTAACAATTCTTT  | 47 | T | 1225 |
| 1410575 | 329443 | 329458 | N/A   | N/A   | GATTTATCGATGTCAC  | 5  | T | 1226 |
| 1410578 | 113538 | 113553 | N/A   | N/A   | ATTACTAATGTTTACC  | 31 | T | 1227 |
| 1410581 | 195410 | 195425 | N/A   | N/A   | TCTAAACTTGAAGTGG  | 53 | T | 1228 |
| 1411081 | 560234 | 560249 | 9223  | 9238  | TCAAATGGTTAAGGCC  | 18 | T | 1229 |
| 1411082 | 457277 | 457292 | 2402  | 2417  | TAGTAGTACTTCCAAT  | 34 | T | 1230 |
| 1411086 | 217416 | 217431 | 382   | 397   | AGTAAGAGGCTGGACA  | 80 | T | 1231 |
| 1411090 | 559268 | 559283 | 8257  | 8272  | CCCAAATTACAGGGAG  | 89 | T | 1232 |
| 1411150 | 557566 | 557581 | 6555  | 6570  | GATTAGGATAACAGTT  | 16 | T | 1233 |
| 1411206 | 554292 | 554307 | 3281  | 3296  | AAAACCCTATTTTGCT  | 68 | T | 1234 |
| 1411224 | 556798 | 556813 | 5787  | 5802  | CCATAGCATAACTCT   | 35 | T | 1235 |
| 1411271 | 558912 | 558927 | 7901  | 7916  | AACAATGGCAGGTGAC  | 30 | T | 1236 |
| 1411291 | 562274 | 562289 | 11263 | 11278 | TTCAAAAGAAGACCAC  | 85 | T | 1237 |
| 1411309 | 556097 | 556112 | 5086  | 5101  | TTTACCCAAACAAGGC  | 36 | T | 1238 |
| 1411312 | 560883 | 560898 | 9872  | 9887  | GAAAATGATGCACACC  | 16 | T | 1239 |
| 1411315 | 559537 | 559552 | 8526  | 8541  | CAAGCGAGTACGGATG  | 15 | T | 1240 |
| 1411317 | 217789 | 217804 | 755   | 770   | CAGTTAACAGCGCGGT  | 6  | T | 1241 |
| 1411431 | 555158 | 555173 | 4147  | 4162  | CACATATGTAGAGTAA  | 41 | T | 1242 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 6  | U | 181  |
| 1408247 | 243311 | 243326 | N/A   | N/A   | ATTAAAAGACGGCCTC  | 80 | U | 1243 |
| 1408251 | 249393 | 249408 | N/A   | N/A   | TTATTAGTATGTCCAC  | 16 | U | 1244 |
| 1408255 | 263011 | 263026 | N/A   | N/A   | AAAGTGATATGAATGG  | 4  | U | 1245 |
|         | 263052 | 263067 |       |       |                   |    |   |      |
| 1408313 | 290675 | 290690 | 2154  | 2169  | GTATTAAGAAGCATTAA | 58 | U | 1246 |
| 1408546 | 288709 | 288724 | 2104  | 2119  | AGCAATGGTATCTGGG  | 15 | U | 1247 |
| 1408604 | 181212 | 181227 | N/A   | N/A   | GCAATGACTAGCAATA  | 29 | U | 1248 |
| 1408616 | 188548 | 188563 | N/A   | N/A   | TAGGCGAGAACACACT  | 44 | U | 1249 |
| 1408758 | 218192 | 218207 | 1158  | 1173  | GTAAACTACTTGAAT   | 62 | U | 1250 |
| 1409089 | 102832 | 102847 | N/A   | N/A   | AAGATATACAACACTC  | 16 | U | 1251 |
| 1409092 | 330574 | 330589 | N/A   | N/A   | GCAAATTGTGTTTCAGT | 6  | U | 1252 |
| 1409105 | 276132 | 276147 | N/A   | N/A   | ATGTAAGATGTCTGGC  | 20 | U | 1253 |

|         |        |        |       |       |                   |     |   |      |
|---------|--------|--------|-------|-------|-------------------|-----|---|------|
| 1409130 | 481056 | 481071 | N/A   | N/A   | CTACATCAAAATCTTG  | 87  | U | 1254 |
| 1409141 | 313763 | 313778 | N/A   | N/A   | CCATACTATATTGGTT  | 64  | U | 1255 |
| 1409199 | 530297 | 530312 | N/A   | N/A   | AAGCTTTAGATTAGG   | 50  | U | 1256 |
| 1409259 | 497352 | 497367 | N/A   | N/A   | GCATAAATGATCCAGG  | 53  | U | 1257 |
| 1409262 | 285988 | 286003 | N/A   | N/A   | TTTTATCCAGATTGTC  | 91  | U | 1258 |
| 1409263 | 199262 | 199277 | N/A   | N/A   | TAGCTAAGCTCATTGT  | 88  | U | 1259 |
| 1409288 | 195435 | 195450 | N/A   | N/A   | CCAGAACAGACATCTG  | 96  | U | 1260 |
| 1409329 | 212636 | 212651 | N/A   | N/A   | GAAGTAGAAATCCAAC  | 63  | U | 1261 |
| 1409381 | 253244 | 253259 | N/A   | N/A   | GCAAATGCTATGACAA  | 8   | U | 1262 |
| 1409405 | 280527 | 280542 | N/A   | N/A   | CATACTAAGATTGGCA  | 9   | U | 1263 |
| 1409443 | 544390 | 544405 | N/A   | N/A   | AGGATAAAAGTTTGTC  | 14  | U | 1264 |
| 1409490 | 207000 | 207015 | N/A   | N/A   | CTATTTGAAAGTGCTG  | 44  | U | 1265 |
| 1409508 | 441384 | 441399 | N/A   | N/A   | GAAAATTTGCAGCAGG  | 27  | U | 1266 |
| 1409511 | 189701 | 189716 | N/A   | N/A   | TTCTTATAGGTATCCT  | 24  | U | 1267 |
| 1409512 | 351591 | 351606 | N/A   | N/A   | GAATTACAATGTTCTA  | 32  | U | 1268 |
| 1409523 | 394249 | 394264 | N/A   | N/A   | GAATTTATCTACCTTG  | 37  | U | 1269 |
| 1409526 | 150250 | 150265 | N/A   | N/A   | TAGAATTTTATCAGAC  | 102 | U | 1270 |
| 1409579 | 222652 | 222667 | N/A   | N/A   | AAGCTACGATCTCTCA  | 34  | U | 1271 |
| 1409588 | 291271 | 291286 | N/A   | N/A   | TATTATGAAGAGTTCG  | 44  | U | 1272 |
| 1409619 | 231767 | 231782 | N/A   | N/A   | AGTTAGGTTTACGCTG  | 44  | U | 1273 |
| 1409647 | 209669 | 209684 | N/A   | N/A   | GCAAATATTGATTACC  | 49  | U | 1274 |
| 1409703 | 190755 | 190770 | N/A   | N/A   | GAATTTCTCTGATATC  | 71  | U | 1275 |
| 1409711 | 562291 | 562306 | 11280 | 11295 | CACAAATTACTGTTCC  | 33  | U | 1276 |
| 1409721 | 513274 | 513289 | N/A   | N/A   | GTAACCTAGATTCCAG  | 12  | U | 1277 |
| 1409738 | 408344 | 408359 | N/A   | N/A   | TCAGTAATTTAGGGTA  | 11  | U | 1278 |
| 1409784 | 72590  | 72605  | N/A   | N/A   | GCTTTATCAAGATCCA  | 86  | U | 1279 |
| 1409831 | 257696 | 257711 | N/A   | N/A   | GCACAGAGGTCATCTA  | 46  | U | 1280 |
| 1409838 | 83468  | 83483  | N/A   | N/A   | AACCATGAGAATTCA   | 21  | U | 1281 |
| 1409897 | 205253 | 205268 | N/A   | N/A   | ATAGTTACAGCTGTGC  | 42  | U | 1282 |
| 1409933 | 167586 | 167601 | N/A   | N/A   | GAGATTAAAGTTCTCA  | 101 | U | 1283 |
| 1409936 | 263463 | 263478 | N/A   | N/A   | ATAAGATTATTCCTCA  | 22  | U | 1284 |
| 1409951 | 271615 | 271630 | N/A   | N/A   | GCTATACATGATCTTA  | 26  | U | 1285 |
| 1409959 | 245272 | 245287 | N/A   | N/A   | GTTAGTTAGAAGCACA  | 28  | U | 1286 |
| 1410035 | 114511 | 114526 | N/A   | N/A   | CCATTTACAACATATGG | 84  | U | 1287 |
| 1410038 | 135027 | 135042 | N/A   | N/A   | ATAACATCAAGGTGCA  | 49  | U | 1288 |
| 1410041 | 290002 | 290017 | N/A   | N/A   | TTTAGTATAGTAGGTG  | 7   | U | 1289 |
| 1410048 | 462958 | 462973 | N/A   | N/A   | GCTATAGAAACTGCC   | 75  | U | 1290 |
| 1410069 | 262462 | 262477 | N/A   | N/A   | TGGTATTATGGAAGGT  | 8   | U | 1291 |
| 1410101 | 234697 | 234712 | N/A   | N/A   | GCAGTAATTTTATTCC  | 8   | U | 1292 |
| 1410143 | 225419 | 225434 | N/A   | N/A   | GAATTCATTAGTCTTA  | 32  | U | 1293 |
| 1410149 | 183364 | 183379 | N/A   | N/A   | TCAAATCAGAAGTGGT  | 16  | U | 1294 |
| 1410187 | 34822  | 34837  | N/A   | N/A   | CATAGAATAGTCTTGC  | 95  | U | 1295 |
| 1410226 | 293430 | 293445 | N/A   | N/A   | GAAATTAGCAGGCCAA  | 65  | U | 1296 |
| 1410326 | 556820 | 556835 | 5809  | 5824  | GCAAATCAGTACTGT   | 19  | U | 1297 |
| 1410336 | 370456 | 370471 | N/A   | N/A   | ACTATAGAATCTCACT  | 35  | U | 1298 |

|         |        |        |      |      |                   |     |   |      |
|---------|--------|--------|------|------|-------------------|-----|---|------|
| 1410350 | 283526 | 283541 | N/A  | N/A  | GATACATTAATTTCCA  | 15  | U | 1299 |
| 1410452 | 221479 | 221494 | N/A  | N/A  | GATTTAAATAAGGCCA  | 84  | U | 1300 |
| 1410475 | 268885 | 268900 | N/A  | N/A  | TATAGGTCATGACATT  | 40  | U | 1301 |
| 1410486 | 202871 | 202886 | N/A  | N/A  | TAGTATTATGCAGCAT  | 50  | U | 1302 |
| 1410509 | 303472 | 303487 | N/A  | N/A  | CATTATCTATGTCAGC  | 7   | U | 1303 |
| 1410545 | 236800 | 236815 | N/A  | N/A  | TGTTATACTGATGGGC  | 7   | U | 1304 |
| 1410547 | 430301 | 430316 | N/A  | N/A  | AGCTTTAAAGAGCCAC  | 94  | U | 1305 |
| 1410560 | 228137 | 228152 | N/A  | N/A  | AGCAATCAGAAGTTCC  | 9   | U | 1306 |
| 1411095 | 217867 | 217882 | 833  | 848  | GACAAGATGGCTCCTG  | 6   | U | 1307 |
| 1411122 | 560886 | 560901 | 9875 | 9890 | TTGGAATAATGATGCAC | 26  | U | 1308 |
| 1411138 | 554300 | 554315 | 3289 | 3304 | GATCTTGAAAAACCCT  | 40  | U | 1309 |
| 1411160 | 217417 | 217432 | 383  | 398  | CAGTAAGAGGCTGGAC  | 86  | U | 1310 |
| 1411270 | 559569 | 559584 | 8558 | 8573 | ATACTTTAGTGCTTGT  | 15  | U | 1311 |
| 1411273 | 556098 | 556113 | 5087 | 5102 | CTTTACCCAAACAAGG  | 80  | U | 1312 |
| 1411294 | 560235 | 560250 | 9224 | 9239 | TTCAAATGGTTAAGGC  | 18  | U | 1313 |
| 1411327 | 222093 | 222108 | 1503 | 1518 | AAATAGCTATCAGGCT  | 37  | U | 1314 |
| 1411341 | 557567 | 557582 | 6556 | 6571 | AGATTAGGATAACAGT  | 14  | U | 1315 |
| 1411382 | 555159 | 555174 | 4148 | 4163 | ACACATATGTAGAGTA  | 91  | U | 1316 |
| 1411389 | 558913 | 558928 | 7902 | 7917 | CAACAATGGCAGGTGA  | 65  | U | 1317 |
| 1411401 | 457280 | 457295 | 2405 | 2420 | GGTTAGTAGTACTTCC  | 30  | U | 1318 |
| 1411412 | 559321 | 559336 | 8310 | 8325 | ACTAAGACTGCACAGG  | 31  | U | 1319 |
| 1173403 | 288679 | 288694 | 2074 | 2089 | TCTATTGGAGAAGTGT  | 5   | V | 181  |
| 1408246 | 243312 | 243327 | N/A  | N/A  | AATTAAGACGCGCCT   | 87  | V | 1320 |
| 1408250 | 249395 | 249410 | N/A  | N/A  | TATTATTAGTATGTCC  | 15  | V | 1321 |
| 1408254 | 263012 | 263027 | N/A  | N/A  | CAAAGTGATATGAATG  | 64  | V | 1322 |
|         | 263053 | 263068 |      |      |                   |     |   |      |
| 1408312 | 290676 | 290691 | 2155 | 2170 | GGTATTAAGAAGCATT  | 8   | V | 1323 |
| 1408334 | 188555 | 188570 | N/A  | N/A  | TTATTGATAGGCGAGA  | 17  | V | 1324 |
| 1408560 | 288710 | 288725 | 2105 | 2120 | AAGCAATGGTATCTGG  | 13  | V | 1325 |
| 1408627 | 189708 | 189723 | N/A  | N/A  | CATGATTTTCTTATAG  | 78  | V | 1326 |
| 1408706 | 217873 | 217888 | 839  | 854  | CCAAAGGACAAGATGG  | 68  | V | 1327 |
| 1408750 | 218202 | 218217 | 1168 | 1183 | AACATTCTCAGTTAAA  | 29  | V | 1328 |
| 1409113 | 290003 | 290018 | N/A  | N/A  | CTTTAGTATAGTAGGT  | 13  | V | 1329 |
| 1409157 | 283535 | 283550 | N/A  | N/A  | ACTAATGAGGATACAT  | 56  | V | 1330 |
| 1409158 | 286178 | 286193 | N/A  | N/A  | GAGTATGGAGCTTCAG  | 22  | V | 1331 |
| 1409237 | 222653 | 222668 | N/A  | N/A  | AAAGCTACGATCTCTC  | 31  | V | 1332 |
| 1409276 | 205254 | 205269 | N/A  | N/A  | AATAGTTACAGCTGTG  | 61  | V | 1333 |
| 1409299 | 231770 | 231785 | N/A  | N/A  | AAGAGTTAGGTTTACG  | 6   | V | 1334 |
| 1409311 | 430475 | 430490 | N/A  | N/A  | GTAAATAACACTTCAT  | 72  | V | 1335 |
| 1409317 | 544828 | 544843 | N/A  | N/A  | TGTATAAGTATTCAGC  | 31  | V | 1336 |
| 1409328 | 556146 | 556161 | 5135 | 5150 | AACTATCCTGTTTGTT  | 101 | V | 1337 |
| 1409369 | 314118 | 314133 | N/A  | N/A  | CTCATAATTTAGAGGT  | 91  | V | 1338 |
| 1409394 | 60916  | 60931  | N/A  | N/A  | AGTAATATTGAGATCA  | 11  | V | 1339 |
|         | 394790 | 394805 |      |      |                   |     |   |      |
| 1409399 | 35730  | 35745  | N/A  | N/A  | CATTTTGGACTGTACA  | 116 | V | 1340 |

|         |        |        |      |      |                   |     |   |      |
|---------|--------|--------|------|------|-------------------|-----|---|------|
| 1409401 | 209688 | 209703 | N/A  | N/A  | AAATTCATTCACGCAT  | 72  | V | 1341 |
| 1409424 | 190869 | 190884 | N/A  | N/A  | CTAGAACTGCTTCTTC  | 80  | V | 1342 |
| 1409450 | 280528 | 280543 | N/A  | N/A  | TCATACTAAGATTGGC  | 9   | V | 1343 |
| 1409454 | 513426 | 513441 | N/A  | N/A  | AGTAATTTAGCATTCC  | 16  | V | 1344 |
| 1409487 | 498113 | 498128 | N/A  | N/A  | AAGGATTATGGGCTCC  | 87  | V | 1345 |
| 1409493 | 330938 | 330953 | N/A  | N/A  | GATTTACATCCTTTCA  | 59  | V | 1346 |
| 1409518 | 263470 | 263485 | N/A  | N/A  | GATGTAAATAAGATTA  | 84  | V | 1347 |
| 1409559 | 84602  | 84617  | N/A  | N/A  | GCAAAATCCAGACTCA  | 35  | V | 1348 |
| 1409590 | 207002 | 207017 | N/A  | N/A  | CTCTATTTGAAAGTGC  | 51  | V | 1349 |
| 1409623 | 221508 | 221523 | N/A  | N/A  | AAACTTTTCATCAGTTG | 93  | V | 1350 |
| 1409642 | 262581 | 262596 | N/A  | N/A  | AGACTACAGGGTGCGA  | 73  | V | 1351 |
| 1409657 | 257800 | 257815 | N/A  | N/A  | GCTGTAAAAGCCCAGT  | 81  | V | 1352 |
| 1409693 | 150328 | 150343 | N/A  | N/A  | GCCAATCAAATTGGTT  | 95  | V | 1353 |
| 1409696 | 74362  | 74377  | N/A  | N/A  | ATCATATAGGAGGCAG  | 106 | V | 1354 |
| 1409704 | 236846 | 236861 | N/A  | N/A  | CTTATTAAGTTATGA   | 78  | V | 1355 |
| 1409722 | 293715 | 293730 | N/A  | N/A  | CATCATAGCACCTCAG  | 33  | V | 1356 |
| 1409725 | 183378 | 183393 | N/A  | N/A  | TAAACTTCATACCTTC  | 45  | V | 1357 |
| 1409776 | 212638 | 212653 | N/A  | N/A  | GTGAAGTAGAAATCCA  | 54  | V | 1358 |
| 1409780 | 370459 | 370474 | N/A  | N/A  | GATACTATAGAATCTC  | 37  | V | 1359 |
| 1409832 | 352780 | 352795 | N/A  | N/A  | AACATATAGCCACAGC  | 21  | V | 1360 |
| 1409862 | 481174 | 481189 | N/A  | N/A  | GTTTATATTTGCATGC  | 68  | V | 1361 |
| 1409904 | 135028 | 135043 | N/A  | N/A  | GATAACATCAAGGTGC  | 65  | V | 1362 |
| 1409905 | 408851 | 408866 | N/A  | N/A  | AACATTAATCCCAGG   | 36  | V | 1363 |
| 1409920 | 167875 | 167890 | N/A  | N/A  | GTTTATTCAAGGATCC  | 43  | V | 1364 |
| 1409986 | 245516 | 245531 | N/A  | N/A  | ACTTTATCTTGACTAA  | 47  | V | 1365 |
| 1410009 | 304705 | 304720 | N/A  | N/A  | CTTACCTAGACCTTCT  | 40  | V | 1366 |
| 1410036 | 463327 | 463342 | N/A  | N/A  | GTTTATAGTGACCATC  | 3   | V | 1367 |
| 1410067 | 234706 | 234721 | N/A  | N/A  | ACTTACCATGCAGTAA  | 72  | V | 1368 |
| 1410074 | 276133 | 276148 | N/A  | N/A  | CATGTAAGATGTCTGG  | 52  | V | 1369 |
| 1410084 | 443331 | 443346 | N/A  | N/A  | ACAACATAATCAGTCT  | 71  | V | 1370 |
| 1410159 | 271616 | 271631 | N/A  | N/A  | AGCTATACATGATCTT  | 53  | V | 1371 |
| 1410221 | 291272 | 291287 | N/A  | N/A  | GTATTATGAAGAGTTC  | 28  | V | 1372 |
| 1410237 | 268890 | 268905 | N/A  | N/A  | TCATTTATAGGTCATG  | 16  | V | 1373 |
| 1410253 | 203374 | 203389 | N/A  | N/A  | ATTACTGTAGCTCCAG  | 27  | V | 1374 |
| 1410265 | 103316 | 103331 | N/A  | N/A  | AAGAGTTAGACACTTC  | 59  | V | 1375 |
| 1410271 | 199322 | 199337 | N/A  | N/A  | ATTACAAGTCACCTGC  | 71  | V | 1376 |
| 1410272 | 195451 | 195466 | N/A  | N/A  | CAACTATGTCAATCAG  | 64  | V | 1377 |
| 1410315 | 225422 | 225437 | N/A  | N/A  | GGAGAATTCATTAGTC  | 14  | V | 1378 |
| 1410329 | 530683 | 530698 | N/A  | N/A  | GCTAATTTTCATAGGTA | 35  | V | 1379 |
| 1410330 | 253907 | 253922 | N/A  | N/A  | AGGTAGAGCTGACCAA  | 79  | V | 1380 |
| 1410364 | 114648 | 114663 | N/A  | N/A  | AATATGTACCATAGGC  | 27  | V | 1381 |
| 1410453 | 228144 | 228159 | N/A  | N/A  | ACCAATAAGCAATCAG  | 17  | V | 1382 |
| 1410498 | 181220 | 181235 | N/A  | N/A  | CCTTATAAGCAATGAC  | 38  | V | 1383 |
| 1411091 | 457301 | 457316 | 2426 | 2441 | CATGAGGAATGTCCAA  | 27  | V | 1384 |
| 1411107 | 555418 | 555433 | 4407 | 4422 | AACAAAGTCACTTTGC  | 57  | V | 1385 |

|         |        |        |       |       |                  |     |   |      |
|---------|--------|--------|-------|-------|------------------|-----|---|------|
| 1411144 | 560921 | 560936 | 9910  | 9925  | AAGGAATGATCTGCAG | 53  | V | 1386 |
| 1411151 | 217418 | 217433 | 384   | 399   | CCAGTAAGAGGCTGGA | 94  | V | 1387 |
| 1411171 | 562292 | 562307 | 11281 | 11296 | ACACAAATTACTGTTC | 80  | V | 1388 |
| 1411176 | 222094 | 222109 | 1504  | 1519  | AAAATAGCTATCAGGC | 17  | V | 1389 |
| 1411187 | 556860 | 556875 | 5849  | 5864  | GAAAATGTGGTTGGCT | 20  | V | 1390 |
| 1411201 | 557569 | 557584 | 6558  | 6573  | CTAGATTAGGATAACA | 36  | V | 1391 |
| 1411213 | 554315 | 554330 | 3304  | 3319  | ACGGATTACCAGAAAG | 14  | V | 1392 |
| 1411241 | 559322 | 559337 | 8311  | 8326  | TACTAAGACTGCACAG | 60  | V | 1393 |
| 1411268 | 558915 | 558930 | 7904  | 7919  | TACAACAATGGCAGGT | 26  | V | 1394 |
| 1411344 | 560270 | 560285 | 9259  | 9274  | TAAACTCCATGGCTTT | 57  | V | 1395 |
| 1411360 | 559570 | 559585 | 8559  | 8574  | TATACTTTAGTGCTTG | 15  | V | 1396 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 6   | W | 181  |
| 1408245 | 243313 | 243328 | N/A   | N/A   | AAATTAAAAGACGGCC | 98  | W | 1397 |
| 1408249 | 249396 | 249411 | N/A   | N/A   | GTATTATTAGTATGTC | 18  | W | 1398 |
| 1408311 | 290678 | 290693 | 2157  | 2172  | TCGGTATTAAGAAGCA | 31  | W | 1399 |
| 1408333 | 188556 | 188571 | N/A   | N/A   | ATTATTGATAGGCGAG | 20  | W | 1400 |
| 1408559 | 288730 | 288745 | N/A   | N/A   | TTGTATCAGATTACCT | 76  | W | 1401 |
| 1408626 | 189718 | 189733 | N/A   | N/A   | AGTCTATAGGCATGAT | 25  | W | 1402 |
| 1408682 | 217923 | 217938 | 889   | 904   | ACCAACACTGCCTGCA | 13  | W | 1403 |
| 1408718 | 263069 | 263084 | N/A   | N/A   | TATTATCAGCTCACAC | 33  | W | 1404 |
| 1408727 | 262869 | 262884 | N/A   | N/A   | ACCATATGAATAAAGA | 53  | W | 1405 |
| 1408744 | 218212 | 218227 | 1178  | 1193  | ATTCATCCCAAACATT | 16  | W | 1406 |
| 1409117 | 513624 | 513639 | N/A   | N/A   | ACTTTATTAAGCCTCC | 26  | W | 1407 |
| 1409185 | 103463 | 103478 | N/A   | N/A   | GTCCATAAGCTCTTTC | 23  | W | 1408 |
| 1409210 | 481482 | 481497 | N/A   | N/A   | GATATTGGAGCCATCA | 86  | W | 1409 |
| 1409211 | 443878 | 443893 | N/A   | N/A   | TAGTATTTCAAGAGGC | 11  | W | 1410 |
| 1409249 | 150517 | 150532 | N/A   | N/A   | GTTACTAGACTCACCA | 67  | W | 1411 |
| 1409257 | 269652 | 269667 | N/A   | N/A   | GTATCTTAGATTCAAA | 48  | W | 1412 |
| 1409282 | 85745  | 85760  | N/A   | N/A   | GTATACATAAGAGTCT | 44  | W | 1413 |
| 1409300 | 276351 | 276366 | N/A   | N/A   | AATTTAGAAGATGCCA | 43  | W | 1414 |
| 1409371 | 205261 | 205276 | N/A   | N/A   | AGTGATTAATAGTTAC | 77  | W | 1415 |
| 1409378 | 499022 | 499037 | N/A   | N/A   | TAGATTTAAACAGTCT | 113 | W | 1416 |
| 1409400 | 544829 | 544844 | N/A   | N/A   | CTGTATAAGTATTCAG | 104 | W | 1417 |
| 1409412 | 287010 | 287025 | N/A   | N/A   | CCAAAGTATCACCTTA | 11  | W | 1418 |
| 1409426 | 284070 | 284085 | N/A   | N/A   | GCCAATAACCATAGTT | 47  | W | 1419 |
| 1409440 | 305987 | 306002 | N/A   | N/A   | GAGTATATTGTATGAC | 13  | W | 1420 |
| 1409455 | 293802 | 293817 | N/A   | N/A   | TATACTTCAGATTGTT | 20  | W | 1421 |
| 1409465 | 463610 | 463625 | N/A   | N/A   | TGTAATATTTGTCATC | 8   | W | 1422 |
| 1409500 | 409387 | 409402 | N/A   | N/A   | CCATATTATGTGCTTC | 6   | W | 1423 |
| 1409538 | 432248 | 432263 | N/A   | N/A   | CCATTTTGAACCCACA | 95  | W | 1424 |
| 1409558 | 183380 | 183395 | N/A   | N/A   | GCTAAACTTCATACCT | 38  | W | 1425 |
| 1409600 | 191393 | 191408 | N/A   | N/A   | GCCTACTATTGACTAG | 90  | W | 1426 |
| 1409626 | 38260  | 38275  | N/A   | N/A   | CCTACTAGACTGCTGG | 97  | W | 1427 |
| 1409659 | 119331 | 119346 | N/A   | N/A   | ATCAGTTAAAGATGAG | 70  | W | 1428 |
| 1409728 | 330969 | 330984 | N/A   | N/A   | AGCTTATAAATCCTGC | 40  | W | 1429 |

|         |        |        |       |       |                   |    |   |      |
|---------|--------|--------|-------|-------|-------------------|----|---|------|
| 1409748 | 135500 | 135515 | N/A   | N/A   | CTCATAAAGATGACCA  | 53 | W | 1430 |
| 1409774 | 77774  | 77789  | N/A   | N/A   | GACAAATCACTTGTGG  | 28 | W | 1431 |
| 1409791 | 228196 | 228211 | N/A   | N/A   | GCAAAGTCTTACCACA  | 12 | W | 1432 |
| 1409835 | 237086 | 237101 | N/A   | N/A   | CACTAGTTAATCCTCA  | 38 | W | 1433 |
| 1409852 | 562304 | 562319 | 11293 | 11308 | TTAACAATATCCACAC  | 28 | W | 1434 |
| 1409856 | 199339 | 199354 | N/A   | N/A   | CATGTAATAAAGAGGT  | 72 | W | 1435 |
| 1409889 | 396085 | 396100 | N/A   | N/A   | ACTTATATTAGATGGT  | 89 | W | 1436 |
| 1409915 | 257810 | 257825 | N/A   | N/A   | CATTTTAGATGCTGTA  | 26 | W | 1437 |
| 1409973 | 222859 | 222874 | N/A   | N/A   | AAGATATCAGCTCTCT  | 66 | W | 1438 |
| 1409987 | 212708 | 212723 | N/A   | N/A   | TAAGAGTTTTGCAGTA  | 25 | W | 1439 |
| 1410016 | 254579 | 254594 | N/A   | N/A   | TTAACTTAGTCTTCCA  | 8  | W | 1440 |
| 1410023 | 203375 | 203390 | N/A   | N/A   | GATTACTGTAGCTCCA  | 22 | W | 1441 |
| 1410080 | 280529 | 280544 | N/A   | N/A   | ATCATACTAAGATTGG  | 27 | W | 1442 |
| 1410089 | 530706 | 530721 | N/A   | N/A   | TGTTATTATACTTGTA  | 53 | W | 1443 |
| 1410121 | 221509 | 221524 | N/A   | N/A   | CAAACCTTTCATCAGTT | 96 | W | 1444 |
| 1410135 | 209690 | 209705 | N/A   | N/A   | CAAATTCATTACACGC  | 51 | W | 1445 |
| 1410155 | 291273 | 291288 | N/A   | N/A   | AGTATTATGAAGAGTT  | 9  | W | 1446 |
| 1410190 | 370615 | 370630 | N/A   | N/A   | TGTTTTAGAGAACTCC  | 10 | W | 1447 |
| 1410203 | 225500 | 225515 | N/A   | N/A   | ACTAACACTTTATACA  | 72 | W | 1448 |
| 1410212 | 353188 | 353203 | N/A   | N/A   | TCAGTAATTAGACTTA  | 12 | W | 1449 |
| 1410242 | 231801 | 231816 | N/A   | N/A   | GATACAAATTTCTGGA  | 9  | W | 1450 |
| 1410274 | 272321 | 272336 | N/A   | N/A   | TGTATACAAAGCTGAA  | 45 | W | 1451 |
| 1410286 | 207434 | 207449 | N/A   | N/A   | TAAATTTTCAGTGGAGA | 31 | W | 1452 |
| 1410309 | 245621 | 245636 | N/A   | N/A   | TATACCTTCCATCAGA  | 96 | W | 1453 |
| 1410313 | 168919 | 168934 | N/A   | N/A   | GATATGAGAAACCTTC  | 36 | W | 1454 |
| 1410339 | 290004 | 290019 | N/A   | N/A   | TCTTTAGTATAGTAGG  | 9  | W | 1455 |
| 1410345 | 316313 | 316328 | N/A   | N/A   | GAGAAATCAGGAGTCC  | 73 | W | 1456 |
| 1410383 | 196438 | 196453 | N/A   | N/A   | AAGTATCAAGTAAAGT  | 92 | W | 1457 |
| 1410433 | 263486 | 263501 | N/A   | N/A   | ACCTTATATTCCTGT   | 26 | W | 1458 |
| 1410487 | 181221 | 181236 | N/A   | N/A   | TCCTTATAAGCAATGA  | 35 | W | 1459 |
| 1410558 | 234711 | 234726 | N/A   | N/A   | ATTATACTTACCATGC  | 46 | W | 1460 |
| 1410576 | 457311 | 457326 | 2436  | 2451  | GCATTTGGATCATGAG  | 12 | W | 1461 |
| 1411127 | 217508 | 217523 | 474   | 489   | TGTAAACTTTGTTTCCT | 6  | W | 1462 |
| 1411186 | 222095 | 222110 | 1505  | 1520  | TAAAATAGCTATCAGG  | 21 | W | 1463 |
| 1411194 | 560272 | 560287 | 9261  | 9276  | TATAAACTCCATGGCT  | 46 | W | 1464 |
| 1411217 | 557046 | 557061 | 6035  | 6050  | ATGGAAGGAAGTCCCA  | 82 | W | 1465 |
| 1411238 | 555444 | 555459 | 4433  | 4448  | CTATCAAGGAGACTGA  | 86 | W | 1466 |
| 1411259 | 556155 | 556170 | 5144  | 5159  | CATATTGGTAACTATC  | 60 | W | 1467 |
| 1411285 | 561062 | 561077 | 10051 | 10066 | GCTGATGGAAAAGTGC  | 91 | W | 1468 |
| 1411297 | 557923 | 557938 | 6912  | 6927  | ACAATGGAGAACTTC   | 47 | W | 1469 |
| 1411306 | 554326 | 554341 | 3315  | 3330  | TAAATATATTCACGGA  | 13 | W | 1470 |
| 1411314 | 559571 | 559586 | 8560  | 8575  | ATATACTTTAGTGCTT  | 21 | W | 1471 |
| 1411325 | 558916 | 558931 | 7905  | 7920  | ATACAACAATGGCAGG  | 22 | W | 1472 |
| 1411409 | 559323 | 559338 | 8312  | 8327  | TTACTAAGACTGCACA  | 70 | W | 1473 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 6  | X | 181  |

|         |        |        |      |      |                   |    |   |      |
|---------|--------|--------|------|------|-------------------|----|---|------|
| 1408244 | 243315 | 243330 | N/A  | N/A  | AGAAATTAAGACGG    | 18 | X | 1474 |
| 1408248 | 249397 | 249412 | N/A  | N/A  | GGTATTATTAGTATGT  | 5  | X | 1475 |
| 1408310 | 290680 | 290695 | 2159 | 2174 | GATCGGTATTAAGAAG  | 85 | X | 1476 |
| 1408332 | 188557 | 188572 | N/A  | N/A  | TATTATTGATAGGCGA  | 32 | X | 1477 |
| 1408545 | 288739 | 288754 | N/A  | N/A  | TTCAAGGATTTGTATC  | 78 | X | 1478 |
| 1408603 | 181222 | 181237 | N/A  | N/A  | CTCCTTATAAGCAATG  | 44 | X | 1479 |
| 1408625 | 189728 | 189743 | N/A  | N/A  | ATCATTGTAGAGTCTA  | 8  | X | 1480 |
| 1408701 | 263070 | 263085 | N/A  | N/A  | ATATTATCAGCTCACA  | 16 | X | 1481 |
| 1408710 | 262900 | 262915 | N/A  | N/A  | ACCAAGCATGCATCCA  | 18 | X | 1482 |
| 1408734 | 218232 | 218247 | 1198 | 1213 | CTCTGAAGGAGCTTTC  | 18 | X | 1483 |
| 1409088 | 78118  | 78133  | N/A  | N/A  | CAGGATAAGAGTGCTG  | 71 | X | 1484 |
| 1409114 | 293998 | 294013 | N/A  | N/A  | TAGATAAAGAGGCATT  | 12 | X | 1485 |
| 1409119 | 263943 | 263958 | N/A  | N/A  | TATCATCCAAAGCCCA  | 59 | X | 1486 |
| 1409137 | 207435 | 207450 | N/A  | N/A  | GTAAATTTCAAGTGGAG | 25 | X | 1487 |
| 1409151 | 221510 | 221525 | N/A  | N/A  | CCAAACTTTCATCAGT  | 57 | X | 1488 |
| 1409171 | 196474 | 196489 | N/A  | N/A  | GTATAAGATTTTCTTC  | 70 | X | 1489 |
| 1409173 | 432780 | 432795 | N/A  | N/A  | CCTTAACATTGTCTCA  | 39 | X | 1490 |
| 1409187 | 191607 | 191622 | N/A  | N/A  | GTTTACTTAAAGTCTG  | 19 | X | 1491 |
| 1409216 | 119463 | 119478 | N/A  | N/A  | CTTTATACAACTCCC   | 27 | X | 1492 |
| 1409238 | 228321 | 228336 | N/A  | N/A  | TCAAATCCTTGCATCT  | 57 | X | 1493 |
| 1409251 | 209712 | 209727 | N/A  | N/A  | CCTATTAAATGCCCAT  | 61 | X | 1494 |
| 1409260 | 269655 | 269670 | N/A  | N/A  | ATAGTATCTTAGATTC  | 21 | X | 1495 |
| 1409278 | 183596 | 183611 | N/A  | N/A  | CAAATTAGAAGGTGTC  | 9  | X | 1496 |
| 1409283 | 169269 | 169284 | N/A  | N/A  | GTAGAATAGTTCTTCC  | 28 | X | 1497 |
| 1409307 | 152301 | 152316 | N/A  | N/A  | GATAATCACAGGTTGT  | 48 | X | 1498 |
| 1409375 | 254580 | 254595 | N/A  | N/A  | TTTAACTTAGTCTTCC  | 10 | X | 1499 |
| 1409473 | 354265 | 354280 | N/A  | N/A  | ACAAATTTATGAGGCT  | 6  | X | 1500 |
| 1409481 | 444567 | 444582 | N/A  | N/A  | TTCAAGTTAATGGTCA  | 6  | X | 1501 |
| 1409494 | 237721 | 237736 | N/A  | N/A  | GAAACTCAGACCAGGC  | 12 | X | 1502 |
| 1409498 | 411528 | 411543 | N/A  | N/A  | CCAACTAACTTCCAGC  | 82 | X | 1503 |
| 1409529 | 272322 | 272337 | N/A  | N/A  | CTGTATACAAAGCTGA  | 18 | X | 1504 |
| 1409587 | 199504 | 199519 | N/A  | N/A  | TCAATAATGATAGTCA  | 47 | X | 1505 |
| 1409698 | 135526 | 135541 | N/A  | N/A  | CTTGAATCAAATCTGG  | 61 | X | 1506 |
| 1409731 | 500464 | 500479 | N/A  | N/A  | TTAGATATGGTCCTTC  | 51 | X | 1507 |
| 1409766 | 284154 | 284169 | N/A  | N/A  | GCTCAAATGTAATCAT  | 32 | X | 1508 |
| 1409839 | 234712 | 234727 | N/A  | N/A  | GATTATACTTACCATG  | 64 | X | 1509 |
| 1409859 | 463909 | 463924 | N/A  | N/A  | TCAGATTTAATAGGTC  | 4  | X | 1510 |
| 1409866 | 205405 | 205420 | N/A  | N/A  | ATGCTAAAGGCACAGA  | 64 | X | 1511 |
| 1409900 | 530803 | 530818 | N/A  | N/A  | TCTTTAAGATGACTGT  | 50 | X | 1512 |
| 1409909 | 396086 | 396101 | N/A  | N/A  | GACTTATATTAGATGG  | 9  | X | 1513 |
| 1409949 | 483370 | 483385 | N/A  | N/A  | AAGAATTCATTTGGAG  | 69 | X | 1514 |
| 1409960 | 316619 | 316634 | N/A  | N/A  | ACACTATTTTACTAC   | 61 | X | 1515 |
| 1410003 | 43215  | 43230  | N/A  | N/A  | GAAATACTGTGACAC   | 76 | X | 1516 |
| 1410160 | 246181 | 246196 | N/A  | N/A  | CACTTACTGGTCCAG   | 11 | X | 1517 |
| 1410164 | 290005 | 290020 | N/A  | N/A  | TTCTTTAGTATAGTAG  | 19 | X | 1518 |

|         |        |        |       |       |                  |     |   |      |
|---------|--------|--------|-------|-------|------------------|-----|---|------|
| 1410169 | 291274 | 291289 | N/A   | N/A   | GAGTATTATGAAGAGT | 3   | X | 1519 |
| 1410195 | 103730 | 103745 | N/A   | N/A   | AGTTATCAAGTTTTCA | 9   | X | 1520 |
| 1410232 | 223036 | 223051 | N/A   | N/A   | GTAGATAACCTGAGGA | 40  | X | 1521 |
| 1410238 | 559572 | 559587 | 8561  | 8576  | GATATACTTTAGTGCT | 18  | X | 1522 |
| 1410288 | 280537 | 280552 | N/A   | N/A   | CCTTTTGAATCATACT | 39  | X | 1523 |
| 1410405 | 231802 | 231817 | N/A   | N/A   | TGATACAAATTTCTGG | 8   | X | 1524 |
| 1410412 | 276879 | 276894 | N/A   | N/A   | GCTATTTAGAAGGTAA | 67  | X | 1525 |
| 1410424 | 85904  | 85919  | N/A   | N/A   | ACTATTTAGATCATGA | 20  | X | 1526 |
| 1410426 | 225646 | 225661 | N/A   | N/A   | ACTAATAGTTCCTTC  | 58  | X | 1527 |
| 1410430 | 372336 | 372351 | N/A   | N/A   | CCACAATACTGGCTTT | 46  | X | 1528 |
| 1410431 | 287022 | 287037 | N/A   | N/A   | GAAGAGTTAATTCCAA | 15  | X | 1529 |
| 1410438 | 212984 | 212999 | N/A   | N/A   | GCTGAATTATTTGTCT | 49  | X | 1530 |
| 1410451 | 306173 | 306188 | N/A   | N/A   | GAAGTAGAGATGGCAT | 30  | X | 1531 |
| 1410493 | 546153 | 546168 | N/A   | N/A   | TATTTACATGGATCTC | 21  | X | 1532 |
| 1410533 | 331862 | 331877 | N/A   | N/A   | ATAGTATGATAGCACA | 5   | X | 1533 |
| 1410557 | 257829 | 257844 | N/A   | N/A   | ACTTTATGAGCCAGCC | 21  | X | 1534 |
| 1410567 | 203476 | 203491 | N/A   | N/A   | TCAATAATACAGACGG | 18  | X | 1535 |
| 1411098 | 457336 | 457351 | 2461  | 2476  | CAAGAATCCACTTTTG | 80† | X | 1536 |
| 1411117 | 217509 | 217524 | 475   | 490   | CTGTAACTTTGTTC   | 10  | X | 1537 |
| 1411153 | 557048 | 557063 | 6037  | 6052  | ATATGGAAGGAAGTCC | 62  | X | 1538 |
| 1411172 | 514823 | 514838 | 2692  | 2707  | TTTAAGTTTAAACACG | 38  | X | 1539 |
| 1411218 | 558917 | 558932 | 7906  | 7921  | AATACAACAATGGCAG | 24  | X | 1540 |
| 1411266 | 554327 | 554342 | 3316  | 3331  | TTAAATATATTCACGG | 17  | X | 1541 |
| 1411275 | 560274 | 560289 | 9263  | 9278  | TTTATAAACTCCATGG | 69  | X | 1542 |
| 1411280 | 222096 | 222111 | 1506  | 1521  | CTAAAATAGCTATCAG | 27  | X | 1543 |
| 1411282 | 557924 | 557939 | 6913  | 6928  | GACAATGGAGAACTT  | 35  | X | 1544 |
| 1411339 | 555466 | 555481 | 4455  | 4470  | GAGTAGTAGCAGAGTG | 38  | X | 1545 |
| 1411340 | 562306 | 562321 | 11295 | 11310 | CTTTAACAATATCCAC | 27  | X | 1546 |
| 1411375 | 556156 | 556171 | 5145  | 5160  | CCATATTGGTAACTAT | 44  | X | 1547 |
| 1411379 | 217926 | 217941 | 892   | 907   | GAAACCAACACTGCCT | 9   | X | 1548 |
| 1411440 | 561174 | 561189 | 10163 | 10178 | GAAGTTAGGGTGCTTA | 35  | X | 1549 |
| 1411444 | 559325 | 559340 | 8314  | 8329  | AGTTACTAAGACTGCA | 59  | X | 1550 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 6   | Y | 181  |
| 1408315 | 290682 | 290697 | 2161  | 2176  | TAGATCGGTATTAAGA | 50  | Y | 1551 |
| 1408331 | 188559 | 188574 | N/A   | N/A   | GGTATTATTGATAGGC | 6   | Y | 1552 |
| 1408558 | 288740 | 288755 | N/A   | N/A   | ATTCAAGGATTTGTAT | 91  | Y | 1553 |
| 1408624 | 189748 | 189763 | N/A   | N/A   | CTAACCTCATTTTTTC | 75  | Y | 1554 |
| 1408672 | 243354 | 243369 | N/A   | N/A   | TTTCAAACATCTTGTG | 62  | Y | 1555 |
| 1408717 | 263079 | 263094 | N/A   | N/A   | GGTATGATAATATTAT | 94  | Y | 1556 |
| 1408726 | 262909 | 262924 | N/A   | N/A   | ATATCAGTTACCAAGC | 41  | Y | 1557 |
| 1408870 | 217932 | 217947 | 898   | 913   | TTTCAAGAAACCAACA | 49  | Y | 1558 |
| 1409095 | 85906  | 85921  | N/A   | N/A   | ACACTATTTAGATCAT | 49  | Y | 1559 |
| 1409120 | 432941 | 432956 | N/A   | N/A   | AGAACTTGAAGGCTTA | 32  | Y | 1560 |
| 1409140 | 306432 | 306447 | N/A   | N/A   | CAGCAATTTAGAGCAA | 50  | Y | 1561 |
| 1409147 | 291275 | 291290 | N/A   | N/A   | AGAGTATTATGAAGAG | 3   | Y | 1562 |

|         |        |        |     |     |                   |    |   |      |
|---------|--------|--------|-----|-----|-------------------|----|---|------|
| 1409193 | 205409 | 205424 | N/A | N/A | GATAATGCTAAAGGCA  | 71 | Y | 1563 |
| 1409204 | 103797 | 103812 | N/A | N/A | TTAACAGTAGAGGTCC  | 24 | Y | 1564 |
| 1409207 | 246258 | 246273 | N/A | N/A | ATGGTAAAATAGAGGT  | 4  | Y | 1565 |
| 1409226 | 276881 | 276896 | N/A | N/A | AAGCTATTTAGAAGGT  | 76 | Y | 1566 |
| 1409266 | 269658 | 269673 | N/A | N/A | TCAATAGTATCTTAGA  | 38 | Y | 1567 |
| 1409320 | 152395 | 152410 | N/A | N/A | TTCTTAAAAGAGCTCC  | 80 | Y | 1568 |
| 1409351 | 223910 | 223925 | N/A | N/A | CAAACCATGTTTGGTC  | 54 | Y | 1569 |
| 1409391 | 254605 | 254620 | N/A | N/A | TTATTAAGTCAGGTCA  | 4  | Y | 1570 |
| 1409408 | 293999 | 294014 | N/A | N/A | GTAGATAAAGAGGCAT  | 4  | Y | 1571 |
| 1409475 | 290310 | 290325 | N/A | N/A | TATACATAGTACAAGG  | 23 | Y | 1572 |
| 1409484 | 213007 | 213022 | N/A | N/A | TTTAGAGACATGCCCA  | 40 | Y | 1573 |
| 1409562 | 447159 | 447174 | N/A | N/A | AACAATGTATTGTCAT  | 48 | Y | 1574 |
| 1409585 | 203697 | 203712 | N/A | N/A | GAAATCAACATTCCAG  | 35 | Y | 1575 |
| 1409595 | 225648 | 225663 | N/A | N/A | ACACTAATAGTTCCTT  | 19 | Y | 1576 |
| 1409603 | 181236 | 181251 | N/A | N/A | TGTAAGTTCATTATCT  | 41 | Y | 1577 |
| 1409638 | 231815 | 231830 | N/A | N/A | ACAATAGAGCAAGTGA  | 13 | Y | 1578 |
| 1409655 | 207436 | 207451 | N/A | N/A | GGTAAATTCAGTGGA   | 16 | Y | 1579 |
| 1409660 | 396498 | 396513 | N/A | N/A | GATTTTAGGCTACTCA  | 30 | Y | 1580 |
| 1409669 | 196476 | 196491 | N/A | N/A | CAGTATAAGATTTTCT  | 72 | Y | 1581 |
| 1409700 | 119464 | 119479 | N/A | N/A | CCTTTATACAACCTCC  | 18 | Y | 1582 |
| 1409747 | 272329 | 272344 | N/A | N/A | CATGAATCTGTATACA  | 69 | Y | 1583 |
| 1409751 | 354971 | 354986 | N/A | N/A | AGAGTAATATTGGCAC  | 6  | Y | 1584 |
| 1409773 | 264213 | 264228 | N/A | N/A | GCATTAGCAAAATCAG  | 26 | Y | 1585 |
| 1409779 | 199598 | 199613 | N/A | N/A | GCTTAATCTAGAGAGA  | 57 | Y | 1586 |
| 1409817 | 183645 | 183660 | N/A | N/A | AAATTTCAATGCACTA  | 43 | Y | 1587 |
| 1409825 | 486662 | 486677 | N/A | N/A | TCTATAACATGCTACT  | 55 | Y | 1588 |
| 1409860 | 546172 | 546187 | N/A | N/A | TTAATCATATCCACAC  | 34 | Y | 1589 |
| 1409881 | 78244  | 78259  | N/A | N/A | GCAAATCAAGCTTCTT  | 9  | Y | 1590 |
| 1409906 | 249398 | 249413 | N/A | N/A | AGGTATTATTAGTATG  | 7  | Y | 1591 |
| 1409908 | 530804 | 530819 | N/A | N/A | ATCTTTAAGATGACTG  | 57 | Y | 1592 |
| 1409955 | 501256 | 501271 | N/A | N/A | TTTACAAAGTTGTCC   | 25 | Y | 1593 |
| 1409962 | 221511 | 221526 | N/A | N/A | ACCAAACCTTTCATCAG | 58 | Y | 1594 |
| 1410014 | 228974 | 228989 | N/A | N/A | AAGGTTTAAACCACAG  | 17 | Y | 1595 |
| 1410062 | 169811 | 169826 | N/A | N/A | CGCTTTAAAACAGCAA  | 84 | Y | 1596 |
| 1410066 | 373262 | 373277 | N/A | N/A | GTTCTATAAACTGTTC  | 8  | Y | 1597 |
| 1410090 | 136556 | 136571 | N/A | N/A | GAAACAATCTGTCCAT  | 81 | Y | 1598 |
| 1410124 | 287024 | 287039 | N/A | N/A | CTGAAGAGTTAATTCC  | 15 | Y | 1599 |
| 1410141 | 257831 | 257846 | N/A | N/A | ATACTTTATGAGCCAG  | 3  | Y | 1600 |
| 1410165 | 281682 | 281697 | N/A | N/A | AGGGAAAATTCATGGC  | 29 | Y | 1601 |
| 1410185 | 209713 | 209728 | N/A | N/A | TCCTATTAAATGCCCA  | 40 | Y | 1602 |
| 1410200 | 284281 | 284296 | N/A | N/A | TCATTATATAACCTTA  | 50 | Y | 1603 |
| 1410222 | 237984 | 237999 | N/A | N/A | GTAAACTAATCACACA  | 86 | Y | 1604 |
| 1410261 | 411529 | 411544 | N/A | N/A | ACCAACTAACTTCCAG  | 55 | Y | 1605 |
| 1410302 | 515145 | 515160 | N/A | N/A | TCTACTAAAACCCTCA  | 66 | Y | 1606 |
| 1410359 | 331863 | 331878 | N/A | N/A | TATAGTATGATAGCAC  | 11 | Y | 1607 |

|         |        |        |       |       |                   |     |   |      |
|---------|--------|--------|-------|-------|-------------------|-----|---|------|
| 1410386 | 43294  | 43309  | N/A   | N/A   | ACCAAATAAAGCTCCA  | 93  | Y | 1608 |
| 1410388 | 191757 | 191772 | N/A   | N/A   | GTTTAAGTGCAATTTA  | 54  | Y | 1609 |
| 1410483 | 317865 | 317880 | N/A   | N/A   | ATAAATCTGTGGATGA  | 49  | Y | 1610 |
| 1410541 | 464142 | 464157 | N/A   | N/A   | TAGGATAAAGCTCTAA  | 86  | Y | 1611 |
| 1410556 | 234740 | 234755 | N/A   | N/A   | TCAAGAATGTTCTGGT  | 6   | Y | 1612 |
| 1411089 | 457338 | 457353 | 2463  | 2478  | GCCAAGAATCCACTTT  | 20† | Y | 1613 |
| 1411124 | 559327 | 559342 | 8316  | 8331  | AAAGTTACTAAGACTG  | 102 | Y | 1614 |
| 1411168 | 555472 | 555487 | 4461  | 4476  | AAAGTTGAGTAGTAGC  | 58  | Y | 1615 |
| 1411195 | 218277 | 218292 | 1243  | 1258  | ATCAAGACGCACAGGG  | 8   | Y | 1616 |
| 1411200 | 557049 | 557064 | 6038  | 6053  | CATATGGAAGGAAGTC  | 57  | Y | 1617 |
| 1411204 | 561181 | 561196 | 10170 | 10185 | AGGAATTGAAGTTAGG  | 9   | Y | 1618 |
| 1411212 | 559573 | 559588 | 8562  | 8577  | TGATATACTTTAGTGC  | 59  | Y | 1619 |
| 1411231 | 217519 | 217534 | 485   | 500   | AGTCAATGGGCTGTAA  | 15  | Y | 1620 |
| 1411239 | 558919 | 558934 | 7908  | 7923  | CAAATACAACAATGGC  | 38  | Y | 1621 |
| 1411242 | 562308 | 562323 | 11297 | 11312 | CACTTTAACAATATCC  | 13  | Y | 1622 |
| 1411255 | 557929 | 557944 | 6918  | 6933  | AGTAAGACAATGGAGA  | 32  | Y | 1623 |
| 1411258 | 222097 | 222112 | 1507  | 1522  | GCTAAAATAGCTATCA  | 39  | Y | 1624 |
| 1411260 | 556166 | 556181 | 5155  | 5170  | GATACATGGGCCATAT  | 23  | Y | 1625 |
| 1411303 | 560275 | 560290 | 9264  | 9279  | CTTTATAAACTCCATG  | 27  | Y | 1626 |
| 1411331 | 554407 | 554422 | 3396  | 3411  | AGACAATCTGTACAGA  | 34  | Y | 1627 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 6   | Z | 181  |
| 1408327 | 181270 | 181285 | N/A   | N/A   | ATTTAATGGTTCCTCG  | 18  | Z | 1628 |
| 1408330 | 188560 | 188575 | N/A   | N/A   | GGGTATTATTGATAGG  | 27  | Z | 1629 |
| 1408573 | 290687 | 290702 | 2166  | 2181  | CCATGTAGATCGGTAT  | 6   | Z | 1630 |
| 1408623 | 189788 | 189803 | N/A   | N/A   | TTAGATCTAACACCTT  | 67  | Z | 1631 |
| 1408650 | 225812 | 225827 | N/A   | N/A   | AAATCATTACCACTTG  | 26  | Z | 1632 |
| 1408671 | 243364 | 243379 | N/A   | N/A   | AACAATCAACTTTCAA  | 26  | Z | 1633 |
| 1408675 | 217933 | 217948 | 899   | 914   | CTTTCAAGAAACCAAC  | 75  | Z | 1634 |
| 1408685 | 249404 | 249419 | N/A   | N/A   | CGAAGTAGGTATTATT  | 12  | Z | 1635 |
| 1408700 | 263080 | 263095 | N/A   | N/A   | TGGTATGATAATATTA  | 98  | Z | 1636 |
| 1408709 | 262910 | 262925 | N/A   | N/A   | GATATCAGTTACCAAG  | 67  | Z | 1637 |
| 1409131 | 191807 | 191822 | N/A   | N/A   | ATCTATCTGATGCTTA  | 42  | Z | 1638 |
| 1409168 | 288743 | 288758 | N/A   | N/A   | GAAATTCAAGGATTTG  | 88  | Z | 1639 |
| 1409175 | 120346 | 120361 | N/A   | N/A   | GTAAATTCAGTATTCA  | 14  | Z | 1640 |
| 1409217 | 238072 | 238087 | N/A   | N/A   | ACTAGATCAAAATTCA  | 48  | Z | 1641 |
| 1409233 | 229011 | 229026 | N/A   | N/A   | ACCAATATCCAGGGAA  | 39  | Z | 1642 |
| 1409292 | 318190 | 318205 | N/A   | N/A   | ACATTAGTATATTAC   | 54  | Z | 1643 |
| 1409298 | 331865 | 331880 | N/A   | N/A   | ACTATAGTATGATAGC  | 61  | Z | 1644 |
| 1409467 | 213008 | 213023 | N/A   | N/A   | TTTTAGAGACATGCCC  | 51  | Z | 1645 |
| 1409491 | 205449 | 205464 | N/A   | N/A   | ACGGTATGTAATCCAG  | 54  | Z | 1646 |
| 1409514 | 232058 | 232073 | N/A   | N/A   | GCATATGAGGTATGGG  | 21  | Z | 1647 |
| 1409540 | 207437 | 207452 | N/A   | N/A   | TGGTAAATTTTCAGTGG | 22  | Z | 1648 |
| 1409546 | 254606 | 254621 | N/A   | N/A   | ATTATTAAGTCAGGTC  | 5   | Z | 1649 |
| 1409553 | 199810 | 199825 | N/A   | N/A   | TGGTAACAATAATTCC  | 47  | Z | 1650 |
| 1409570 | 531052 | 531067 | N/A   | N/A   | GATTTATCTACATGTA  | 69  | Z | 1651 |

|         |        |        |       |       |                   |    |   |      |
|---------|--------|--------|-------|-------|-------------------|----|---|------|
| 1409572 | 272383 | 272398 | N/A   | N/A   | AGCTATCAACTTGAGT  | 66 | Z | 1652 |
| 1409601 | 103914 | 103929 | N/A   | N/A   | GTAACAAAACCTCATT  | 26 | Z | 1653 |
| 1409668 | 170914 | 170929 | N/A   | N/A   | AGAATATCTAGAGTGG  | 5  | Z | 1654 |
| 1409718 | 234755 | 234770 | N/A   | N/A   | ATGTAATATGCCCTTT  | 28 | Z | 1655 |
| 1409759 | 152934 | 152949 | N/A   | N/A   | AGAACTACAAAGGTGA  | 71 | Z | 1656 |
| 1409781 | 515904 | 515919 | N/A   | N/A   | ACTCATAAATGAATGG  | 60 | Z | 1657 |
| 1409789 | 411530 | 411545 | N/A   | N/A   | CACCAACTAACTTCCA  | 54 | Z | 1658 |
| 1409796 | 562338 | 562353 | 11327 | 11342 | GTAAACTTAATTGTCA  | 18 | Z | 1659 |
| 1409799 | 196477 | 196492 | N/A   | N/A   | TCAGTATAAGATTTTC  | 11 | Z | 1660 |
| 1409823 | 210696 | 210711 | N/A   | N/A   | TCAGATAAGAGGGAGA  | 65 | Z | 1661 |
| 1409828 | 447161 | 447176 | N/A   | N/A   | CAAACAATGTATTGTC  | 11 | Z | 1662 |
| 1409918 | 264510 | 264525 | N/A   | N/A   | ACCGTAACTACCTTGT  | 44 | Z | 1663 |
| 1409958 | 373374 | 373389 | N/A   | N/A   | TTTGATAAGGAGTCTA  | 31 | Z | 1664 |
| 1409991 | 397727 | 397742 | N/A   | N/A   | AGACATTAATCAATCA  | 17 | Z | 1665 |
| 1409997 | 137149 | 137164 | N/A   | N/A   | CAAACAACCTTATTGAG | 66 | Z | 1666 |
| 1410081 | 291309 | 291324 | N/A   | N/A   | AATTACTTCATAGTCC  | 15 | Z | 1667 |
| 1410087 | 464562 | 464577 | N/A   | N/A   | GGTATAAGGCTACAGG  | 4  | Z | 1668 |
| 1410112 | 246404 | 246419 | N/A   | N/A   | TACAATTTTCAGTCCTC | 14 | Z | 1669 |
| 1410116 | 87056  | 87071  | N/A   | N/A   | ACTTTAAGAAGGGCAA  | 6  | Z | 1670 |
| 1410134 | 221538 | 221553 | N/A   | N/A   | GATACGGCAAAATTTTC | 44 | Z | 1671 |
| 1410139 | 294001 | 294016 | N/A   | N/A   | TTGTAGATAAAGAGGC  | 5  | Z | 1672 |
| 1410158 | 457759 | 457774 | N/A   | N/A   | GCAAAATCAACCTTTC  | 18 | Z | 1673 |
| 1410178 | 433324 | 433339 | N/A   | N/A   | GCATTACAAAGGTCCT  | 28 | Z | 1674 |
| 1410194 | 503309 | 503324 | N/A   | N/A   | ACCAATTTGATTCATT  | 65 | Z | 1675 |
| 1410201 | 306687 | 306702 | N/A   | N/A   | CCAATAGTAATGCCCT  | 10 | Z | 1676 |
| 1410206 | 355691 | 355706 | N/A   | N/A   | GTAATAACTTTTCA    | 18 | Z | 1677 |
| 1410230 | 487349 | 487364 | N/A   | N/A   | AAGAGTAAGGTACTAT  | 68 | Z | 1678 |
| 1410241 | 269663 | 269678 | N/A   | N/A   | CCCAATCAATAGTATC  | 20 | Z | 1679 |
| 1410283 | 203698 | 203713 | N/A   | N/A   | TGAAATCAACATTCCA  | 58 | Z | 1680 |
| 1410293 | 183646 | 183661 | N/A   | N/A   | GAAATTTCAATGCACT  | 35 | Z | 1681 |
| 1410312 | 287446 | 287461 | N/A   | N/A   | TCAGAATGCAAGGCAA  | 45 | Z | 1682 |
| 1410408 | 45139  | 45154  | N/A   | N/A   | CTTAAGCATGTTCCAA  | 90 | Z | 1683 |
| 1410428 | 257849 | 257864 | N/A   | N/A   | ATTATAGGTGGAGTTC  | 25 | Z | 1684 |
| 1410464 | 223912 | 223927 | N/A   | N/A   | CCCAAACCATGTTTGG  | 93 | Z | 1685 |
| 1410471 | 290312 | 290327 | N/A   | N/A   | TCTATACATAGTACAA  | 31 | Z | 1686 |
| 1410499 | 79260  | 79275  | N/A   | N/A   | AAGATATGGGCACTCC  | 12 | Z | 1687 |
| 1410505 | 284300 | 284315 | N/A   | N/A   | AAACATGTGTTGACAC  | 34 | Z | 1688 |
| 1410530 | 281715 | 281730 | N/A   | N/A   | CTTAATTAAACCACTA  | 73 | Z | 1689 |
| 1410569 | 547512 | 547527 | N/A   | N/A   | ATTATATCTTCGCTTT  | 29 | Z | 1690 |
| 1410574 | 276953 | 276968 | N/A   | N/A   | AGAATAGTACAGTCAA  | 89 | Z | 1691 |
| 1411085 | 222098 | 222113 | 1508  | 1523  | AGCTAAAATAGCTATC  | 91 | Z | 1692 |
| 1411156 | 561201 | 561216 | 10190 | 10205 | CTCCATTAACCAACAT  | 27 | Z | 1693 |
| 1411162 | 557050 | 557065 | 6039  | 6054  | TCATATGGAAGGAAGT  | 24 | Z | 1694 |
| 1411163 | 554411 | 554426 | 3400  | 3415  | GCAAAGACAATCTGTA  | 40 | Z | 1695 |
| 1411185 | 555474 | 555489 | 4463  | 4478  | AGAAAGTTGAGTAGTA  | 66 | Z | 1696 |

|         |        |        |      |      |                   |     |    |      |
|---------|--------|--------|------|------|-------------------|-----|----|------|
| 1411248 | 558934 | 558949 | 7923 | 7938 | AACTATAAATACCCAC  | 34  | Z  | 1697 |
| 1411257 | 218278 | 218293 | 1244 | 1259 | CATCAAGACGCACAGG  | 17  | Z  | 1698 |
| 1411265 | 559646 | 559661 | 8635 | 8650 | TTTTACCTGTGACACT  | 35  | Z  | 1699 |
| 1411302 | 217524 | 217539 | 490  | 505  | CAAAGAGTCAATGGGC  | 8   | Z  | 1700 |
| 1411311 | 556241 | 556256 | 5230 | 5245 | AGATTATCAGGTAGAA  | 63  | Z  | 1701 |
| 1411336 | 558045 | 558060 | 7034 | 7049 | TGCAAAGCTAAACTTC  | 80  | Z  | 1702 |
| 1411369 | 559328 | 559343 | 8317 | 8332 | TAAAGTTACTAAGACT  | 102 | Z  | 1703 |
| 1411443 | 560276 | 560291 | 9265 | 9280 | GCTTTATAAACTCCAT  | 11  | Z  | 1704 |
| 1173403 | 288679 | 288694 | 2074 | 2089 | TCTATTGGAGAAGTGT  | 5   | AA | 181  |
| 1408326 | 181271 | 181286 | N/A  | N/A  | TATTTAATGGTTCCTC  | 9   | AA | 1705 |
| 1408329 | 188561 | 188576 | N/A  | N/A  | AGGGTATTATTGATAG  | 41  | AA | 1706 |
| 1408544 | 288759 | 288774 | N/A  | N/A  | CCATTGATATAAAAAA  | 95  | AA | 1707 |
| 1408571 | 290707 | 290722 | N/A  | N/A  | ACAAATCCACACTTAC  | 83  | AA | 1708 |
| 1408649 | 225872 | 225887 | N/A  | N/A  | GCAAAGCAAATACATT  | 25  | AA | 1709 |
| 1408670 | 243374 | 243389 | N/A  | N/A  | GACCAAAAAGTAACAAT | 70  | AA | 1710 |
| 1408684 | 249414 | 249429 | N/A  | N/A  | AACAATCCTGCGAAGT  | 28  | AA | 1711 |
| 1408716 | 263089 | 263104 | N/A  | N/A  | TGATATCAATGGTATG  | 71  | AA | 1712 |
| 1408863 | 217952 | 217967 | 918  | 933  | CCAAGAGCAGACCTCT  | 67  | AA | 1713 |
| 1409098 | 103971 | 103986 | N/A  | N/A  | TCACAAAATGTAGGGT  | 18  | AA | 1714 |
| 1409123 | 200164 | 200179 | N/A  | N/A  | ACAAATGATTACTCAC  | 43  | AA | 1715 |
| 1409153 | 319852 | 319867 | N/A  | N/A  | ACACTAACATCTGTCC  | 58  | AA | 1716 |
| 1409156 | 306721 | 306736 | N/A  | N/A  | ACAATATTCACCTTACA | 16  | AA | 1717 |
| 1409178 | 79261  | 79276  | N/A  | N/A  | CAAGATATGGGCACTC  | 15  | AA | 1718 |
| 1409243 | 269838 | 269853 | N/A  | N/A  | AGTTAATTGCTGGCAT  | 12  | AA | 1719 |
| 1409252 | 238679 | 238694 | N/A  | N/A  | CCATATTCAGCACCTT  | 13  | AA | 1720 |
| 1409275 | 281759 | 281774 | N/A  | N/A  | TCCTATCATGTAGTAA  | 44  | AA | 1721 |
| 1409296 | 120651 | 120666 | N/A  | N/A  | AAATTTTCGATGCAACA | 58  | AA | 1722 |
| 1409305 | 232059 | 232074 | N/A  | N/A  | AGCATATGAGGTATGG  | 7   | AA | 1723 |
| 1409333 | 433982 | 433997 | N/A  | N/A  | GAAAATATGGTCTTGT  | 27  | AA | 1724 |
| 1409336 | 466181 | 466196 | N/A  | N/A  | CAGAAGTAACAACCAT  | 8   | AA | 1725 |
| 1409342 | 411631 | 411646 | N/A  | N/A  | CCAATGTAAACAGTAA  | 5   | AA | 1726 |
| 1409370 | 272384 | 272399 | N/A  | N/A  | CAGCTATCAACTTGAG  | 35  | AA | 1727 |
| 1409395 | 47446  | 47461  | N/A  | N/A  | TCAATAAAGTTGACCA  | 81  | AA | 1728 |
| 1409404 | 457966 | 457981 | N/A  | N/A  | AGATAATCATGCCTCA  | 37  | AA | 1729 |
| 1409458 | 203699 | 203714 | N/A  | N/A  | CTGAAATCAACATTCC  | 27  | AA | 1730 |
| 1409472 | 517135 | 517150 | N/A  | N/A  | AAGCTATGATCATCAC  | 77  | AA | 1731 |
| 1409521 | 213009 | 213024 | N/A  | N/A  | TTTTTAGAGACATGCC  | 33  | AA | 1732 |
| 1409532 | 218518 | 218533 | N/A  | N/A  | TTAGCTTAGAAGGACC  | 44  | AA | 1733 |
| 1409539 | 234756 | 234771 | N/A  | N/A  | CATGTAATATGCCCTT  | 23  | AA | 1734 |
| 1409584 | 224434 | 224449 | N/A  | N/A  | TTATCATATGCCAACC  | 17  | AA | 1735 |
| 1409605 | 262911 | 262926 | N/A  | N/A  | TGATATCAGTTACCAA  | 54  | AA | 1736 |
| 1409621 | 547514 | 547529 | N/A  | N/A  | GTATTATATCTTCGCT  | 9   | AA | 1737 |
| 1409710 | 205450 | 205465 | N/A  | N/A  | TACGGTATGTAATCCA  | 39  | AA | 1738 |
| 1409737 | 503588 | 503603 | N/A  | N/A  | CGAATTGAATTATTCT  | 93  | AA | 1739 |
| 1409767 | 257852 | 257867 | N/A  | N/A  | TTTATTATAGGTGGAG  | 5   | AA | 1740 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1409793 | 447360 | 447375 | N/A   | N/A   | ATAATCACATTCCATC  | 38 | AA | 1741 |
| 1409801 | 487414 | 487429 | N/A   | N/A   | GCTATAAAAGCACTGC  | 65 | AA | 1742 |
| 1409834 | 87130  | 87145  | N/A   | N/A   | CCATAAAGCACACCTG  | 53 | AA | 1743 |
| 1409854 | 373830 | 373845 | N/A   | N/A   | AGGTATTAAACAGTTG  | 5  | AA | 1744 |
| 1409896 | 284302 | 284317 | N/A   | N/A   | CAAAACATGTGTTGAC  | 28 | AA | 1745 |
| 1409939 | 532131 | 532146 | N/A   | N/A   | ATCAACTATGTTATGG  | 56 | AA | 1746 |
| 1409981 | 189795 | 189810 | N/A   | N/A   | TCCAAGTTTAGATCTA  | 16 | AA | 1747 |
| 1409998 | 153514 | 153529 | N/A   | N/A   | ACTATATTTTGGCTGG  | 57 | AA | 1748 |
| 1410008 | 264511 | 264526 | N/A   | N/A   | CACCGTAACTACCTTG  | 39 | AA | 1749 |
| 1410025 | 291486 | 291501 | N/A   | N/A   | GAAATTATGTGACTAG  | 25 | AA | 1750 |
| 1410028 | 355954 | 355969 | N/A   | N/A   | CAGGTATTAAAGTCTA  | 8  | AA | 1751 |
| 1410086 | 294161 | 294176 | N/A   | N/A   | CCATTTCAAACAAGGT  | 71 | AA | 1752 |
| 1410097 | 254643 | 254658 | N/A   | N/A   | CTTTTACAGATCCTTA  | 9  | AA | 1753 |
| 1410102 | 246406 | 246421 | N/A   | N/A   | GATACAATTTTCAGTCC | 45 | AA | 1754 |
| 1410108 | 287453 | 287468 | N/A   | N/A   | AACTACATCAGAATGC  | 41 | AA | 1755 |
| 1410132 | 397941 | 397956 | N/A   | N/A   | TTAATAATGTCAAGCC  | 9  | AA | 1756 |
| 1410180 | 207452 | 207467 | N/A   | N/A   | ACAAAGTTCAGGCAGT  | 41 | AA | 1757 |
| 1410250 | 211140 | 211155 | N/A   | N/A   | AATGTTTAAACCATCA  | 65 | AA | 1758 |
| 1410256 | 184895 | 184910 | N/A   | N/A   | AAGTAGCTTATAGCCA  | 23 | AA | 1759 |
| 1410301 | 277639 | 277654 | N/A   | N/A   | CCACTATGGAGACTGG  | 55 | AA | 1760 |
| 1410333 | 290313 | 290328 | N/A   | N/A   | ATCTATACATAGTACA  | 25 | AA | 1761 |
| 1410343 | 137232 | 137247 | N/A   | N/A   | CTTTATTTCAGGAGAGC | 50 | AA | 1762 |
| 1410380 | 171304 | 171319 | N/A   | N/A   | CCAATAACATCCATTC  | 18 | AA | 1763 |
| 1410488 | 191881 | 191896 | N/A   | N/A   | TACCTAACTTGCTGAG  | 66 | AA | 1764 |
| 1410542 | 196822 | 196837 | N/A   | N/A   | GAGAAACTGCTTTCGC  | 57 | AA | 1765 |
| 1410563 | 332271 | 332286 | N/A   | N/A   | CCTAAACAATTCTTCA  | 29 | AA | 1766 |
| 1410564 | 229086 | 229101 | N/A   | N/A   | ATCATTTGATGCCATT  | 13 | AA | 1767 |
| 1410570 | 221544 | 221559 | N/A   | N/A   | AAACTTGATACGGCAA  | 22 | AA | 1768 |
| 1411178 | 559667 | 559682 | 8656  | 8671  | TTAAACCTGGTCCTGA  | 33 | AA | 1769 |
| 1411188 | 558935 | 558950 | 7924  | 7939  | CAACTATAAATACCCA  | 14 | AA | 1770 |
| 1411228 | 562339 | 562354 | 11328 | 11343 | TGTAAACTTAATTGTC  | 30 | AA | 1771 |
| 1411240 | 222101 | 222116 | 1511  | 1526  | CAAAGCTAAAATAGCT  | 83 | AA | 1772 |
| 1411251 | 217525 | 217540 | 491   | 506   | TCAAAGAGTCAATGGG  | 8  | AA | 1773 |
| 1411253 | 557051 | 557066 | 6040  | 6055  | ATCATATGGAAGGAAG  | 22 | AA | 1774 |
| 1411278 | 558068 | 558083 | 7057  | 7072  | GTAAATTACAGAGAT   | 50 | AA | 1775 |
| 1411284 | 556245 | 556260 | 5234  | 5249  | ATTTAGATTATCAGGT  | 80 | AA | 1776 |
| 1411296 | 555475 | 555490 | 4464  | 4479  | GAGAAAGTTGAGTAGT  | 61 | AA | 1777 |
| 1411329 | 560291 | 560306 | 9280  | 9295  | TCAAATGGTTACTTGG  | 34 | AA | 1778 |
| 1411367 | 559329 | 559344 | 8318  | 8333  | CTAAAGTTACTAAGAC  | 85 | AA | 1779 |
| 1411381 | 554412 | 554427 | 3401  | 3416  | AGCAAAGACAATCTGT  | 17 | AA | 1780 |
| 1411415 | 561223 | 561238 | 10212 | 10227 | TTAAGTGAAACTCCAA  | 15 | AA | 1781 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 4  | AB | 181  |
| 1408325 | 181273 | 181288 | N/A   | N/A   | TCTATTTAATGGTTCC  | 3  | AB | 1782 |
| 1408350 | 225894 | 225909 | N/A   | N/A   | ATTTAAGTAAATCTAG  | 77 | AB | 1783 |
| 1408472 | 222102 | 222117 | 1512  | 1527  | TCAAAGCTAAAATAGC  | 60 | AB | 1784 |

|         |        |        |     |     |                  |    |    |      |
|---------|--------|--------|-----|-----|------------------|----|----|------|
| 1408557 | 288760 | 288775 | N/A | N/A | ACCATTGATATAAAAA | 93 | AB | 1785 |
| 1408582 | 290527 | 290542 | N/A | N/A | TGCTAGGTACAATTAG | 59 | AB | 1786 |
| 1408587 | 290709 | 290724 | N/A | N/A | TCACAAATCCACACTT | 81 | AB | 1787 |
| 1408615 | 188568 | 188583 | N/A | N/A | ACATTCAAGGGTATTA | 25 | AB | 1788 |
| 1408642 | 224923 | 224938 | N/A | N/A | CGATCAAAAGAAGAAT | 81 | AB | 1789 |
| 1408668 | 243394 | 243409 | N/A | N/A | TGCCAACAAATCAGTA | 75 | AB | 1790 |
| 1408669 | 217953 | 217968 | 919 | 934 | CCCAAGAGCAGACCTC | 14 | AB | 1791 |
| 1408683 | 249444 | 249459 | N/A | N/A | TTTACAGGCATTAACA | 26 | AB | 1792 |
| 1408699 | 263090 | 263105 | N/A | N/A | GTGATATCAATGGTAT | 33 | AB | 1793 |
| 1409096 | 120951 | 120966 | N/A | N/A | AAGTATATAGCCTTCC | 20 | AB | 1794 |
| 1409118 | 434232 | 434247 | N/A | N/A | ACCAAGTAATTCCTTC | 16 | AB | 1795 |
| 1409179 | 189806 | 189821 | N/A | N/A | GCATTACATTCTCAA  | 7  | AB | 1796 |
| 1409200 | 466182 | 466197 | N/A | N/A | CCAGAAGTAACAACCA | 7  | AB | 1797 |
| 1409227 | 254817 | 254832 | N/A | N/A | ATATCCTAAGAACCAG | 25 | AB | 1798 |
| 1409229 | 272839 | 272854 | N/A | N/A | CAATTTCAAAGTAGTC | 27 | AB | 1799 |
| 1409285 | 532200 | 532215 | N/A | N/A | GTCAAAAATGCTTCAG | 19 | AB | 1800 |
| 1409308 | 411688 | 411703 | N/A | N/A | GCTCATTAGACTGAGG | 48 | AB | 1801 |
| 1409376 | 447362 | 447377 | N/A | N/A | ACATAATCACATTCCA | 17 | AB | 1802 |
| 1409377 | 200587 | 200602 | N/A | N/A | GATATACAAACCAACC | 67 | AB | 1803 |
| 1409398 | 306835 | 306850 | N/A | N/A | ATTACTAACTCTTCA  | 24 | AB | 1804 |
| 1409445 | 211179 | 211194 | N/A | N/A | GCATAATGTTACTCAC | 28 | AB | 1805 |
| 1409448 | 247568 | 247583 | N/A | N/A | AAGATAAATAGCTCTC | 59 | AB | 1806 |
| 1409451 | 457967 | 457982 | N/A | N/A | AAGATAATCATGCCTC | 25 | AB | 1807 |
| 1409480 | 336174 | 336189 | N/A | N/A | CATTTTTGATGACTCA | 2  | AB | 1808 |
| 1409485 | 203773 | 203788 | N/A | N/A | GTAAGATTACAGGTAA | 46 | AB | 1809 |
| 1409528 | 287913 | 287928 | N/A | N/A | TCTATTAAAGCCACTA | 12 | AB | 1810 |
| 1409547 | 218775 | 218790 | N/A | N/A | GCCAAGGTTGGAAGTA | 64 | AB | 1811 |
| 1409555 | 79404  | 79419  | N/A | N/A | CTTAATTTGGAGCTTG | 8  | AB | 1812 |
| 1409573 | 229087 | 229102 | N/A | N/A | TATCATTTGATGCCAT | 15 | AB | 1813 |
| 1409593 | 104001 | 104016 | N/A | N/A | AAGATTACAGTTGTAT | 13 | AB | 1814 |
| 1409622 | 271044 | 271059 | N/A | N/A | GAATTCAGGGCATGTC | 76 | AB | 1815 |
| 1409640 | 196893 | 196908 | N/A | N/A | CAAATTGCAAGGTCAA | 39 | AB | 1816 |
| 1409679 | 284303 | 284318 | N/A | N/A | GCAAAACATGTGTTGA | 26 | AB | 1817 |
| 1409689 | 137245 | 137260 | N/A | N/A | GCAATTAAATACACTT | 31 | AB | 1818 |
| 1409730 | 205451 | 205466 | N/A | N/A | CTACGGTATGTAATCC | 26 | AB | 1819 |
| 1409750 | 232104 | 232119 | N/A | N/A | AGTAGAATACCTGCAA | 35 | AB | 1820 |
| 1409752 | 356426 | 356441 | N/A | N/A | GATTATTCTGAGTCCC | 5  | AB | 1821 |
| 1409807 | 257853 | 257868 | N/A | N/A | CTTTATTATAGGTGGA | 4  | AB | 1822 |
| 1409864 | 87132  | 87147  | N/A | N/A | TTCCATAAAGCACACC | 33 | AB | 1823 |
| 1409891 | 235004 | 235019 | N/A | N/A | AGAAACCAGGGACAGC | 18 | AB | 1824 |
| 1409948 | 174913 | 174928 | N/A | N/A | AAGGTATCAAGGACAC | 28 | AB | 1825 |
| 1409952 | 503623 | 503638 | N/A | N/A | CTTTACTATTACTCTC | 39 | AB | 1826 |
| 1409992 | 374016 | 374031 | N/A | N/A | GCAAATACATTGGTTG | 28 | AB | 1827 |
| 1410047 | 213627 | 213642 | N/A | N/A | ATAAGTTTCAGGGTCT | 34 | AB | 1828 |
| 1410058 | 397942 | 397957 | N/A | N/A | CTTAATAATGTCAAGC | 52 | AB | 1829 |

|         |        |        |       |       |                  |     |    |      |
|---------|--------|--------|-------|-------|------------------|-----|----|------|
| 1410061 | 487477 | 487492 | N/A   | N/A   | CAACCTATAATCCTCC | 53  | AB | 1830 |
| 1410133 | 320907 | 320922 | N/A   | N/A   | CAAACAAGGTGTCTCA | 25  | AB | 1831 |
| 1410198 | 264525 | 264540 | N/A   | N/A   | GCTATAAGCATCCTCA | 64  | AB | 1832 |
| 1410239 | 47708  | 47723  | N/A   | N/A   | TAGAATTACATTCTGC | 73  | AB | 1833 |
| 1410244 | 262913 | 262928 | N/A   | N/A   | ACTGATATCAGTTACC | 58  | AB | 1834 |
| 1410245 | 221579 | 221594 | N/A   | N/A   | CCTAATTATAACAGAA | 85  | AB | 1835 |
| 1410277 | 281833 | 281848 | N/A   | N/A   | TACAATCAAGTACTTT | 30  | AB | 1836 |
| 1410342 | 291487 | 291502 | N/A   | N/A   | GGAAATTATGTGACTA | 7   | AB | 1837 |
| 1410358 | 207456 | 207471 | N/A   | N/A   | GCAAACAAAGTTCAGG | 18  | AB | 1838 |
| 1410368 | 277816 | 277831 | N/A   | N/A   | CACAATCTGATGTTGA | 25  | AB | 1839 |
| 1410387 | 184997 | 185012 | N/A   | N/A   | GTGTATTAGGTTTTTC | 5   | AB | 1840 |
| 1410403 | 239047 | 239062 | N/A   | N/A   | TCTTATGCATACCAGG | 18  | AB | 1841 |
| 1410446 | 547516 | 547531 | N/A   | N/A   | AAGTATTATATCTTCG | 52  | AB | 1842 |
| 1410461 | 191883 | 191898 | N/A   | N/A   | CTTACCTAACTTGCTG | 53  | AB | 1843 |
| 1410516 | 153620 | 153635 | N/A   | N/A   | TCTATAGGGAAGTCAG | 53  | AB | 1844 |
| 1410561 | 294165 | 294180 | N/A   | N/A   | CATACCATTTCAAACA | 48  | AB | 1845 |
| 1411092 | 559669 | 559684 | 8658  | 8673  | GTTTAAACCTGGTCCT | 44  | AB | 1846 |
| 1411103 | 562399 | 562414 | 11388 | 11403 | AGTGAAATAGGGTAAT | 24  | AB | 1847 |
| 1411111 | 560391 | 560406 | 9380  | 9395  | TAATTACTCTTGTTC  | 19  | AB | 1848 |
| 1411141 | 559336 | 559351 | 8325  | 8340  | CTTAATACTAAAGTTA | 81  | AB | 1849 |
| 1411177 | 557052 | 557067 | 6041  | 6056  | TATCATATGGAAGGAA | 28  | AB | 1850 |
| 1411202 | 517372 | 517387 | 2786  | 2801  | AAAATACAGCTGCCAC | 45  | AB | 1851 |
| 1411277 | 558936 | 558951 | 7925  | 7940  | ACAACTATAAATACCC | 15  | AB | 1852 |
| 1411279 | 561224 | 561239 | 10213 | 10228 | ATTAAGTGAACTCCA  | 18  | AB | 1853 |
| 1411295 | 217526 | 217541 | 492   | 507   | ATCAAAGAGTCAATGG | 4   | AB | 1854 |
| 1411343 | 555476 | 555491 | 4465  | 4480  | GGAGAAAGTTGAGTAG | 55  | AB | 1855 |
| 1411358 | 558070 | 558085 | 7059  | 7074  | GAGTTAAATTACAGAG | 5   | AB | 1856 |
| 1411392 | 556246 | 556261 | 5235  | 5250  | AATTTAGATTATCAGG | 78  | AB | 1857 |
| 1411437 | 554413 | 554428 | 3402  | 3417  | GAGCAAAGACAATCTG | 21  | AB | 1858 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 5   | AC | 181  |
| 1408276 | 217980 | 217995 | 946   | 961   | TCGATCACATCCCCCT | 19  | AC | 1859 |
| 1408324 | 181274 | 181289 | N/A   | N/A   | TTCTATTTAATGGTTC | 16  | AC | 1860 |
| 1408349 | 225895 | 225910 | N/A   | N/A   | GATTTAAGTAAATCTA | 104 | AC | 1861 |
| 1408543 | 288769 | 288784 | N/A   | N/A   | AGGAAAATAACCATTG | 24  | AC | 1862 |
| 1408570 | 290717 | 290732 | N/A   | N/A   | TCTAAGTTTCACAAAT | 62  | AC | 1863 |
| 1408591 | 290539 | 290554 | N/A   | N/A   | AAAACAGTACTGTGCT | 55  | AC | 1864 |
| 1408601 | 217531 | 217546 | 497   | 512   | CTGAAATCAAAGAGTC | 13  | AC | 1865 |
| 1408614 | 188578 | 188593 | N/A   | N/A   | TAATCCATTGACATTC | 82  | AC | 1866 |
| 1408622 | 189808 | 189823 | N/A   | N/A   | TGGCATTACATTCTCC | 7   | AC | 1867 |
| 1408641 | 224953 | 224968 | N/A   | N/A   | GCTTTATCAACACATG | 35  | AC | 1868 |
| 1408667 | 243404 | 243419 | N/A   | N/A   | GATCAACAAATGCCAA | 59  | AC | 1869 |
| 1408681 | 249484 | 249499 | N/A   | N/A   | TGTACTAAGCACTTCC | 12  | AC | 1870 |
| 1408715 | 263017 | 263032 | N/A   | N/A   | CATACCAAAGTGATAT | 92  | AC | 1871 |
|         | 263099 | 263114 |       |       |                  |     |    |      |
| 1408725 | 262929 | 262944 | N/A   | N/A   | AAAACAAAGTTCTCTC | 47  | AC | 1872 |

|         |        |        |      |      |                  |    |    |      |
|---------|--------|--------|------|------|------------------|----|----|------|
| 1409094 | 50081  | 50096  | N/A  | N/A  | TATATGGTATCAAGGA | 88 | AC | 1873 |
| 1409101 | 205606 | 205621 | N/A  | N/A  | TAACCCATTTTGCCCA | 38 | AC | 1874 |
| 1409111 | 264526 | 264541 | N/A  | N/A  | GGCTATAAGCATCCTC | 63 | AC | 1875 |
| 1409124 | 559018 | 559033 | 8007 | 8022 | ACTGATTAAGGACAAA | 25 | AC | 1876 |
| 1409127 | 185302 | 185317 | N/A  | N/A  | TTTACTCAAGGTCAGC | 4  | AC | 1877 |
| 1409170 | 80733  | 80748  | N/A  | N/A  | CCAATATTCAGATTCC | 4  | AC | 1878 |
| 1409174 | 277817 | 277832 | N/A  | N/A  | GCACAATCTGATGTTG | 33 | AC | 1879 |
| 1409190 | 321207 | 321222 | N/A  | N/A  | TACAATGACAGTGCTG | 24 | AC | 1880 |
| 1409203 | 489497 | 489512 | N/A  | N/A  | GAATCTAAATGATCAA | 84 | AC | 1881 |
| 1409256 | 532356 | 532371 | N/A  | N/A  | GACAAGATTCATTTCT | 68 | AC | 1882 |
| 1409284 | 381929 | 381944 | N/A  | N/A  | TTTATTCACAATCTCG | 8  | AC | 1883 |
| 1409510 | 411739 | 411754 | N/A  | N/A  | TGATATTTTGACCTAA | 80 | AC | 1884 |
| 1409549 | 287915 | 287930 | N/A  | N/A  | TCTCTATTAAGCCAC  | 9  | AC | 1885 |
| 1409563 | 104004 | 104019 | N/A  | N/A  | ACCAAGATTACAGTTG | 12 | AC | 1886 |
| 1409569 | 232106 | 232121 | N/A  | N/A  | CCAGTAGAATACCTGC | 46 | AC | 1887 |
| 1409611 | 284304 | 284319 | N/A  | N/A  | TGCAAAACATGTGTTG | 65 | AC | 1888 |
| 1409646 | 221591 | 221606 | N/A  | N/A  | ACTACCAGCATTCCTA | 52 | AC | 1889 |
| 1409673 | 201558 | 201573 | N/A  | N/A  | CCAATTATGTTACCTT | 27 | AC | 1890 |
| 1409685 | 254819 | 254834 | N/A  | N/A  | GCATATCCTAAGAACC | 14 | AC | 1891 |
| 1409687 | 248056 | 248071 | N/A  | N/A  | AATACTTCAGACCAGT | 37 | AC | 1892 |
| 1409695 | 281835 | 281850 | N/A  | N/A  | ATTACAATCAAGTACT | 60 | AC | 1893 |
| 1409712 | 239197 | 239212 | N/A  | N/A  | ATCAATAGCAGAGTTG | 66 | AC | 1894 |
| 1409719 | 337082 | 337097 | N/A  | N/A  | GCTTTTAGAATAGGTA | 5  | AC | 1895 |
| 1409778 | 214480 | 214495 | N/A  | N/A  | AACTGTACAACATCA  | 59 | AC | 1896 |
| 1409783 | 271047 | 271062 | N/A  | N/A  | GCAGAATTCAGGGCAT | 88 | AC | 1897 |
| 1409802 | 219940 | 219955 | N/A  | N/A  | CACATATCAAGGCCGC | 70 | AC | 1898 |
| 1409812 | 549486 | 549501 | N/A  | N/A  | ACAATAAAAGCTTTGC | 57 | AC | 1899 |
| 1409829 | 222123 | 222138 | 1533 | 1548 | ATCATTGGAGTGAGGG | 9  | AC | 1900 |
| 1409893 | 356715 | 356730 | N/A  | N/A  | ACTTTTAGGGTCATA  | 8  | AC | 1901 |
| 1409901 | 272971 | 272986 | N/A  | N/A  | ACAAATGCAGGCCTGG | 72 | AC | 1902 |
| 1409926 | 457970 | 457985 | N/A  | N/A  | ATCAAGATAATCATGC | 29 | AC | 1903 |
| 1409965 | 447369 | 447384 | N/A  | N/A  | GCTACTAACATAATCA | 47 | AC | 1904 |
| 1410045 | 192053 | 192068 | N/A  | N/A  | GATCATTTATCTGGCT | 77 | AC | 1905 |
| 1410078 | 121480 | 121495 | N/A  | N/A  | CTTTATAGACATCTCA | 23 | AC | 1906 |
| 1410094 | 87216  | 87231  | N/A  | N/A  | ATATTTTGATCTGAGG | 6  | AC | 1907 |
| 1410098 | 203774 | 203789 | N/A  | N/A  | AGTAAGATTACAGGTA | 35 | AC | 1908 |
| 1410118 | 176757 | 176772 | N/A  | N/A  | CCTTTTGAAAATCCTC | 16 | AC | 1909 |
| 1410161 | 291674 | 291689 | N/A  | N/A  | GAGTATTTTGAGATAT | 18 | AC | 1910 |
| 1410214 | 153621 | 153636 | N/A  | N/A  | ATCTATAGGGAAGTCA | 57 | AC | 1911 |
| 1410263 | 211180 | 211195 | N/A  | N/A  | AGCATAATGTTACTCA | 21 | AC | 1912 |
| 1410267 | 229161 | 229176 | N/A  | N/A  | AAGTATTAACCACCAT | 9  | AC | 1913 |
| 1410289 | 207457 | 207472 | N/A  | N/A  | CGCAAACAAAGTTCAG | 20 | AC | 1914 |
| 1410349 | 306836 | 306851 | N/A  | N/A  | GATTACTAAACTCTTC | 40 | AC | 1915 |
| 1410392 | 397944 | 397959 | N/A  | N/A  | TCCTTAATAATGTCAA | 9  | AC | 1916 |
| 1410410 | 196973 | 196988 | N/A  | N/A  | TCCAAGAAGTCAGTGA | 48 | AC | 1917 |

|         |        |        |       |       |                  |     |    |      |
|---------|--------|--------|-------|-------|------------------|-----|----|------|
| 1410439 | 504124 | 504139 | N/A   | N/A   | ATTAGTTAAGTGACAG | 57  | AC | 1918 |
| 1410443 | 294383 | 294398 | N/A   | N/A   | ATCTATCTCACTCCTC | 21  | AC | 1919 |
| 1410467 | 257854 | 257869 | N/A   | N/A   | TCTTTATTATAGGTGG | 5   | AC | 1920 |
| 1410482 | 137272 | 137287 | N/A   | N/A   | CCAAAGCATACATGTT | 41  | AC | 1921 |
| 1410524 | 235010 | 235025 | N/A   | N/A   | CATCCGAGAAACCAGG | 12  | AC | 1922 |
| 1410562 | 466984 | 466999 | N/A   | N/A   | ATGCTATAATGATGGC | 69  | AC | 1923 |
| 1411108 | 559348 | 559363 | 8337  | 8352  | ACTTTAAGTGCTCTTA | 13  | AC | 1924 |
| 1411121 | 562402 | 562417 | 11391 | 11406 | AACAGTGAAATAGGGT | 17  | AC | 1925 |
| 1411125 | 517373 | 517388 | 2787  | 2802  | GAAAATACAGCTGCCA | 30  | AC | 1926 |
| 1411152 | 554471 | 554486 | 3460  | 3475  | CACAGAAAAGGTGCAT | 54  | AC | 1927 |
| 1411198 | 556247 | 556262 | 5236  | 5251  | TAATTTAGATTATCAG | 93  | AC | 1928 |
| 1411203 | 558276 | 558291 | 7265  | 7280  | ATACTATTTAACTCC  | 29  | AC | 1929 |
| 1411207 | N/A    | N/A    | 2269  | 2284  | GTACAGAGCTTTCAGC | 50  | AC | 1930 |
| 1411222 | 557053 | 557068 | 6042  | 6057  | TTATCATATGGAAGGA | 17  | AC | 1931 |
| 1411387 | 555526 | 555541 | 4515  | 4530  | CATTTTGAGTAGACAG | 41  | AC | 1932 |
| 1411427 | 560392 | 560407 | 9381  | 9396  | CTAATTACTCTTGTC  | 19  | AC | 1933 |
| 1411445 | 561586 | 561601 | 10575 | 10590 | TCAGAGAATCTTTGTC | 32  | AC | 1934 |
| 1411447 | 559672 | 559687 | 8661  | 8676  | AAAGTTTAAACCTGGT | 21  | AC | 1935 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT | 5   | AD | 181  |
| 1408268 | 217981 | 217996 | 947   | 962   | TTGATCACATCCCCC  | 16  | AD | 1936 |
| 1408323 | 181275 | 181290 | N/A   | N/A   | CTTCTATTTAATGGTT | 24  | AD | 1937 |
| 1408341 | 189825 | 189840 | N/A   | N/A   | ATCGAACCATCTTTTG | 57  | AD | 1938 |
| 1408556 | 288770 | 288785 | N/A   | N/A   | AAGGAAAATAACCATT | 76  | AD | 1939 |
| 1408586 | 290719 | 290734 | N/A   | N/A   | GATCTAAGTTTCACAA | 65  | AD | 1940 |
| 1408597 | 217561 | 217576 | 527   | 542   | AAATGATTCTGGCTTC | 5   | AD | 1941 |
| 1408613 | 188588 | 188603 | N/A   | N/A   | GTGGAGAATTTAATCC | 57  | AD | 1942 |
| 1408640 | 224983 | 224998 | N/A   | N/A   | TTCTTGAAAACAGACC | 30  | AD | 1943 |
| 1408647 | 225902 | 225917 | N/A   | N/A   | AGAAAAGGATTTAAGT | 93  | AD | 1944 |
| 1408664 | 235089 | 235104 | N/A   | N/A   | GTCCAAAGCCTGCTTC | 16  | AD | 1945 |
| 1408666 | 243454 | 243469 | N/A   | N/A   | CTCTGGGAGGTTGTAT | 36  | AD | 1946 |
| 1408680 | 249494 | 249509 | N/A   | N/A   | ATAGTTAGTGTGTACT | 28  | AD | 1947 |
| 1408698 | 263018 | 263033 | N/A   | N/A   | TCATACCAAAGTGATA | 66  | AD | 1948 |
|         | 263100 | 263115 |       |       |                  |     |    |      |
| 1408708 | 262930 | 262945 | N/A   | N/A   | GAAAACAAAGTTCTCT | 87  | AD | 1949 |
| 1408739 | 271049 | 271064 | N/A   | N/A   | AAGCAGAATTCAGGGC | 44  | AD | 1950 |
| 1409109 | 87217  | 87232  | N/A   | N/A   | CATATTTTGATCTGAG | 5   | AD | 1951 |
| 1409186 | 284416 | 284431 | N/A   | N/A   | AATCTAAATTTGTGTC | 41  | AD | 1952 |
| 1409270 | 272972 | 272987 | N/A   | N/A   | AACAAATGCAGGCCTG | 65  | AD | 1953 |
| 1409322 | 137480 | 137495 | N/A   | N/A   | CTTACATCAATTTACA | 67  | AD | 1954 |
| 1409348 | 307383 | 307398 | N/A   | N/A   | GATATTGGTAAAAGCA | 65  | AD | 1955 |
| 1409355 | 232276 | 232291 | N/A   | N/A   | GCAGATTCTAATGTAG | 21  | AD | 1956 |
| 1409356 | 290541 | 290556 | N/A   | N/A   | TGAAAACAGTACTGTG | 85  | AD | 1957 |
| 1409409 | 322554 | 322569 | N/A   | N/A   | AATACAAAGTGTACCA | 48  | AD | 1958 |
| 1409411 | 383230 | 383245 | N/A   | N/A   | GACATTAAACAGTCAC | 85  | AD | 1959 |
| 1409415 | 264802 | 264817 | N/A   | N/A   | CAGACCTAAAGTTTGA | 101 | AD | 1960 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1409425 | 281965 | 281980 | N/A   | N/A   | TCATTATCGACAGTAT  | 14 | AD | 1961 |
| 1409446 | 287995 | 288010 | N/A   | N/A   | TCAATACATCATCATA  | 27 | AD | 1962 |
| 1409477 | 504149 | 504164 | N/A   | N/A   | GATAATTAACCTGCTCC | 67 | AD | 1963 |
| 1409499 | 229163 | 229178 | N/A   | N/A   | TAAAGTATTAACCACC  | 5  | AD | 1964 |
| 1409557 | 239384 | 239399 | N/A   | N/A   | GTTATTTAAAAGGAGG  | 30 | AD | 1965 |
| 1409567 | 201680 | 201695 | N/A   | N/A   | GCCTTAAAACCTTTCCA | 54 | AD | 1966 |
| 1409589 | 207475 | 207490 | N/A   | N/A   | CTATATATACTGTCTG  | 28 | AD | 1967 |
| 1409665 | 121481 | 121496 | N/A   | N/A   | TCTTTATAGACATCTC  | 11 | AD | 1968 |
| 1409676 | 549518 | 549533 | N/A   | N/A   | GATAATTCTTAAGTGG  | 37 | AD | 1969 |
| 1409754 | 219941 | 219956 | N/A   | N/A   | CCACATATCAAGGCCG  | 73 | AD | 1970 |
| 1409797 | 203776 | 203791 | N/A   | N/A   | GAAGTAAGATTACAGG  | 27 | AD | 1971 |
| 1409815 | 53231  | 53246  | N/A   | N/A   | GACTATCTCATTGCCA  | 86 | AD | 1972 |
| 1409842 | 257866 | 257881 | N/A   | N/A   | CTTGAAATATGGTCTT  | 4  | AD | 1973 |
| 1409857 | 198095 | 198110 | N/A   | N/A   | GATATATTGAGTATTC  | 65 | AD | 1974 |
| 1409878 | 104015 | 104030 | N/A   | N/A   | TCTATTTAAAAGACCAA | 11 | AD | 1975 |
| 1409880 | 397957 | 397972 | N/A   | N/A   | GAATTTCTATCAGTCC  | 11 | AD | 1976 |
| 1409931 | 176852 | 176867 | N/A   | N/A   | CCTATTTCAATGCATT  | 45 | AD | 1977 |
| 1410010 | 458017 | 458032 | N/A   | N/A   | CTATATAAGCATGCTC  | 35 | AD | 1978 |
| 1410017 | 185324 | 185339 | N/A   | N/A   | AATTATGTTACAGCTG  | 46 | AD | 1979 |
| 1410030 | 532816 | 532831 | N/A   | N/A   | GAAAATGTATGACTCC  | 29 | AD | 1980 |
| 1410088 | 358502 | 358517 | N/A   | N/A   | ATCAAACATGATCTCA  | 6  | AD | 1981 |
| 1410095 | 467368 | 467383 | N/A   | N/A   | GTACATAAGTGTACAA  | 79 | AD | 1982 |
| 1410197 | 278098 | 278113 | N/A   | N/A   | CCATTTAGTAACAGAA  | 30 | AD | 1983 |
| 1410259 | 221592 | 221607 | N/A   | N/A   | AACTACCAGCATTCCCT | 70 | AD | 1984 |
| 1410268 | 214517 | 214532 | N/A   | N/A   | ACCTTTTAAGATTTCAG | 32 | AD | 1985 |
| 1410314 | 80930  | 80945  | N/A   | N/A   | CTTTATTGTGAATTCC  | 5  | AD | 1986 |
| 1410327 | 337106 | 337121 | N/A   | N/A   | CTCAAGGAATAATTGC  | 6  | AD | 1987 |
| 1410376 | 447418 | 447433 | N/A   | N/A   | CATAATTCCTTGCTCC  | 45 | AD | 1988 |
| 1410397 | 211471 | 211486 | N/A   | N/A   | CCTAATACACACTGGA  | 87 | AD | 1989 |
| 1410407 | 294533 | 294548 | N/A   | N/A   | GATGTTAAAAGGTACA  | 6  | AD | 1990 |
| 1410411 | 192171 | 192186 | N/A   | N/A   | GTATATAGAAACACCA  | 24 | AD | 1991 |
| 1410495 | 414826 | 414841 | N/A   | N/A   | TTTACTTATGCTGGGA  | 5  | AD | 1992 |
| 1410515 | 248317 | 248332 | N/A   | N/A   | ATAATGAAGATAGCCA  | 8  | AD | 1993 |
| 1410518 | 254884 | 254899 | N/A   | N/A   | CATACATTAAAGGCAG  | 37 | AD | 1994 |
| 1410566 | 291717 | 291732 | N/A   | N/A   | TCTAAATTCACCTCTT  | 23 | AD | 1995 |
| 1410584 | 205616 | 205631 | N/A   | N/A   | GAGGATAATCTAACCC  | 61 | AD | 1996 |
| 1411110 | 559349 | 559364 | 8338  | 8353  | GACTTTAAGTGCTCTT  | 10 | AD | 1997 |
| 1411126 | 559027 | 559042 | 8016  | 8031  | TCATATCACACTGATT  | 36 | AD | 1998 |
| 1411137 | 555527 | 555542 | 4516  | 4531  | CCATTTTGAGTAGACA  | 17 | AD | 1999 |
| 1411234 | 559747 | 559762 | 8736  | 8751  | CAAACAACCTAAGGCCA | 59 | AD | 2000 |
| 1411247 | 434321 | 434336 | 2281  | 2296  | CTTGATTGAGTTGTAC  | 41 | AD | 2001 |
| 1411256 | 554493 | 554508 | 3482  | 3497  | GAAATCACGATCCCCT  | 30 | AD | 2002 |
| 1411261 | 558277 | 558292 | 7266  | 7281  | GATACTATTTAACTC   | 28 | AD | 2003 |
| 1411288 | 562413 | 562428 | 11402 | 11417 | TTTACTTGAACAACAG  | 19 | AD | 2004 |
| 1411293 | 517418 | 517433 | 2832  | 2847  | CTAAACTTCTTCTGAG  | 77 | AD | 2005 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1411300 | 153861 | 153876 | 127   | 142   | CCAAACAAATGTCTCT  | 9   | AD | 2006 |
| 1411316 | 489611 | 489626 | 2558  | 2573  | AAAGAACTGTTCCCTT  | 45† | AD | 2007 |
| 1411335 | 557056 | 557071 | 6045  | 6060  | GATTTATCATATGGAA  | 16  | AD | 2008 |
| 1411348 | 222124 | 222139 | 1534  | 1549  | TATCATTGGAGTGAGG  | 6   | AD | 2009 |
| 1411356 | 560394 | 560409 | 9383  | 9398  | GTCTAATTACTCTTGT  | 18  | AD | 2010 |
| 1411380 | 556249 | 556264 | 5238  | 5253  | GATAATTTAGATTATC  | 91  | AD | 2011 |
| 1411417 | 561617 | 561632 | 10606 | 10621 | GCAAAGGTAAAATACG  | 20  | AD | 2012 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 9   | AE | 181  |
| 1408243 | 217984 | 217999 | 950   | 965   | TGCTTCGATCACATCC  | 21  | AE | 2013 |
| 1408302 | 222139 | 222154 | 1549  | 1564  | TTTAATGCGCTGTTGT  | 13  | AE | 2014 |
| 1408322 | 82197  | 82212  | N/A   | N/A   | ATTAGCTCATGGAAAG  | 36  | AE | 2015 |
| 1408340 | 189826 | 189841 | N/A   | N/A   | TATCGAACCATCTTTT  | 52  | AE | 2016 |
| 1408551 | 288529 | 288544 | N/A   | N/A   | TTTATATAAACCTAAG  | 84  | AE | 2017 |
| 1408555 | 288780 | 288795 | N/A   | N/A   | CTTTCATAATAAGGAA  | 90  | AE | 2018 |
| 1408602 | 181302 | 181317 | N/A   | N/A   | ATCATTTGGCACTTAA  | 49  | AE | 2019 |
| 1408612 | 188608 | 188623 | N/A   | N/A   | AGCCAGTCTATATCTT  | 62  | AE | 2020 |
| 1408639 | 224993 | 225008 | N/A   | N/A   | AGAACTTAGTTTCTTG  | 71  | AE | 2021 |
| 1408646 | 225922 | 225937 | N/A   | N/A   | GTAAAGACAGATCTTG  | 21  | AE | 2022 |
| 1408663 | 235109 | 235124 | N/A   | N/A   | TATTTATTGTCCTGTT  | 17  | AE | 2023 |
| 1408665 | 243464 | 243479 | N/A   | N/A   | CCATGAATGTCTCTGG  | 82  | AE | 2024 |
| 1408679 | 249504 | 249519 | N/A   | N/A   | GACAAAAACGATAGTT  | 66  | AE | 2025 |
| 1408714 | 263109 | 263124 | N/A   | N/A   | AGTACCAGCTCATACC  | 59  | AE | 2026 |
| 1408724 | 262939 | 262954 | N/A   | N/A   | GCTTAAGAGGAAAACA  | 56  | AE | 2027 |
| 1408738 | 271059 | 271074 | N/A   | N/A   | ACAGGTAAACAAGCAG  | 57  | AE | 2028 |
| 1409103 | 290545 | 290560 | N/A   | N/A   | CCTATGAAAACAGTAC  | 88  | AE | 2029 |
| 1409107 | 337133 | 337148 | N/A   | N/A   | AGAGTAACAATGTACC  | 13  | AE | 2030 |
| 1409108 | 307518 | 307533 | N/A   | N/A   | GTGGATAAAGCTGTGG  | 16  | AE | 2031 |
| 1409145 | 239542 | 239557 | N/A   | N/A   | GCAGATTATAGGCAAG  | 20  | AE | 2032 |
| 1409192 | 290720 | 290735 | N/A   | N/A   | GGATCTAAGTTTCACA  | 59  | AE | 2033 |
| 1409224 | 229260 | 229275 | N/A   | N/A   | GCTAAGAGACCTCTGC  | 74  | AE | 2034 |
| 1409232 | 211473 | 211488 | N/A   | N/A   | ATCCTAATACACACTG  | 74  | AE | 2035 |
| 1409250 | 458018 | 458033 | N/A   | N/A   | ACTATATAAGCATGCT  | 63  | AE | 2036 |
| 1409327 | 467986 | 468001 | N/A   | N/A   | AACTTTTGATGACAGG  | 5   | AE | 2037 |
| 1409476 | 278273 | 278288 | N/A   | N/A   | CATGTTAGATGTGTGA  | 92  | AE | 2038 |
| 1409542 | 549802 | 549817 | N/A   | N/A   | TCTGATAGAAGGTGGT  | 24  | AE | 2039 |
| 1409571 | 176938 | 176953 | N/A   | N/A   | TTAATCTAAACAACCTT | 81  | AE | 2040 |
| 1409615 | 205660 | 205675 | N/A   | N/A   | CAAATTTGCAATGCAA  | 82  | AE | 2041 |
| 1409617 | 121633 | 121648 | N/A   | N/A   | GCAGAATGTGTATATC  | 12  | AE | 2042 |
| 1409629 | 322556 | 322571 | N/A   | N/A   | TGAATACAAAGTGTAC  | 54  | AE | 2043 |
| 1409671 | 284417 | 284432 | N/A   | N/A   | GAATCTAAATTTGTGT  | 70  | AE | 2044 |
| 1409708 | 360233 | 360248 | N/A   | N/A   | ACAAATGCCATTCTGG  | 24  | AE | 2045 |
| 1409727 | 192172 | 192187 | N/A   | N/A   | GGTATATAGAAACACC  | 84  | AE | 2046 |
| 1409746 | 416547 | 416562 | N/A   | N/A   | TACGAATCTATCTCTA  | 79  | AE | 2047 |
| 1409765 | 88243  | 88258  | N/A   | N/A   | CTCAGAGAAGGAAGGT  | 28  | AE | 2048 |
| 1409786 | 272974 | 272989 | N/A   | N/A   | CAAACAAATGCAGGCC  | 66  | AE | 2049 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1409809 | 219960 | 219975 | N/A   | N/A   | ATAAACACTGGGCCAC  | 80  | AE | 2050 |
| 1409867 | 208111 | 208126 | N/A   | N/A   | TCAATTATGAATGTCC  | 25  | AE | 2051 |
| 1409875 | 221593 | 221608 | N/A   | N/A   | CAACTACCAGCATTCC  | 60  | AE | 2052 |
| 1409877 | 203825 | 203840 | N/A   | N/A   | ACAGAATTGTGTGTC   | 49  | AE | 2053 |
| 1409924 | 198159 | 198174 | N/A   | N/A   | AATGTAAGACCACTCC  | 62  | AE | 2054 |
| 1409954 | 137509 | 137524 | N/A   | N/A   | AGTAAAATCTGGTTCA  | 31  | AE | 2055 |
| 1409982 | 505317 | 505332 | N/A   | N/A   | ATGTATAATGCTCTGA  | 32  | AE | 2056 |
| 1409988 | 264954 | 264969 | N/A   | N/A   | GATTTATTTGACTATG  | 39  | AE | 2057 |
| 1410011 | 384074 | 384089 | N/A   | N/A   | CACAAATATCTACTGC  | 52  | AE | 2058 |
| 1410033 | 434410 | 434425 | N/A   | N/A   | GGCATAAAGACAGTAG  | 27  | AE | 2059 |
| 1410039 | 294740 | 294755 | N/A   | N/A   | TAAACTCAGACCACAG  | 36  | AE | 2060 |
| 1410136 | 257938 | 257953 | N/A   | N/A   | CCAACAAAACAGCACC  | 14  | AE | 2061 |
| 1410145 | 248352 | 248367 | N/A   | N/A   | CTAGTATCAACCAGTC  | 61  | AE | 2062 |
| 1410150 | 185326 | 185341 | N/A   | N/A   | GTAATTATGTTACAGC  | 57  | AE | 2063 |
| 1410229 | 54647  | 54662  | N/A   | N/A   | TTTAATTAGTTGTTGG  | 96  | AE | 2064 |
| 1410249 | 532985 | 533000 | N/A   | N/A   | CATTATTATAGGTACC  | 76  | AE | 2065 |
| 1410281 | 397964 | 397979 | N/A   | N/A   | CACTTATGAATTTCTA  | 41  | AE | 2066 |
| 1410290 | 232653 | 232668 | N/A   | N/A   | GCAAATTTTGCTCGAG  | 48  | AE | 2067 |
| 1410347 | 291803 | 291818 | N/A   | N/A   | CCCAAGAATGCTTCCT  | 16  | AE | 2068 |
| 1410395 | 254899 | 254914 | N/A   | N/A   | AGAAATACAGGCACTC  | 73  | AE | 2069 |
| 1410398 | 281969 | 281984 | N/A   | N/A   | ATAATCATTATCGACA  | 38  | AE | 2070 |
| 1410460 | 104404 | 104419 | N/A   | N/A   | ACATTAGTTTACTTGT  | 86  | AE | 2071 |
| 1410500 | 202027 | 202042 | N/A   | N/A   | ACTACTAAAACCTCAAG | 79  | AE | 2072 |
| 1410510 | 448071 | 448086 | N/A   | N/A   | AGAAAGCATGTAGTTA  | 29  | AE | 2073 |
| 1410549 | 153862 | 153877 | 128   | 143   | CCCAAACAAATGTCTC  | 9   | AE | 2074 |
| 1410568 | 214518 | 214533 | N/A   | N/A   | CACCTTTTAAGATTCA  | 51  | AE | 2075 |
| 1411114 | 489613 | 489628 | 2560  | 2575  | GTAAAGAACTGTTCCC  | 28† | AE | 2076 |
| 1411123 | 559058 | 559073 | 8047  | 8062  | ATAATCAGTCCTATGA  | 62  | AE | 2077 |
| 1411139 | 556251 | 556266 | 5240  | 5255  | CTGATAATTTAGATTA  | 91  | AE | 2078 |
| 1411197 | 217562 | 217577 | 528   | 543   | GAAATGATTCTGGCTT  | 7   | AE | 2079 |
| 1411211 | 559756 | 559771 | 8745  | 8760  | CAGTAAGCTCAAACAA  | 39  | AE | 2080 |
| 1411215 | 562484 | 562499 | 11473 | 11488 | CACAATAAATGTACTC  | 53  | AE | 2081 |
| 1411220 | 558363 | 558378 | 7352  | 7367  | AGGTAGGAGGCCCAGA  | 38  | AE | 2082 |
| 1411262 | 517419 | 517434 | 2833  | 2848  | GCTAAACTTCTTCTGA  | 54  | AE | 2083 |
| 1411289 | 554496 | 554511 | 3485  | 3500  | TCTGAAATCACGATCC  | 37  | AE | 2084 |
| 1411292 | 557226 | 557241 | 6215  | 6230  | CCTGTAAAAGCCAGCA  | 34  | AE | 2085 |
| 1411310 | 559376 | 559391 | 8365  | 8380  | TTGTAATAAGCCCAAA  | 46  | AE | 2086 |
| 1411328 | 555529 | 555544 | 4518  | 4533  | AACCATTTTGAGTAGA  | 28  | AE | 2087 |
| 1411337 | 560442 | 560457 | 9431  | 9446  | ACCCTAAATGGAAAGC  | 43  | AE | 2088 |
| 1411349 | 561749 | 561764 | 10738 | 10753 | GCTAAGCTAGCACTTG  | 48  | AE | 2089 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 4   | AF | 181  |
| 1408301 | 222140 | 222155 | 1550  | 1565  | CTTTAATGCGCTGTTG  | 8   | AF | 2090 |
| 1408321 | 82198  | 82213  | N/A   | N/A   | TATTAGCTCATGGAAA  | 49  | AF | 2091 |
| 1408339 | 189827 | 189842 | N/A   | N/A   | TTATCGAACCATCTTT  | 46  | AF | 2092 |
| 1408347 | 217986 | 218001 | 952   | 967   | GCTGCTTCGATCACAT  | 29  | AF | 2093 |

|         |        |        |     |     |                   |    |    |      |
|---------|--------|--------|-----|-----|-------------------|----|----|------|
| 1408531 | 288809 | 288824 | N/A | N/A | GATACATAATTTCTCA  | 43 | AF | 2094 |
| 1408550 | 288549 | 288564 | N/A | N/A | CTTTCATAGTTAAAAG  | 92 | AF | 2095 |
| 1408569 | 290727 | 290742 | N/A | N/A | ATGTTTTGGATCTAAG  | 28 | AF | 2096 |
| 1408581 | 290547 | 290562 | N/A | N/A | AACCTATGAAAACAGT  | 64 | AF | 2097 |
| 1408600 | 181392 | 181407 | N/A | N/A | TCAAACAGTCTGTCTC  | 25 | AF | 2098 |
| 1408611 | 188668 | 188683 | N/A | N/A | ACAGGTAAAGTGAGTT  | 46 | AF | 2099 |
| 1408638 | 225003 | 225018 | N/A | N/A | CTCTACATTTAGAACT  | 66 | AF | 2100 |
| 1408645 | 225932 | 225947 | N/A | N/A | TAATGACAAAAGTAAAG | 82 | AF | 2101 |
| 1408662 | 235179 | 235194 | N/A | N/A | TAATCTCATGTAATTT  | 84 | AF | 2102 |
| 1408678 | 249514 | 249529 | N/A | N/A | AAAGCATTGAGACAAA  | 27 | AF | 2103 |
| 1408697 | 263110 | 263125 | N/A | N/A | TAGTACCAGCTCATAC  | 54 | AF | 2104 |
| 1408707 | 262940 | 262955 | N/A | N/A | AGCTTAAGAGGAAAAC  | 65 | AF | 2105 |
| 1408737 | 271129 | 271144 | N/A | N/A | ATAGGAATCCCCTTGG  | 53 | AF | 2106 |
| 1409121 | 417048 | 417063 | N/A | N/A | ACCTATATATGCTGTC  | 70 | AF | 2107 |
| 1409122 | 205698 | 205713 | N/A | N/A | ATCAATAAACTTCACC  | 52 | AF | 2108 |
| 1409146 | 211477 | 211492 | N/A | N/A | TCTAATCCTAATACAC  | 85 | AF | 2109 |
| 1409196 | 177169 | 177184 | N/A | N/A | ATCTACCCACTATTCC  | 41 | AF | 2110 |
| 1409197 | 337228 | 337243 | N/A | N/A | GCAAATAACCTTTCGA  | 11 | AF | 2111 |
| 1409198 | 258634 | 258649 | N/A | N/A | CATATAGTAATTTAC   | 34 | AF | 2112 |
| 1409206 | 434480 | 434495 | N/A | N/A | TAGGTAAGACACTTGG  | 8  | AF | 2113 |
| 1409209 | 398484 | 398499 | N/A | N/A | GCATTATAAACTCTTC  | 16 | AF | 2114 |
| 1409235 | 254931 | 254946 | N/A | N/A | AGCACTTAGACAAAGG  | 51 | AF | 2115 |
| 1409261 | 448129 | 448144 | N/A | N/A | TATACCACGAGGCAGG  | 64 | AF | 2116 |
| 1409460 | 273425 | 273440 | N/A | N/A | AAGTATACACAACCAA  | 85 | AF | 2117 |
| 1409554 | 208112 | 208127 | N/A | N/A | ATCAATTATGAATGTC  | 51 | AF | 2118 |
| 1409599 | 233129 | 233144 | N/A | N/A | ACTGATAATAGCCAAC  | 4  | AF | 2119 |
| 1409602 | 214738 | 214753 | N/A | N/A | ATGGAATCTAACAAGC  | 76 | AF | 2120 |
| 1409686 | 458019 | 458034 | N/A | N/A | AACTATATAAGCATGC  | 90 | AF | 2121 |
| 1409692 | 221602 | 221617 | N/A | N/A | GATTATTTGCAACTAC  | 59 | AF | 2122 |
| 1409772 | 198160 | 198175 | N/A | N/A | TAATGTAAGACCACTC  | 62 | AF | 2123 |
| 1409816 | 384868 | 384883 | N/A | N/A | GCACAAAAACATCTGC  | 84 | AF | 2124 |
| 1409836 | 239693 | 239708 | N/A | N/A | CTCTATTTGAGCCACC  | 52 | AF | 2125 |
| 1409868 | 550824 | 550839 | N/A | N/A | AGGTATTAGTTTTCAGC | 11 | AF | 2126 |
| 1409913 | 505318 | 505333 | N/A | N/A | GATGTATAATGCTCTG  | 7  | AF | 2127 |
| 1409916 | 265119 | 265134 | N/A | N/A | CCTTTTAGTCAAGTAT  | 20 | AF | 2128 |
| 1409942 | 185327 | 185342 | N/A | N/A | TGTAATTATGTTACAG  | 79 | AF | 2129 |
| 1409971 | 137512 | 137527 | N/A | N/A | GATAGTAAAATCTGGT  | 10 | AF | 2130 |
| 1410019 | 292076 | 292091 | N/A | N/A | AATGTTATATGTGGCC  | 25 | AF | 2131 |
| 1410040 | 361754 | 361769 | N/A | N/A | TGAAATACTCATTGCA  | 35 | AF | 2132 |
| 1410138 | 88874  | 88889  | N/A | N/A | TTAGATAAGATCTTGC  | 35 | AF | 2133 |
| 1410189 | 203856 | 203871 | N/A | N/A | TATATCACAAACAGGG  | 65 | AF | 2134 |
| 1410218 | 229271 | 229286 | N/A | N/A | GCAAATATGGTGCTAA  | 6  | AF | 2135 |
| 1410231 | 243928 | 243943 | N/A | N/A | GCTTATCAATTTGACT  | 16 | AF | 2136 |
| 1410234 | 284425 | 284440 | N/A | N/A | GCAATATGGAATCTAA  | 13 | AF | 2137 |
| 1410257 | 282017 | 282032 | N/A | N/A | TTAACACTACCATTCA  | 48 | AF | 2138 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1410292 | 202056 | 202071 | N/A   | N/A   | TACTATGATTAACCCA  | 23  | AF | 2139 |
| 1410308 | 54920  | 54935  | N/A   | N/A   | GACTATCAGATTCAGT  | 86  | AF | 2140 |
| 1410324 | 105365 | 105380 | N/A   | N/A   | GAATTTTGTAGTCTTA  | 5   | AF | 2141 |
| 1410334 | 322573 | 322588 | N/A   | N/A   | GCAAAATGTAGTCCAA  | 15  | AF | 2142 |
| 1410344 | 294826 | 294841 | N/A   | N/A   | CCAGTAAGTTGTACTA  | 43  | AF | 2143 |
| 1410406 | 124981 | 124996 | N/A   | N/A   | CTCATAAAAAGGTTCA  | 35  | AF | 2144 |
| 1410422 | 278692 | 278707 | N/A   | N/A   | TTTACTACTATCCATT  | 47  | AF | 2145 |
| 1410425 | 308221 | 308236 | N/A   | N/A   | TTTACCTATTATTTCG  | 33  | AF | 2146 |
| 1410473 | 219964 | 219979 | N/A   | N/A   | GAATATAAACACTGGG  | 77  | AF | 2147 |
| 1410508 | 248354 | 248369 | N/A   | N/A   | AGCTAGTATCAACCAG  | 56  | AF | 2148 |
| 1410536 | 532986 | 533001 | N/A   | N/A   | GCATTATTATAGGTAC  | 92  | AF | 2149 |
| 1410537 | 154040 | 154055 | N/A   | N/A   | AGAAAGTAATGCAGGT  | 7   | AF | 2150 |
| 1410572 | 192451 | 192466 | N/A   | N/A   | GATGAATGACACTGGT  | 5   | AF | 2151 |
| 1410587 | 467988 | 468003 | N/A   | N/A   | TAAACTTTTGATGACA  | 60  | AF | 2152 |
| 1411109 | 561960 | 561975 | 10949 | 10964 | ATTATAATAGGCTGGA  | 10  | AF | 2153 |
| 1411166 | 517420 | 517435 | 2834  | 2849  | GGCTAAACTTCTCTG   | 43  | AF | 2154 |
| 1411179 | 562539 | 562554 | 11528 | 11543 | ACAAAATATCCCCAAC  | 62  | AF | 2155 |
| 1411189 | 559081 | 559096 | 8070  | 8085  | TATACTCTCAACAACT  | 48  | AF | 2156 |
| 1411225 | 556252 | 556267 | 5241  | 5256  | CCTGATAATTTAGATT  | 86  | AF | 2157 |
| 1411254 | 560460 | 560475 | 9449  | 9464  | CTAACCACATGCATGG  | 60  | AF | 2158 |
| 1411264 | 558440 | 558455 | 7429  | 7444  | GTGGAAAGAAATTTGC  | 27  | AF | 2159 |
| 1411274 | 557265 | 557280 | 6254  | 6269  | ATTAAGTTTTGATTGC  | 18  | AF | 2160 |
| 1411283 | 217564 | 217579 | 530   | 545   | CGGAAATGATTCTGGC  | 13  | AF | 2161 |
| 1411388 | 489614 | 489629 | 2561  | 2576  | AGTAAAGAACTGTTCC  | 39† | AF | 2162 |
| 1411397 | 555533 | 555548 | 4522  | 4537  | ATAGAACCATTTTGAG  | 57  | AF | 2163 |
| 1411432 | 554554 | 554569 | 3543  | 3558  | AACAACCTGAGCAGACT | 23  | AF | 2164 |
| 1411433 | 559761 | 559776 | 8750  | 8765  | ATAAGCAGTAAGCTCA  | 36  | AF | 2165 |
| 1411436 | 559377 | 559392 | 8366  | 8381  | TTTGTAAATAAGCCCAA | 20  | AF | 2166 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 7   | AG | 181  |
| 1408300 | 222141 | 222156 | 1551  | 1566  | TCTTTAATGCGCTGTT  | 8   | AG | 2167 |
| 1408320 | 82199  | 82214  | N/A   | N/A   | ATATTAGCTCATGGAA  | 15  | AG | 2168 |
| 1408337 | 189829 | 189844 | N/A   | N/A   | AATTATCGAACCATCT  | 49  | AG | 2169 |
| 1408554 | 288810 | 288825 | N/A   | N/A   | AGATACATAATTTCTC  | 77  | AG | 2170 |
| 1408568 | 290737 | 290752 | N/A   | N/A   | TAAGCCCGACATGTTT  | 63  | AG | 2171 |
| 1408590 | 290549 | 290564 | N/A   | N/A   | AGAACCTATGAAAACA  | 59  | AG | 2172 |
| 1408637 | 225013 | 225028 | N/A   | N/A   | CAACAAGCAGCTCTAC  | 61  | AG | 2173 |
| 1408643 | 226002 | 226017 | N/A   | N/A   | CAGCCGAGAACAGTGT  | 45  | AG | 2174 |
| 1408659 | 235182 | 235197 | N/A   | N/A   | ACTTAATCTCATGTAA  | 71  | AG | 2175 |
| 1408705 | 262950 | 262965 | N/A   | N/A   | TAAGAGCAGCAGCTTA  | 79  | AG | 2176 |
| 1408713 | 263119 | 263134 | N/A   | N/A   | TAATATAATTAGTACC  | 97  | AG | 2177 |
| 1408736 | 271139 | 271154 | N/A   | N/A   | GTAAATTTAAATAGGA  | 107 | AG | 2178 |
| 1409115 | 387073 | 387088 | N/A   | N/A   | GCTATAGGTACTCTTT  | 8   | AG | 2179 |
|         | 387391 | 387406 |       |       |                   |     |    |      |
| 1409166 | 155024 | 155039 | N/A   | N/A   | TTAACAGGATGAGCTC  | 68  | AG | 2180 |
| 1409180 | 105598 | 105613 | N/A   | N/A   | CAAATTTATAGCCCAT  | 12  | AG | 2181 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1409228 | 458503 | 458518 | N/A   | N/A   | TGTATAAAGGACCTCA  | 21  | AG | 2182 |
| 1409312 | 278791 | 278806 | N/A   | N/A   | GAAACAGGCAATAGTA  | 30  | AG | 2183 |
| 1409388 | 418701 | 418716 | N/A   | N/A   | TCAAATGCAAGATGCT  | 51  | AG | 2184 |
| 1409461 | 361863 | 361878 | N/A   | N/A   | TATCATTATAGGTTCA  | 8   | AG | 2185 |
| 1409596 | 259054 | 259069 | N/A   | N/A   | GAAACCATTTCATTCTA | 40  | AG | 2186 |
| 1409627 | 185536 | 185551 | N/A   | N/A   | CAGGATACAAGACATG  | 50  | AG | 2187 |
| 1409717 | 294827 | 294842 | N/A   | N/A   | ACCAGTAAGTTGTACT  | 73  | AG | 2188 |
| 1409724 | 233179 | 233194 | N/A   | N/A   | GACTTTGAAGAGGTTT  | 30  | AG | 2189 |
| 1409732 | 219965 | 219980 | N/A   | N/A   | GGAATATAAACACTGG  | 59  | AG | 2190 |
| 1409745 | 181434 | 181449 | N/A   | N/A   | ATAACCACATATCCCT  | 38  | AG | 2191 |
| 1409769 | 198251 | 198266 | N/A   | N/A   | GTTATTTCAAGCTCAT  | 12  | AG | 2192 |
| 1409775 | 561963 | 561978 | 10952 | 10967 | GTTATTATAATAGGCT  | 17  | AG | 2193 |
| 1409819 | 192509 | 192524 | N/A   | N/A   | CTATCCAGGGTATTGT  | 67  | AG | 2194 |
| 1409820 | 265364 | 265379 | N/A   | N/A   | CAGAATAAATTCAGGG  | 21  | AG | 2195 |
| 1409821 | 215856 | 215871 | N/A   | N/A   | CATTAGTTGTTACCAT  | 64  | AG | 2196 |
| 1409822 | 202220 | 202235 | N/A   | N/A   | GCCAAACAGGGTGCTG  | 86  | AG | 2197 |
| 1409843 | 244047 | 244062 | N/A   | N/A   | GTAATAATCTCCACTC  | 27  | AG | 2198 |
| 1409851 | 448132 | 448147 | N/A   | N/A   | CATTATACCACGAGGC  | 32  | AG | 2199 |
| 1409872 | 469120 | 469135 | N/A   | N/A   | GAATTTGACACACTGC  | 7   | AG | 2200 |
| 1409890 | 506047 | 506062 | N/A   | N/A   | GTAAATTTATGGCCCT  | 30  | AG | 2201 |
| 1409950 | 249874 | 249889 | N/A   | N/A   | GCAAAATCACTCCACA  | 30  | AG | 2202 |
| 1409990 | 518152 | 518167 | N/A   | N/A   | AATCTTTAACTAGTCA  | 31  | AG | 2203 |
| 1410013 | 221791 | 221806 | N/A   | N/A   | ACATATTTGGGAAGGA  | 38  | AG | 2204 |
| 1410022 | 124982 | 124997 | N/A   | N/A   | GCTCATAAAAAGGTTTC | 25  | AG | 2205 |
| 1410037 | 322574 | 322589 | N/A   | N/A   | AGCAAAATGTAGTCCA  | 23  | AG | 2206 |
| 1410050 | 208573 | 208588 | N/A   | N/A   | AATTATCCTGTTTGAG  | 79  | AG | 2207 |
| 1410051 | 282020 | 282035 | N/A   | N/A   | GACTTAACACTACCAT  | 46  | AG | 2208 |
| 1410128 | 205748 | 205763 | N/A   | N/A   | GTAACATAATCCTTA   | 60  | AG | 2209 |
| 1410137 | 292176 | 292191 | N/A   | N/A   | AGTTAACAGATGCTAA  | 29  | AG | 2210 |
| 1410157 | 177209 | 177224 | N/A   | N/A   | ACAAATTTCAAGCTAG  | 74  | AG | 2211 |
| 1410172 | 194965 | 194980 | N/A   | N/A   | CATTATCTCAGAAGGC  | 36  | AG | 2212 |
|         | 551688 | 551703 |       |       |                   |     |    |      |
| 1410173 | 284901 | 284916 | N/A   | N/A   | AATCTTAGGCAAGCAG  | 65  | AG | 2213 |
| 1410188 | 239900 | 239915 | N/A   | N/A   | ACACAGGATAGATGTA  | 90  | AG | 2214 |
| 1410209 | 337573 | 337588 | N/A   | N/A   | AGTGATAAGCAATACC  | 11  | AG | 2215 |
| 1410210 | 248743 | 248758 | N/A   | N/A   | CAATATTCATGCATGC  | 71  | AG | 2216 |
| 1410255 | 229362 | 229377 | N/A   | N/A   | GTGTAAAACACCTTCA  | 38  | AG | 2217 |
| 1410291 | 140033 | 140048 | N/A   | N/A   | CCAGTAAAGTCATTCT  | 19  | AG | 2218 |
| 1410296 | 58074  | 58089  | N/A   | N/A   | TTGGATAGAAACATCA  | 102 | AG | 2219 |
| 1410357 | 308262 | 308277 | N/A   | N/A   | TATATCTAGATGTCTG  | 67  | AG | 2220 |
| 1410371 | 89933  | 89948  | N/A   | N/A   | GATATACAAGCCACAC  | 31  | AG | 2221 |
| 1410442 | 435648 | 435663 | N/A   | N/A   | CCCAAGTTATGATTCT  | 10  | AG | 2222 |
| 1410447 | 204003 | 204018 | N/A   | N/A   | GATACTAAGCTGTACT  | 70  | AG | 2223 |
| 1410481 | 559394 | 559409 | 8383  | 8398  | GCTTTAAAGCATCACA  | 97  | AG | 2224 |
| 1410502 | 273427 | 273442 | N/A   | N/A   | TTAAGTATACACAACC  | 68  | AG | 2225 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1410517 | 211591 | 211606 | N/A   | N/A   | TACAATCCCAATCCAT  | 92  | AG | 2226 |
| 1410519 | 254956 | 254971 | N/A   | N/A   | GCCATTAAATTGGTTA  | 92  | AG | 2227 |
| 1410525 | 188669 | 188684 | N/A   | N/A   | AACAGGTAAAGTGAGT  | 31  | AG | 2228 |
| 1410532 | 398645 | 398660 | N/A   | N/A   | AGAACAAAGACGGCCT  | 72  | AG | 2229 |
| 1410543 | 288566 | 288581 | N/A   | N/A   | GAAAATGCTATCACAC  | 79  | AG | 2230 |
| 1411078 | 557268 | 557283 | 6257  | 6272  | GTAATTAAGTTTTGAT  | 57  | AG | 2231 |
| 1411088 | 533706 | 533721 | 2945  | 2960  | GATATGAGCGGTGCTC  | 58  | AG | 2232 |
| 1411100 | 559086 | 559101 | 8075  | 8090  | CTATATATACTCTCAA  | 34  | AG | 2233 |
| 1411130 | 554555 | 554570 | 3544  | 3559  | AAACAACCTGAGCAGAC | 41  | AG | 2234 |
| 1411135 | 559782 | 559797 | 8771  | 8786  | TACCTATTTACACTCT  | 22  | AG | 2235 |
| 1411175 | 560461 | 560476 | 9450  | 9465  | ACTAACCACATGCATG  | 42  | AG | 2236 |
| 1411182 | 556339 | 556354 | 5328  | 5343  | CTTTAGTTACTGAAGC  | 25  | AG | 2237 |
| 1411299 | 217565 | 217580 | 531   | 546   | CCGGAAATGATTCTGG  | 65  | AG | 2238 |
| 1411330 | 558465 | 558480 | 7454  | 7469  | GATCATGTAAGATGCT  | 46  | AG | 2239 |
| 1411384 | 555539 | 555554 | 4528  | 4543  | AAGTTAATAGAACCAT  | 71  | AG | 2240 |
| 1411394 | 489615 | 489630 | 2562  | 2577  | AAGTAAAGAACTGTTC  | 88† | AG | 2241 |
| 1411428 | 562576 | 562591 | 11565 | 11580 | ACCATTTAAATGCAAT  | 52  | AG | 2242 |
| 1411429 | 218026 | 218041 | 992   | 1007  | GAAATTCCACATGTTT  | 9   | AG | 2243 |
| 1173082 | 533769 | 533784 | 3008  | 3023  | CCAGATAGTGGTCTTT  | 70  | AH | 2244 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 6   | AH | 181  |
| 1408298 | 222144 | 222159 | 1554  | 1569  | CCTTCTTTAATGCGCT  | 17  | AH | 2245 |
| 1408318 | 82201  | 82216  | N/A   | N/A   | AGATATTAGCTCATGG  | 8   | AH | 2246 |
| 1408336 | 189830 | 189845 | N/A   | N/A   | AAATTATCGAACCATC  | 58  | AH | 2247 |
| 1408528 | 288819 | 288834 | N/A   | N/A   | GGTAACTGAAGATACA  | 55  | AH | 2248 |
| 1408549 | 288569 | 288584 | N/A   | N/A   | TTCGAAAATGCTATCA  | 112 | AH | 2249 |
| 1408580 | 290557 | 290572 | N/A   | N/A   | ATACACTCAGAACCTA  | 69  | AH | 2250 |
| 1408585 | 290739 | 290754 | N/A   | N/A   | GATAAGCCCGACATGT  | 38  | AH | 2251 |
| 1408592 | 217571 | 217586 | 537   | 552   | AATGTTCCGGAAATGA  | 9   | AH | 2252 |
| 1408610 | 188678 | 188693 | N/A   | N/A   | TTAATAGTCAACAGGT  | 25  | AH | 2253 |
| 1408636 | 225043 | 225058 | N/A   | N/A   | ATTGAATGCATACACC  | 10  | AH | 2254 |
| 1408658 | 235222 | 235237 | N/A   | N/A   | GTCATTAATATTATAC  | 25  | AH | 2255 |
|         | 235295 | 235310 |       |       |                   |     |    |      |
| 1408696 | 263120 | 263135 | N/A   | N/A   | ATAATATAATTAGTAC  | 98  | AH | 2256 |
| 1408735 | 271149 | 271164 | N/A   | N/A   | GATTGTTAGAGTAAAT  | 82  | AH | 2257 |
| 1408835 | 218032 | 218047 | 998   | 1013  | CTCCTTGAAATTCCAC  | 8   | AH | 2258 |
| 1409100 | 177457 | 177472 | N/A   | N/A   | ATCTTTAATTAGGTGA  | 28  | AH | 2259 |
| 1409128 | 471053 | 471068 | N/A   | N/A   | CCAAAGATATCACGGA  | 103 | AH | 2260 |
| 1409150 | 552536 | 552551 | N/A   | N/A   | AGTCAAAGGCCATTCT  | 95  | AH | 2261 |
| 1409161 | 298307 | 298322 | N/A   | N/A   | CATGATTAAGATGTCA  | 52  | AH | 2262 |
| 1409205 | 418880 | 418895 | N/A   | N/A   | ACACAATTATGATGGG  | 46  | AH | 2263 |
| 1409213 | 341056 | 341071 | N/A   | N/A   | GTAGATATGGAGCTTT  | 4   | AH | 2264 |
| 1409271 | 208709 | 208724 | N/A   | N/A   | AAGTAGTCATCTGTTT  | 72  | AH | 2265 |
| 1409323 | 250092 | 250107 | N/A   | N/A   | AGCAATACTTTGTGGT  | 25  | AH | 2266 |
| 1409350 | 266298 | 266313 | N/A   | N/A   | CCATTTAAAACTTGCC  | 37  | AH | 2267 |
| 1409360 | 254972 | 254987 | N/A   | N/A   | TCAGATAGCTTTTTCA  | 28  | AH | 2268 |

|         |        |        |      |      |                   |     |    |      |
|---------|--------|--------|------|------|-------------------|-----|----|------|
| 1409361 | 308264 | 308279 | N/A  | N/A  | CCTATATCTAGATGTC  | 64  | AH | 2269 |
| 1409382 | 323357 | 323372 | N/A  | N/A  | GATTTACACTACTTTC  | 42  | AH | 2270 |
| 1409531 | 244579 | 244594 | N/A  | N/A  | GACATAAGCAGGGTGG  | 15  | AH | 2271 |
| 1409536 | 198252 | 198267 | N/A  | N/A  | AGTTATTTCAAGCTCA  | 13  | AH | 2272 |
| 1409537 | 204004 | 204019 | N/A  | N/A  | AGATACTAAGCTGTAC  | 82  | AH | 2273 |
| 1409624 | 215857 | 215872 | N/A  | N/A  | ACATTAGTTGTTACCA  | 49  | AH | 2274 |
| 1409635 | 219966 | 219981 | N/A  | N/A  | GGGAATATAAACACTG  | 88  | AH | 2275 |
| 1409670 | 206047 | 206062 | N/A  | N/A  | GTTAGTAAACACCTTA  | 12  | AH | 2276 |
| 1409713 | 202269 | 202284 | N/A  | N/A  | CAAACCACTTCACAGT  | 73  | AH | 2277 |
| 1409729 | 285149 | 285164 | 1784 | 1799 | AAATTTTCAGTGCTCCC | 10  | AH | 2278 |
| 1409755 | 273445 | 273460 | N/A  | N/A  | TTTACTATGGTTGCAT  | 45  | AH | 2279 |
| 1409808 | 239913 | 239928 | N/A  | N/A  | GACTAAAATGTCCACA  | 89  | AH | 2280 |
| 1409840 | 278796 | 278811 | N/A  | N/A  | CTTATGAAACAGGCAA  | 17  | AH | 2281 |
| 1409885 | 262953 | 262968 | N/A  | N/A  | AGTTAAGAGCAGCAGC  | 72  | AH | 2282 |
| 1409888 | 363709 | 363724 | N/A  | N/A  | GTAATAAGCAGCCAGA  | 13  | AH | 2283 |
| 1409975 | 448133 | 448148 | N/A  | N/A  | ACATTATACCACGAGG  | 20  | AH | 2284 |
| 1409976 | 125506 | 125521 | N/A  | N/A  | ACTAATGCTTTACTCC  | 23  | AH | 2285 |
| 1409984 | 233265 | 233280 | N/A  | N/A  | AGGAATTGAAGGCTCT  | 9   | AH | 2286 |
| 1409995 | 106668 | 106683 | N/A  | N/A  | GCAATAAGGCTTCTGC  | 93  | AH | 2287 |
| 1410027 | 211593 | 211608 | N/A  | N/A  | TTTACAATCCCAATCC  | 74  | AH | 2288 |
| 1410032 | 398700 | 398715 | N/A  | N/A  | ATGTTTTAGACCAGAG  | 7   | AH | 2289 |
| 1410082 | 181831 | 181846 | N/A  | N/A  | TCTATAAATTTGTGCC  | 19  | AH | 2290 |
| 1410130 | 506084 | 506099 | N/A  | N/A  | ATCTTATATATGCACT  | 35  | AH | 2291 |
| 1410162 | 387393 | 387408 | N/A  | N/A  | TAGCTATAGGTACTCT  | 28  | AH | 2292 |
| 1410264 | 94387  | 94402  | N/A  | N/A  | AGGCTGCTATTAAAGA  | 66  | AH | 2293 |
| 1410266 | 259182 | 259197 | N/A  | N/A  | CTAATCACAGACTGGA  | 34  | AH | 2294 |
| 1410275 | 140037 | 140052 | N/A  | N/A  | ATTACCAGTAAAGTCA  | 11  | AH | 2295 |
| 1410298 | 458504 | 458519 | N/A  | N/A  | ATGTATAAAGGACCTC  | 16  | AH | 2296 |
| 1410311 | 192564 | 192579 | N/A  | N/A  | GTATATTTTGGAGTCC  | 24  | AH | 2297 |
| 1410362 | 282171 | 282186 | N/A  | N/A  | ACATTACATGGCTGGG  | 18  | AH | 2298 |
| 1410367 | 292254 | 292269 | N/A  | N/A  | GCTCTAAGAGATCTGC  | 46  | AH | 2299 |
| 1410417 | 229417 | 229432 | N/A  | N/A  | AAGATTAAAGTACTGT  | 71  | AH | 2300 |
| 1410435 | 226299 | 226314 | N/A  | N/A  | ACCTTACACAGAGTGA  | 53  | AH | 2301 |
| 1410444 | 522311 | 522326 | N/A  | N/A  | TTTTTATAACTATGGC  | 27  | AH | 2302 |
| 1410455 | 248744 | 248759 | N/A  | N/A  | CCAATATTCATGCATG  | 24  | AH | 2303 |
| 1410490 | 435818 | 435833 | N/A  | N/A  | CTTAACCTTTGACTCC  | 19  | AH | 2304 |
| 1410504 | 559087 | 559102 | 8076 | 8091 | ACTATATATACTCTCA  | 16  | AH | 2305 |
| 1410528 | 186451 | 186466 | N/A  | N/A  | CAGGATACAAGAGCTG  | 91  | AH | 2306 |
| 1410538 | 59655  | 59670  | N/A  | N/A  | ATGTACTATTGTATTA  | 104 | AH | 2307 |
| 1410539 | 221828 | 221843 | N/A  | N/A  | GAAGATCTAACTCTTC  | 102 | AH | 2308 |
| 1410585 | 155818 | 155833 | N/A  | N/A  | GTCAAAAATGTGTAGT  | 5   | AH | 2309 |
| 1411120 | 556341 | 556356 | 5330 | 5345 | TTCTTTAGTTACTGAA  | 83  | AH | 2310 |
| 1411167 | 555541 | 555556 | 4530 | 4545 | CAAAGTTAATAGAACC  | 31  | AH | 2311 |
| 1411221 | 559413 | 559428 | 8402 | 8417 | ACAACAATAAAGAACG  | 87  | AH | 2312 |
| 1411223 | 559783 | 559798 | 8772 | 8787 | TTACCTATTTACACTC  | 34  | AH | 2313 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1411250 | 557290 | 557305 | 6279  | 6294  | AAAGTAAGGACTCTGC  | 20  | AH | 2314 |
| 1411267 | 561964 | 561979 | 10953 | 10968 | AGTTATTATAATAGGC  | 22  | AH | 2315 |
| 1411318 | 554557 | 554572 | 3546  | 3561  | TAAAACAACTGAGCAG  | 34  | AH | 2316 |
| 1411334 | 562655 | 562670 | 11644 | 11659 | TCTAAAGTTTGTACAT  | 61  | AH | 2317 |
| 1411413 | 558603 | 558618 | 7592  | 7607  | ACAAAAGGAGAATGCC  | 49  | AH | 2318 |
| 1411430 | 560462 | 560477 | 9451  | 9466  | GACTAACCACATGCAT  | 65  | AH | 2319 |
| 1411438 | 489616 | 489631 | 2563  | 2578  | CAAGTAAAGAACTGTT  | 65† | AH | 2320 |
| 1004291 | 458505 | 458520 | N/A   | N/A   | CATGTATAAAGGACCT  | 61  | AI | 2321 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 4   | AI | 181  |
| 1408265 | 271176 | 271191 | N/A   | N/A   | ATTAGTGACAGTCAGA  | 8   | AI | 2322 |
| 1408297 | 222145 | 222160 | 1555  | 1570  | ACCTTCTTTAATGCGC  | 15  | AI | 2323 |
| 1408317 | 82202  | 82217  | N/A   | N/A   | CAGATATTAGCTCATG  | 6   | AI | 2324 |
| 1408335 | 189831 | 189846 | N/A   | N/A   | AAAATTATCGAACCAT  | 73  | AI | 2325 |
| 1408514 | 222012 | 222027 | 1422  | 1437  | AACTGGGAGCTGTACA  | 11  | AI | 2326 |
| 1408553 | 288820 | 288835 | N/A   | N/A   | AGGTAAGTGAAGATAC  | 42  | AI | 2327 |
| 1408564 | 288570 | 288585 | N/A   | N/A   | TTTCGAAAATGCTATC  | 90  | AI | 2328 |
| 1408579 | 290567 | 290582 | N/A   | N/A   | CACTAATAGGATACAC  | 63  | AI | 2329 |
| 1408635 | 225063 | 225078 | N/A   | N/A   | CCTGGTAAATTTTCCT  | 24  | AI | 2330 |
| 1408648 | 218033 | 218048 | 999   | 1014  | ACTCCTTGAAATTCCA  | 6   | AI | 2331 |
| 1408657 | 235232 | 235247 | N/A   | N/A   | ATAGATTTAAGTCATT  | 46  | AI | 2332 |
|         | 235305 | 235320 |       |       |                   |     |    |      |
| 1408712 | 263129 | 263144 | N/A   | N/A   | TTAAGTGCTATAATAT  | 58  | AI | 2333 |
| 1409165 | 215871 | 215886 | N/A   | N/A   | CTTTATGAAAGAGGAC  | 48  | AI | 2334 |
| 1409169 | 262954 | 262969 | N/A   | N/A   | CAGTTAAGAGCAGCAG  | 43  | AI | 2335 |
| 1409223 | 140053 | 140068 | N/A   | N/A   | CTTAATACTCCTGTCA  | 40  | AI | 2336 |
| 1409225 | 522566 | 522581 | N/A   | N/A   | CATATTTTAGTTGGAT  | 22  | AI | 2337 |
| 1409267 | 177713 | 177728 | N/A   | N/A   | AGAGTATTAAGTCCGA  | 65  | AI | 2338 |
| 1409301 | 127240 | 127255 | N/A   | N/A   | GACTATATACTATGAG  | 40  | AI | 2339 |
| 1409332 | 204006 | 204021 | N/A   | N/A   | TCAGATACTAAGCTGT  | 96  | AI | 2340 |
| 1409337 | 60248  | 60263  | N/A   | N/A   | TTAAGTTTATACCCAA  | 95  | AI | 2341 |
| 1409341 | 436648 | 436663 | N/A   | N/A   | CATATGAACAAGAGAG  | 39  | AI | 2342 |
| 1409346 | 273446 | 273461 | N/A   | N/A   | GTTTACTATGTTGCA   | 51  | AI | 2343 |
| 1409347 | 285150 | 285165 | 1785  | 1800  | AAAATTTTCAGTGCTCC | 7   | AI | 2344 |
| 1409397 | 255160 | 255175 | N/A   | N/A   | GGATATAAACCCAACG  | 52  | AI | 2345 |
| 1409423 | 248745 | 248760 | N/A   | N/A   | GCCAATATTCATGCAT  | 75  | AI | 2346 |
| 1409468 | 250919 | 250934 | N/A   | N/A   | GGAAGTAAAGCTCCAA  | 85  | AI | 2347 |
| 1409486 | 220171 | 220186 | N/A   | N/A   | ACCTATTAGCATGTTT  | 77  | AI | 2348 |
| 1409520 | 193659 | 193674 | N/A   | N/A   | TATACCAAGTGGTAGG  | 84  | AI | 2349 |
| 1409564 | 419083 | 419098 | N/A   | N/A   | GACAATTTGAATGTTG  | 87  | AI | 2350 |
| 1409604 | 233266 | 233281 | N/A   | N/A   | AAGGAATTGAAGGCTC  | 7   | AI | 2351 |
| 1409606 | 155819 | 155834 | N/A   | N/A   | AGTCAAAAATGTGTAG  | 5   | AI | 2352 |
| 1409645 | 181832 | 181847 | N/A   | N/A   | ATCTATAAATTTGTGC  | 54  | AI | 2353 |
| 1409667 | 202270 | 202285 | N/A   | N/A   | ACAAACCACTTCACAG  | 71  | AI | 2354 |
| 1409682 | 471082 | 471097 | N/A   | N/A   | TGGAATACGCTTATCC  | 78  | AI | 2355 |
| 1409691 | 400103 | 400118 | N/A   | N/A   | TTCTATAGATGACTCC  | 59  | AI | 2356 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1409694 | 198283 | 198298 | N/A   | N/A   | TCCATAAGCATTCCAA  | 33  | AI | 2357 |
| 1409707 | 292389 | 292404 | N/A   | N/A   | CTTTATTGGTTGCTAC  | 4   | AI | 2358 |
| 1409723 | 106669 | 106684 | N/A   | N/A   | AGCAATAAGGCTTCTG  | 76  | AI | 2359 |
| 1409743 | 290742 | 290757 | N/A   | N/A   | AGAGATAAGCCCGACA  | 22  | AI | 2360 |
| 1409762 | 299798 | 299813 | N/A   | N/A   | CTTAGATAAGGATTCC  | 32  | AI | 2361 |
| 1409787 | 282172 | 282187 | N/A   | N/A   | AACATTACATGGCTGG  | 15  | AI | 2362 |
| 1409794 | 278797 | 278812 | N/A   | N/A   | TCTTATGAAACAGGCA  | 13  | AI | 2363 |
| 1409803 | 187088 | 187103 | N/A   | N/A   | GAGACTTAGATGAGGG  | 18  | AI | 2364 |
| 1409858 | 552935 | 552950 | N/A   | N/A   | GTAATTTAGAAGTGCT  | 30  | AI | 2365 |
| 1409863 | 363710 | 363725 | N/A   | N/A   | AGTAATAAGCAGCCAG  | 10  | AI | 2366 |
| 1409902 | 211595 | 211610 | N/A   | N/A   | CCTTTACAATCCCAAT  | 71  | AI | 2367 |
| 1409934 | 229419 | 229434 | N/A   | N/A   | ACAAGATTAAAGTACT  | 69  | AI | 2368 |
| 1410020 | 450199 | 450214 | N/A   | N/A   | GATATACTTAGATGCT  | 43  | AI | 2369 |
| 1410068 | 244751 | 244766 | N/A   | N/A   | TAAAGGGTATTGATCA  | 25  | AI | 2370 |
| 1410117 | 508259 | 508274 | N/A   | N/A   | ATAATACTGGTCTTCT  | 49  | AI | 2371 |
| 1410170 | 239914 | 239929 | N/A   | N/A   | AGACTAAAATGTCCAC  | 99  | AI | 2372 |
| 1410174 | 324217 | 324232 | N/A   | N/A   | ACTACTAACATGTTTA  | 59  | AI | 2373 |
| 1410204 | 308341 | 308356 | N/A   | N/A   | GACTTTTAACAGITCG  | 71  | AI | 2374 |
| 1410223 | 95121  | 95136  | N/A   | N/A   | GTAGAATTTACAGGAA  | 3   | AI | 2375 |
| 1410224 | 206102 | 206117 | N/A   | N/A   | GATATTCATAAATGCA  | 54  | AI | 2376 |
| 1410284 | 208710 | 208725 | N/A   | N/A   | TAAGTAGTCATCTGTT  | 64  | AI | 2377 |
| 1410372 | 226332 | 226347 | N/A   | N/A   | CCAGATTTATTCCAGG  | 16  | AI | 2378 |
| 1410375 | 266299 | 266314 | N/A   | N/A   | ACCATTTAAAACCTGTC | 17  | AI | 2379 |
| 1410389 | 342566 | 342581 | N/A   | N/A   | CATAATAGATGGGCAA  | 14  | AI | 2380 |
| 1410393 | 387789 | 387804 | N/A   | N/A   | ATGTTTAAGATCATCT  | 33  | AI | 2381 |
| 1410420 | 259183 | 259198 | N/A   | N/A   | TCTAATCACAGACTGG  | 39  | AI | 2382 |
| 1410441 | 188693 | 188708 | N/A   | N/A   | TCAAAACCTGTGTTGT  | 84  | AI | 2383 |
| 1411097 | 559423 | 559438 | 8412  | 8427  | ACTAATTACAACAACA  | 61  | AI | 2384 |
| 1411129 | 533771 | 533786 | 3010  | 3025  | CTCCAGATAGTGGTCT  | 52  | AI | 2385 |
| 1411165 | 561965 | 561980 | 10954 | 10969 | CAGTTATTATAATAGG  | 19  | AI | 2386 |
| 1411170 | 562678 | 562693 | 11667 | 11682 | GAAATTTGTTGGATTT  | 77  | AI | 2387 |
| 1411219 | 559785 | 559800 | 8774  | 8789  | AGTTACCTATTTACAC  | 68  | AI | 2388 |
| 1411243 | 559088 | 559103 | 8077  | 8092  | CACTATATATACTCTC  | 14  | AI | 2389 |
| 1411304 | 560512 | 560527 | 9501  | 9516  | CTTATACACCTAAGGG  | 80  | AI | 2390 |
| 1411313 | 557295 | 557310 | 6284  | 6299  | GCGATAAAGTAAGGAC  | 14  | AI | 2391 |
| 1411347 | 558604 | 558619 | 7593  | 7608  | TACAAAAGGAGAATGC  | 64  | AI | 2392 |
| 1411350 | 555558 | 555573 | 4547  | 4562  | GAACAAGCTCATGACT  | 53  | AI | 2393 |
| 1411365 | 217607 | 217622 | 573   | 588   | GAAACAGCATCTTGGT  | 4   | AI | 2394 |
| 1411368 | 554644 | 554659 | 3633  | 3648  | AAACTACAGTTTGTCC  | 17  | AI | 2395 |
| 1411390 | 489617 | 489632 | 2564  | 2579  | GCAAGTAAAGAACTGT  | 27† | AI | 2396 |
| 1411442 | 556413 | 556428 | 5402  | 5417  | CATACAGACATTCTAT  | 24  | AI | 2397 |
| 1173403 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5   | AJ | 181  |
| 1408264 | 271177 | 271192 | N/A   | N/A   | TATTAGTGACAGTCAG  | 10  | AJ | 2398 |
| 1408316 | 82203  | 82218  | N/A   | N/A   | TCAGATATTAGCTCAT  | 5   | AJ | 2399 |
| 1408348 | 225070 | 225085 | N/A   | N/A   | TTATTGACCTGGTAAA  | 59  | AJ | 2400 |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1408552 | 288830 | 288845 | N/A  | N/A  | AGTTATCACTAGGTAA  | 34 | AJ | 2401 |
| 1408563 | 288610 | 288625 | N/A  | N/A  | GAAATACCTACAAGAG  | 77 | AJ | 2402 |
| 1408567 | 290747 | 290762 | N/A  | N/A  | AAAGCAGAGATAAGCC  | 59 | AJ | 2403 |
| 1408576 | 217611 | 217626 | 577  | 592  | ACTAGAAACAGCATCT  | 18 | AJ | 2404 |
| 1408589 | 290569 | 290584 | N/A  | N/A  | ATCACTAATAGGATAC  | 88 | AJ | 2405 |
| 1408621 | 189868 | 189883 | N/A  | N/A  | CTGTTATCTTGACATT  | 66 | AJ | 2406 |
| 1408644 | 218043 | 218058 | 1009 | 1024 | CAGTATTTCCACTCCT  | 5  | AJ | 2407 |
| 1408656 | 235242 | 235257 | N/A  | N/A  | AGACAACAAAATAGAT  | 51 | AJ | 2408 |
|         | 235315 | 235330 |      |      |                   |    |    |      |
| 1408695 | 263130 | 263145 | N/A  | N/A  | CTTAAGTGCTATAATA  | 67 | AJ | 2409 |
| 1408723 | 262969 | 262984 | N/A  | N/A  | CCAATATTAATGTCAC  | 5  | AJ | 2410 |
| 1409090 | 282174 | 282189 | N/A  | N/A  | TTAACATTACATGGCT  | 60 | AJ | 2411 |
| 1409139 | 436649 | 436664 | N/A  | N/A  | GCATATGAACAAGAGA  | 9  | AJ | 2412 |
| 1409188 | 198284 | 198299 | N/A  | N/A  | CTCCATAAGCATTCCA  | 40 | AJ | 2413 |
| 1409189 | 229498 | 229513 | N/A  | N/A  | GCAATAAAGCTAAGTG  | 10 | AJ | 2414 |
| 1409202 | 193661 | 193676 | N/A  | N/A  | TATATACCAAGTGGTA  | 91 | AJ | 2415 |
| 1409218 | 188937 | 188952 | N/A  | N/A  | GTATATAAGTTTTGAT  | 73 | AJ | 2416 |
| 1409231 | 240021 | 240036 | N/A  | N/A  | ACAGATTTAACTCTTC  | 16 | AJ | 2417 |
| 1409236 | 299998 | 300013 | N/A  | N/A  | ACTGATTAAAGCTACC  | 47 | AJ | 2418 |
| 1409319 | 522567 | 522582 | N/A  | N/A  | TCATATTTTAGTTGGA  | 19 | AJ | 2419 |
| 1409335 | 108190 | 108205 | N/A  | N/A  | AATACTGACAATCATC  | 78 | AJ | 2420 |
| 1409338 | 208711 | 208726 | N/A  | N/A  | TTAAGTAGTCATCTGT  | 38 | AJ | 2421 |
| 1409340 | 387855 | 387870 | N/A  | N/A  | CCAATAACTTGTCCAT  | 6  | AJ | 2422 |
| 1409407 | 220173 | 220188 | N/A  | N/A  | ATACCTATTAGCATGT  | 84 | AJ | 2423 |
| 1409566 | 400224 | 400239 | N/A  | N/A  | TTCAAGAGGCTAGTGC  | 21 | AJ | 2424 |
| 1409644 | 278798 | 278813 | N/A  | N/A  | GTCTTATGAAACAGGC  | 45 | AJ | 2425 |
| 1409663 | 226628 | 226643 | N/A  | N/A  | CTAATTTTGAGCCAT   | 43 | AJ | 2426 |
| 1409697 | 308470 | 308485 | N/A  | N/A  | TTGTATAGACTTTTCC  | 20 | AJ | 2427 |
| 1409701 | 273496 | 273511 | N/A  | N/A  | GTGTATATAGGAACAA  | 33 | AJ | 2428 |
| 1409720 | 471322 | 471337 | N/A  | N/A  | ACCTTAAGGTTTTTGC  | 64 | AJ | 2429 |
| 1409798 | 458514 | 458529 | N/A  | N/A  | GCTAATAACCATGTAT  | 42 | AJ | 2430 |
| 1409811 | 127336 | 127351 | N/A  | N/A  | AAGTTTAAATACCTCC  | 64 | AJ | 2431 |
| 1409844 | 552936 | 552951 | N/A  | N/A  | AGTAATTTAGAAGTGC  | 30 | AJ | 2432 |
| 1409849 | 419949 | 419964 | N/A  | N/A  | GATAATTCTGTCACCT  | 32 | AJ | 2433 |
| 1409853 | 364532 | 364547 | N/A  | N/A  | CATTATACTTCCTTCA  | 21 | AJ | 2434 |
| 1409855 | 508260 | 508275 | N/A  | N/A  | CATAATACTGGTCTTC  | 40 | AJ | 2435 |
| 1409869 | 248788 | 248803 | N/A  | N/A  | GCTTAGCAGACTGCTG  | 61 | AJ | 2436 |
| 1409912 | 202275 | 202290 | N/A  | N/A  | ACAATACAAACCACTT  | 63 | AJ | 2437 |
| 1409968 | 267518 | 267533 | N/A  | N/A  | AATACTCCACCTGGTG  | 76 | AJ | 2438 |
| 1410127 | 60915  | 60930  | N/A  | N/A  | GTAATATTGAGATCAA  | 16 | AJ | 2439 |
| 1410147 | 206180 | 206195 | N/A  | N/A  | GTTCATCGGATTTTCA  | 47 | AJ | 2440 |
| 1410151 | 187203 | 187218 | N/A  | N/A  | AGCAATAACTGTGGGT  | 24 | AJ | 2441 |
| 1410163 | 181869 | 181884 | N/A  | N/A  | AACCAGATGTAGTTTC  | 32 | AJ | 2442 |
| 1410168 | 204011 | 204026 | N/A  | N/A  | GCTATTCAGATACTAA  | 49 | AJ | 2443 |
| 1410202 | 255321 | 255336 | N/A  | N/A  | GCTGAACCTAAGTGGCA | 92 | AJ | 2444 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1410216 | 180689 | 180704 | N/A   | N/A   | CCATTAACACCACTGT  | 71  | AJ | 2445 |
| 1410319 | 215892 | 215907 | N/A   | N/A   | AATACAGTGTACTCAC  | 55  | AJ | 2446 |
| 1410321 | 244760 | 244775 | N/A   | N/A   | TTTATGAGTTAAAGGG  | 20  | AJ | 2447 |
| 1410331 | 259386 | 259401 | N/A   | N/A   | CAATCAATCACTTTCA  | 22  | AJ | 2448 |
| 1410356 | 233288 | 233303 | N/A   | N/A   | ATCATTAAACCTCCTC  | 32  | AJ | 2449 |
| 1410366 | 95490  | 95505  | N/A   | N/A   | GCATATACACCTGTGC  | 91  | AJ | 2450 |
| 1410414 | 141624 | 141639 | N/A   | N/A   | GATTTAAGTCGGGTCA  | 95  | AJ | 2451 |
| 1410419 | 155847 | 155862 | N/A   | N/A   | GTTATTAAATAATCCC  | 6   | AJ | 2452 |
| 1410469 | 292551 | 292566 | N/A   | N/A   | AAGAAGCAGGATGCTT  | 86  | AJ | 2453 |
| 1410474 | 450538 | 450553 | N/A   | N/A   | TTTAATTCAGTCCCCA  | 62  | AJ | 2454 |
| 1410534 | 342700 | 342715 | N/A   | N/A   | GATATTACAAACAAGG  | 12  | AJ | 2455 |
| 1410573 | 251701 | 251716 | N/A   | N/A   | ATTACCTAAAGGTCAG  | 38  | AJ | 2456 |
| 1410579 | 211617 | 211632 | N/A   | N/A   | GTGGATAAAAGCTTTA  | 67  | AJ | 2457 |
| 1411075 | 559089 | 559104 | 8078  | 8093  | CCACTATATATACTCT  | 17  | AJ | 2458 |
| 1411084 | 557367 | 557382 | 6356  | 6371  | TTAATTAGACACTGCT  | 20  | AJ | 2459 |
| 1411159 | 559424 | 559439 | 8413  | 8428  | GACTAATTACAACAAC  | 56  | AJ | 2460 |
| 1411196 | 558605 | 558620 | 7594  | 7609  | GTACAAAAGGAGAATG  | 83  | AJ | 2461 |
| 1411205 | 556414 | 556429 | 5403  | 5418  | ACATACAGACATTCTA  | 16  | AJ | 2462 |
| 1411263 | 533773 | 533788 | 3012  | 3027  | AACTCCAGATAGTGGT  | 84  | AJ | 2463 |
| 1411269 | 560513 | 560528 | 9502  | 9517  | CCTTATACACCTAAGG  | 91  | AJ | 2464 |
| 1411286 | 285151 | 285166 | 1786  | 1801  | CAAAATTTTCAGTGCTC | 8   | AJ | 2465 |
| 1411332 | 554645 | 554660 | 3634  | 3649  | AAAACCTACAGTTTGTC | 72  | AJ | 2466 |
| 1411352 | 555809 | 555824 | 4798  | 4813  | TCATAGTACCTTCAAC  | 32  | AJ | 2467 |
| 1411373 | 562681 | 562696 | 11670 | 11685 | ATTGAAATTTGTTGGA  | 87  | AJ | 2468 |
| 1411377 | 559823 | 559838 | 8812  | 8827  | ATATACCAAACATGCT  | 43  | AJ | 2469 |
| 1411396 | 489618 | 489633 | 2565  | 2580  | TGCAAGTAAAGAACTG  | 44† | AJ | 2470 |
| 1411398 | 222016 | 222031 | 1426  | 1441  | TTCAAACCTGGGAGCTG | 6   | AJ | 2471 |
| 1411402 | 222157 | 222172 | 1567  | 1582  | CAAGAACTGACCACCT  | 7   | AJ | 2472 |
| 1411423 | N/A    | N/A    | 2179  | 2194  | TCCAATATTGTGGCCA  | 22  | AJ | 2473 |
| 1411434 | 562017 | 562032 | 11006 | 11021 | GTAAAGAAATGTTCCA  | 16  | AJ | 2474 |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 4   | AK | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 3   | AL | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 3   | AM | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 3   | AN | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 2   | AO | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 3   | AP | 686  |
| 1410423 | 285254 | 285269 | 1889  | 1904  | ATCTTTTGAATCTGTC  | 4   | AQ | 686  |
| 1441240 | 366243 | 366258 | N/A   | N/A   | ACTATCATATGAAAGC  | 13  | AQ | 2475 |
| 1441241 | 366242 | 366257 | N/A   | N/A   | CTATCATATGAAAGCC  | 4   | AQ | 2476 |
| 1441242 | 366241 | 366256 | N/A   | N/A   | TATCATATGAAAGCCA  | 5   | AQ | 2477 |
| 1441243 | 181932 | 181947 | N/A   | N/A   | ATGCAGAATTGATAAC  | 51  | AQ | 2478 |
| 1441244 | 365701 | 365716 | N/A   | N/A   | GCAGTAATATTAAAGC  | 28  | AQ | 2479 |
| 1441245 | 365700 | 365715 | N/A   | N/A   | CAGTAATATTAAAGCC  | 10  | AQ | 2480 |
| 1441246 | 508287 | 508302 | N/A   | N/A   | TTTTAAGAGTCCACTA  | 63  | AQ | 2481 |
| 1441247 | 508286 | 508301 | N/A   | N/A   | TTTAAGAGTCCACTAG  | 80  | AQ | 2482 |

|         |        |        |      |      |                  |    |    |      |
|---------|--------|--------|------|------|------------------|----|----|------|
| 1441248 | 222040 | 222055 | 1450 | 1465 | TAAAGAAGTGTGTGCC | 4  | AQ | 2483 |
| 1441249 | 155903 | 155918 | N/A  | N/A  | AAGTTATTATATGGCT | 17 | AQ | 2484 |
| 1441250 | 155901 | 155916 | N/A  | N/A  | GTTATTATATGGCTGT | 5  | AQ | 2485 |
| 1441251 | 251926 | 251941 | N/A  | N/A  | GGTTTTAAGTTATCTC | 3  | AQ | 2486 |
| 1441252 | N/A    | N/A    | 2003 | 2018 | AATACCTGAGTGACTG | 4  | AQ | 2487 |
| 1441253 | 285468 | 285483 | 2002 | 2017 | ATACCTGAGTGACTGA | 4  | AQ | 2488 |
| 1441318 | 235205 | 235220 | N/A  | N/A  | CAATTTAGCTCTATTA | 39 | AQ | 2489 |
| 1441551 | 222154 | 222169 | 1564 | 1579 | GAACTGACCACCTTCT | 12 | AQ | 2490 |
| 1441552 | 222149 | 222164 | 1559 | 1574 | GACCACCTTCTTTAAT | 35 | AQ | 2491 |
| 1441553 | 244768 | 244783 | N/A  | N/A  | ATAGGTAATTTATGAG | 19 | AQ | 2492 |
| 1441554 | 342929 | 342944 | N/A  | N/A  | TGAGATAATGTGAAGC | 3  | AQ | 2493 |
| 1441555 | 342928 | 342943 | N/A  | N/A  | GAGATAATGTGAAGCT | 3  | AQ | 2494 |
| 1441556 | 342925 | 342940 | N/A  | N/A  | ATAATGTGAAGCTTAG | 5  | AQ | 2495 |
| 1441557 | 218086 | 218101 | 1052 | 1067 | AATCTATAGGATGCTG | 6  | AQ | 2496 |
| 1441558 | 229904 | 229919 | N/A  | N/A  | ACATTTAGAGGCATTG | 9  | AQ | 2497 |
| 1441559 | 229902 | 229917 | N/A  | N/A  | ATTTAGAGGCATTGCA | 20 | AQ | 2498 |
| 1441560 | 222047 | 222062 | 1457 | 1472 | TGTAGTATAAAGAAGT | 12 | AQ | 2499 |
| 1441561 | 97753  | 97768  | N/A  | N/A  | TCTCATTAAATCAAGG | 21 | AQ | 2500 |
| 1441562 | 97751  | 97766  | N/A  | N/A  | TCATTAAATCAAGGCA | 8  | AQ | 2501 |
| 1441563 | 350508 | 350523 | N/A  | N/A  | TTATTATAGGGTTGAA | 6  | AQ | 2502 |
| 1441564 | 350507 | 350522 | N/A  | N/A  | TATTATAGGGTTGAAA | 66 | AQ | 2503 |
| 1441565 | 290653 | 290668 | 2132 | 2147 | AGGTAAGGCAATGGAC | 5  | AQ | 2504 |
| 1441566 | 290652 | 290667 | 2131 | 2146 | GGTAAGGCAATGGACT | 22 | AQ | 2505 |
| 1441567 | 82465  | 82480  | N/A  | N/A  | TGAACAATGCTGATTC | 56 | AQ | 2506 |
| 1441568 | 82462  | 82477  | N/A  | N/A  | ACAATGCTGATTCAGG | 4  | AQ | 2507 |
| 1441569 | 368430 | 368445 | N/A  | N/A  | GGTGATATTGTATAAG | 4  | AQ | 2508 |
| 1441570 | 368428 | 368443 | N/A  | N/A  | TGATATTGTATAAGGT | 7  | AQ | 2509 |
| 1441571 | 368425 | 368440 | N/A  | N/A  | TATTGTATAAGGTTAG | 10 | AQ | 2510 |
| 1441572 | 368424 | 368439 | N/A  | N/A  | ATTGTATAAGGTTAGG | 3  | AQ | 2511 |
| 1441573 | 242390 | 242405 | N/A  | N/A  | CGTCAAGTAATGAGTT | 7  | AQ | 2512 |
| 1441574 | 285255 | 285270 | 1890 | 1905 | GATCTTTTGAATCTGT | 10 | AQ | 2513 |
| 1441575 | 285253 | 285268 | 1888 | 1903 | TCTTTTGAATCTGTCC | 6  | AQ | 2514 |
| 1441576 | 285188 | 285203 | 1823 | 1838 | TGGTACCATTACTGAG | 37 | AQ | 2515 |
| 1441577 | 217792 | 217807 | 758  | 773  | CTCCAGTTAACAGCGC | 19 | AQ | 2516 |
| 1441578 | 217788 | 217803 | 754  | 769  | AGTTAACAGCGCGGTG | 12 | AQ | 2517 |
| 1441579 | 217787 | 217802 | 753  | 768  | GTTAACAGCGCGGTGA | 23 | AQ | 2518 |
| 1441580 | 217786 | 217801 | 752  | 767  | TTAACAGCGCGGTGAG | 14 | AQ | 2519 |
| 1441700 | 222231 | 222246 | 1641 | 1656 | GAATAGCCCATCACGA | 20 | AQ | 2520 |
| 1441702 | 222230 | 222245 | 1640 | 1655 | AATAGCCCATCACGAT | 12 | AQ | 2521 |
| 1441714 | 218175 | 218190 | 1141 | 1156 | ACACAAACCAGCTGAT | 10 | AQ | 2522 |
| 1441718 | 218174 | 218189 | 1140 | 1155 | CACAAACCAGCTGATG | 8  | AQ | 2523 |
| 1441722 | 218173 | 218188 | 1139 | 1154 | ACAAACCAGCTGATGA | 8  | AQ | 2524 |
| 1441737 | 218170 | 218185 | 1136 | 1151 | AACCAGCTGATGAGAT | 7  | AQ | 2525 |
| 1441853 | 263335 | 263350 | N/A  | N/A  | GTTTGAAGAATGCATG | 8  | AQ | 2526 |
| 1441854 | 344746 | 344761 | N/A  | N/A  | CTAAATTTAGTATCCT | 10 | AQ | 2527 |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1441855 | 391184 | 391199 | N/A  | N/A  | AATTAGGATTAAGGAG  | 37 | AQ | 2528 |
| 1441856 | 391183 | 391198 | N/A  | N/A  | ATTAGGATTAAGGAGT  | 10 | AQ | 2529 |
| 1441857 | 391182 | 391197 | N/A  | N/A  | TTAGGATTAAGGAGTT  | 4  | AQ | 2530 |
| 1441858 | 391180 | 391195 | N/A  | N/A  | AGGATTAAGGAGTTCT  | 36 | AQ | 2531 |
| 1441859 | 391179 | 391194 | N/A  | N/A  | GGATTAAGGAGTTCTG  | 11 | AQ | 2532 |
| 1441860 | 391178 | 391193 | N/A  | N/A  | GATTAAGGAGTTCTGT  | 14 | AQ | 2533 |
| 1441861 | 222013 | 222028 | 1423 | 1438 | AAACTGGGAGCTGTAC  | 8  | AQ | 2534 |
| 1441977 | 229160 | 229175 | N/A  | N/A  | AGTATTAACCACCATT  | 5  | AQ | 2535 |
| 1441978 | 463907 | 463922 | N/A  | N/A  | AGATTTAATAGGTCTT  | 73 | AQ | 2536 |
| 1441979 | 331864 | 331879 | N/A  | N/A  | CTATAGTATGATAGCA  | 31 | AQ | 2537 |
| 1441980 | 331861 | 331876 | N/A  | N/A  | TAGTATGATAGCACAA  | 4  | AQ | 2538 |
| 1441981 | 331860 | 331875 | N/A  | N/A  | AGTATGATAGCACAAA  | 3  | AQ | 2539 |
| 1441982 | 331859 | 331874 | N/A  | N/A  | GTATGATAGCACAAAC  | 5  | AQ | 2540 |
| 1441983 | 236803 | 236818 | N/A  | N/A  | AATTGTTATACTGATG  | 24 | AQ | 2541 |
| 1441984 | 236802 | 236817 | N/A  | N/A  | ATTGTTATACTGATGG  | 5  | AQ | 2542 |
| 1441985 | 236801 | 236816 | N/A  | N/A  | TTGTTATACTGATGGG  | 5  | AQ | 2543 |
| 1441986 | 236799 | 236814 | N/A  | N/A  | GTTATACTGATGGGCT  | 8  | AQ | 2544 |
| 1441987 | 236798 | 236813 | N/A  | N/A  | TTATACTGATGGGCTA  | 6  | AQ | 2545 |
| 1441988 | 236797 | 236812 | N/A  | N/A  | TATACTGATGGGCTAG  | 34 | AQ | 2546 |
| 1441989 | 217510 | 217525 | 476  | 491  | GCTGTAAACTTTGTTC  | 13 | AQ | 2547 |
| 1441990 | 222017 | 222032 | 1427 | 1442 | TTTCAAACCTGGGAGCT | 14 | AQ | 2548 |
| 1442015 | 226037 | 226052 | N/A  | N/A  | CCCAACCTCTTGCACC  | 41 | AQ | 2549 |
| 1442048 | 508284 | 508299 | N/A  | N/A  | TAAGAGTCCACTAGCC  | 71 | AQ | 2550 |
| 1442085 | 222237 | 222252 | 1647 | 1662 | CCACTAGAATAGCCCA  | 4  | AQ | 2551 |
| 1410423 | 285254 | 285269 | 1889 | 1904 | ATCTTTTGAATCTGTC  | 3  | AR | 686  |
| 1410423 | 285254 | 285269 | 1889 | 1904 | ATCTTTTGAATCTGTC  | 5  | AS | 686  |
| 1410423 | 285254 | 285269 | 1889 | 1904 | ATCTTTTGAATCTGTC  | 4  | AT | 686  |
| 1410423 | 285254 | 285269 | 1889 | 1904 | ATCTTTTGAATCTGTC  | 3  | AU | 686  |
| 1410423 | 285254 | 285269 | 1889 | 1904 | ATCTTTTGAATCTGTC  | 4  | AV | 686  |
| 1442123 | 326723 | 326738 | N/A  | N/A  | GATTATGAGGAAACCT  | 4  | AV | 2552 |
| 1442124 | 263003 | 263018 | N/A  | N/A  | ATGAATGGTATGATGG  | 6  | AV | 2553 |
| 1442125 | 263333 | 263348 | N/A  | N/A  | TTGAAGAATGCATGTC  | 3  | AV | 2554 |
| 1442126 | 391186 | 391201 | N/A  | N/A  | TTAATTAGGATTAAGG  | 31 | AV | 2555 |
| 1442127 | 391176 | 391191 | N/A  | N/A  | TTAAGGAGTTCTGTGT  | 3  | AV | 2556 |
| 1442128 | 229900 | 229915 | N/A  | N/A  | TTAGAGGCATTGCAGG  | 6  | AV | 2557 |
| 1442129 | 350504 | 350519 | N/A  | N/A  | TATAGGGTTGAAAATA  | 38 | AV | 2558 |
| 1442130 | 368422 | 368437 | N/A  | N/A  | TGTATAAGGTTAGGTG  | 3  | AV | 2559 |
| 1442131 | 222238 | 222253 | 1648 | 1663 | GCCACTAGAATAGCCC  | 28 | AV | 2560 |
| 1442152 | 229158 | 229173 | N/A  | N/A  | TATTAACCACCATTCC  | 6  | AV | 2561 |
| 1442153 | 236795 | 236810 | N/A  | N/A  | TACTGATGGGCTAGCC  | 60 | AV | 2562 |
| 1442154 | 217567 | 217582 | 533  | 548  | TTCCGGAAATGATTCT  | 11 | AV | 2563 |
| 1442155 | 222021 | 222036 | 1431 | 1446 | ATGGTTTCAAACCTGGG | 4  | AV | 2564 |

The modified oligonucleotides in Table 3 below are 16 nucleosides in length. The sugar motif for the modified oligonucleotides is (from 5' to 3'): kkkdyddddd kkk; wherein each "d" represents a 2'-β-D-deoxyribose sugar moiety, each "k" represents a cEt modified sugar moiety, and each "y" represents a 2'-O-methylribose sugar moiety. The internucleoside linkage motif for the modified oligonucleotides is (from 5' to 3'): sssssssssssss; wherein each "s" represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine unless otherwise indicated. *Non-methylated cytosines are represented in **C** font as "C".*

**Table 3.** Reduction of PSD3 RNA by mixed sugar modified oligonucleotides with uniform phosphorothioate internucleoside linkages

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3')       | DMPK (% UTC) RTS41435 | AID | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|---------------------------|-----------------------|-----|-----------|
| 1408272      | 217983                  | 217998                 | 949                     | 964                    | GCTT <u>C</u> GATCACATCCC | 25                    | E   | 22        |
| 1408278      | 218080                  | 218095                 | 1046                    | 1061                   | TAGGATGCTGGGTCTC          | 10                    | E   | 474       |
| 1408280      | 222145                  | 222160                 | 1555                    | 1570                   | ACCTUCTTTAATGCGC          | 28                    | E   | 2565      |
| 1408294      | 225074                  | 225089                 | N/A                     | N/A                    | TGTAUTATTGACCTGG          | 12                    | E   | 2566      |
| 1408299      | 249397                  | 249412                 | N/A                     | N/A                    | GGTAUTATTAGTATGT          | 8                     | E   | 2567      |
| 1408367      | 271174                  | 271189                 | N/A                     | N/A                    | TAGTGACAGTCAGAAC          | 91                    | E   | 378       |
| 1408400      | 217666                  | 217681                 | 632                     | 647                    | TCTGUGTTTACGACT           | 10                    | E   | 2568      |
| 1408402      | 217988                  | 218003                 | 954                     | 969                    | GAGCUGCTTCGATCAC          | 35                    | E   | 2569      |
| 1408408      | 290684                  | 290699                 | 2163                    | 2178                   | TGTAGATCGGTATTAA          | 42                    | E   | 354       |
| 1408410      | 181277                  | 181292                 | N/A                     | N/A                    | ATCTUCTATTTAATGG          | 76                    | E   | 2570      |
| 1408417      | 189818                  | 189833                 | N/A                     | N/A                    | CATCUTTTGCTGGCAT          | 51                    | E   | 2571      |
| 1408421      | 189758                  | 189773                 | N/A                     | N/A                    | TTGT <u>C</u> ATACACTAACC | 78                    | E   | 2572      |
| 1408424      | 225203                  | 225218                 | N/A                     | N/A                    | AGTG <u>C</u> TTGGCTGAAGG | 28                    | E   | 2573      |
| 1408428      | 225153                  | 225168                 | N/A                     | N/A                    | TCGG <u>C</u> AGAGGGATGTT | 64                    | E   | 2574      |
| 1408431      | 225033                  | 225048                 | N/A                     | N/A                    | TACA <u>C</u> CACCACCGACA | 79                    | E   | 2575      |
| 1408435      | 224933                  | 224948                 | N/A                     | N/A                    | GAGAGAAATCCGATCA          | 79                    | E   | 2576      |
| 1408439      | 226012                  | 226027                 | N/A                     | N/A                    | AAGAGCAATTCAGCCG          | 101                   | E   | 2577      |
| 1408443      | 225882                  | 225897                 | N/A                     | N/A                    | CTAGGCAATAGCAAAG          | 81                    | E   | 2578      |
| 1408448      | 225802                  | 225817                 | N/A                     | N/A                    | CACTUGGTCCAGTTCA          | 30                    | E   | 2579      |
| 1408452      | 225762                  | 225777                 | N/A                     | N/A                    | TCTGGAGGCTGACTGC          | 47                    | E   | 2580      |
| 1408457      | 235402                  | 235417                 | N/A                     | N/A                    | ATAG <u>C</u> ACTAAAGTTTT | 29                    | E   | 2581      |
| 1408464      | 235202                  | 235217                 | N/A                     | N/A                    | TTTAGCTCTATTAAAT          | 90                    | E   | 2582      |
| 1408466      | 235349                  | 235364                 | N/A                     | N/A                    | ACACACAGCCTGGTCC          | 56                    | E   | 2583      |
| 1408468      | 235269                  | 235284                 | N/A                     | N/A                    | TCTGUTAAATTCACAC          | 62                    | E   | 2584      |
| 1408474      | 235059                  | 235074                 | N/A                     | N/A                    | CCAGGCAACACACACA          | 52                    | E   | 2585      |
| 1408478      | 243424                  | 243439                 | N/A                     | N/A                    | GTC <u>A</u> CGGACTGCTGAC | 80                    | E   | 2586      |
| 1408482      | 243334                  | 243349                 | N/A                     | N/A                    | CCTGGACTTAGTGCTG          | 56                    | E   | 2587      |
| 1408486      | 243284                  | 243299                 | N/A                     | N/A                    | AAGTUGCAGGATGCAC          | 83                    | E   | 2588      |
| 1408491      | 243204                  | 243219                 | N/A                     | N/A                    | GGGT <u>C</u> TTGCTCATGAA | 70                    | E   | 2589      |

|         |        |        |      |      |                           |     |   |      |
|---------|--------|--------|------|------|---------------------------|-----|---|------|
| 1408494 | 249534 | 249549 | N/A  | N/A  | ATTTGTCCCCACTGTC          | 67  | E | 2590 |
| 1408502 | 249324 | 249339 | N/A  | N/A  | GCCAGTGGCAGAGCTG          | 66  | E | 2591 |
| 1408506 | 249254 | 249269 | N/A  | N/A  | TCCTGCCTCTCTGGGA          | 79  | E | 2592 |
| 1408508 | 263180 | 263195 | N/A  | N/A  | GCCAGAGGCAGTGTAC          | 66  | E | 2593 |
| 1408511 | 263140 | 263155 | N/A  | N/A  | AGTCCTGGGCCTTAAG          | 68  | E | 2594 |
| 1408513 | 263000 | 263015 | N/A  | N/A  | AATGGTATGATGGTTC          | 49  | E | 2595 |
| 1408522 | 262959 | 262974 | N/A  | N/A  | TGTCACAGTTAAGAGC          | 76  | E | 2596 |
| 1408525 | 262899 | 262914 | N/A  | N/A  | CCAAGCATGCATCCAC          | 30  | E | 2597 |
| 1408532 | 271229 | 271244 | N/A  | N/A  | TGCAUTTTCTGGCTTT          | 68  | E | 2598 |
| 1408539 | 271079 | 271094 | N/A  | N/A  | AGTCATCCCTGCCAGG          | 54  | E | 2599 |
| 1408742 | 217791 | 217806 | 757  | 772  | TCCAGTTAACAGCGCG          | 26  | E | 2600 |
| 1408747 | 217741 | 217756 | 707  | 722  | CCTCCGTTGTTACTTC          | 9   | E | 2601 |
| 1408752 | 217651 | 217666 | 617  | 632  | TGGCAGTGTCCAGCTC          | 26  | E | 2602 |
| 1408756 | 217591 | 217606 | 557  | 572  | CCAGUACCTTTGTAGC          | 63  | E | 2603 |
| 1408761 | 217521 | 217536 | 487  | 502  | AGAGUCAATGGGCTGT          | 31  | E | 2604 |
| 1408764 | 218123 | 218138 | 1089 | 1104 | CTGT <u>C</u> AGGAGAGGCTG | 35  | E | 2605 |
| 1408767 | 218103 | 218118 | 1069 | 1084 | TTGCAGTGATGTCTCA          | 13  | E | 2606 |
| 1408773 | 218013 | 218028 | 979  | 994  | TTTGACCCGGCCTGGG          | 71  | E | 2607 |
| 1408776 | 217973 | 217988 | 939  | 954  | CATC <u>C</u> CCCTGGGTGCT | 45  | E | 2608 |
| 1408778 | 217943 | 217958 | 909  | 924  | GACCUCTGCTCTTTCA          | 72  | E | 2609 |
| 1408783 | 217893 | 217908 | 859  | 874  | TGCTGAGCTCCCAGG           | 62  | E | 2610 |
| 1408787 | 217843 | 217858 | 809  | 824  | CAGC <u>C</u> CCTTTCCTCCC | 34  | E | 2611 |
| 1408795 | 218072 | 218087 | 1038 | 1053 | TGGGUCTCTCTTTGT           | 55  | E | 2612 |
| 1408797 | 218052 | 218067 | 1018 | 1033 | TCCTGTCCACAGTATT          | 18  | E | 2613 |
| 1408808 | 222222 | 222237 | 1632 | 1647 | ATCA <u>C</u> GATGCCACCAT | 18  | E | 180  |
| 1408812 | 222182 | 222197 | 1592 | 1607 | GATGUCCTCCCCCTGA          | 33  | E | 2614 |
| 1408816 | 222082 | 222097 | 1492 | 1507 | AGGCUCTGAGTATAAT          | 28  | E | 2615 |
| 1408820 | 221992 | 222007 | 1402 | 1417 | GGTGGAGTCCTCCGTA          | 52  | E | 2616 |
| 1408823 | 288729 | 288744 | N/A  | N/A  | TGTAUCAGATTACCTT          | 62  | E | 2617 |
| 1408825 | 288699 | 288714 | 2094 | 2109 | TCTGGGTTACAATAAA          | 69  | E | 2618 |
| 1408826 | 288639 | 288654 | 2034 | 2049 | GTTT <u>T</u> TCCCACAAGAG | 42  | E | 2619 |
| 1408828 | 288559 | 288574 | N/A  | N/A  | CTAT <u>C</u> ACACTCTTTCA | 86  | E | 2620 |
| 1408837 | 290807 | 290822 | N/A  | N/A  | CATGGGAACCATGTAG          | 92  | E | 2621 |
| 1408848 | 290659 | 290674 | 2138 | 2153 | TTGCACAGGTAAGGCA          | 112 | E | 2622 |
| 1408850 | 290599 | 290614 | N/A  | N/A  | TCGCUTTTCACTGTTG          | 79  | E | 2623 |
| 1408853 | 290559 | 290574 | N/A  | N/A  | GGATACACTCAGAACC          | 75  | E | 2624 |
| 1408857 | 82330  | 82345  | N/A  | N/A  | CTAGGTCAGTGGACAA          | 88  | E | 2625 |
| 1408861 | 82230  | 82245  | N/A  | N/A  | TGTA <u>C</u> TTCAAGGCTG  | 48  | E | 2626 |
| 1408865 | 82170  | 82185  | N/A  | N/A  | TTTT <u>C</u> TTCAAGGGAGA | 23  | E | 2627 |
| 1408866 | 181422 | 181437 | N/A  | N/A  | CCCTGACTTCCCGTTC          | 72  | E | 2628 |
| 1408871 | 181362 | 181377 | N/A  | N/A  | TCTGUCTCTGTGCAGG          | 81  | E | 2629 |
| 1408878 | 181142 | 181157 | N/A  | N/A  | TATTUCCTGCCCTCCC          | 60  | E | 2630 |
| 1408881 | 188688 | 188703 | N/A  | N/A  | ACCTGTGTTGTTAATA          | 62  | E | 2631 |

|         |        |        |      |      |                           |     |   |      |
|---------|--------|--------|------|------|---------------------------|-----|---|------|
| 1408885 | 188628 | 188643 | N/A  | N/A  | TCATGTTTTTTCATCC          | 42  | E | 2632 |
| 1408887 | 188538 | 188553 | N/A  | N/A  | CACA <u>C</u> TCTTGTTATT  | 67  | E | 2633 |
| 1408893 | 189928 | 189943 | N/A  | N/A  | TGATUTTCTTAATGGT          | 70  | E | 2634 |
| 1408897 | 189888 | 189903 | N/A  | N/A  | TTGG <u>C</u> TGTCTGCTGCT | 67  | E | 2635 |
| 1408271 | 217984 | 217999 | 950  | 965  | TGCTUCGATCACATCC          | 22  | F | 2636 |
| 1408275 | 217980 | 217995 | 946  | 961  | TCGAUCACATCCCCCT          | 68  | F | 2637 |
| 1408277 | 218081 | 218096 | 1047 | 1062 | ATAGGATGCTGGGTCT          | 11  | F | 551  |
| 1408289 | 188559 | 188574 | N/A  | N/A  | GGTAUTATTGATAGGC          | 40  | F | 2638 |
| 1408291 | 225076 | 225091 | N/A  | N/A  | TGTGUATTATTGACCT          | 7   | F | 2639 |
| 1408401 | 217656 | 217671 | 622  | 637  | ACGA <u>C</u> TGGCAGTGTCC | 35  | F | 358  |
| 1408404 | 222147 | 222162 | 1557 | 1572 | CCAC <u>C</u> TTCTTTAATGC | 19  | F | 347  |
| 1408416 | 189848 | 189863 | N/A  | N/A  | AAGG <u>C</u> AAATCTCTTTC | 91  | F | 2640 |
| 1408420 | 189768 | 189783 | N/A  | N/A  | TTGCUTTAAGTTGTCA          | 32  | F | 2641 |
| 1408423 | 225213 | 225228 | N/A  | N/A  | TTGGGCCCTCAGTGCT          | 79  | F | 2642 |
| 1408427 | 225163 | 225178 | N/A  | N/A  | CTTC <u>C</u> TTGCCTCGGCA | 91  | F | 2643 |
| 1408430 | 225053 | 225068 | N/A  | N/A  | TTTC <u>C</u> TTCAAATTGAA | 84  | F | 2644 |
| 1408434 | 224943 | 224958 | N/A  | N/A  | CACAUGGCATGAGAGA          | 38  | F | 2645 |
| 1408438 | 226022 | 226037 | N/A  | N/A  | CTTT <u>C</u> TTAAAAGAGC  | 107 | F | 2646 |
| 1408442 | 225952 | 225967 | N/A  | N/A  | ACCG <u>C</u> CACTGAAATAA | 37  | F | 2647 |
| 1408447 | 225832 | 225847 | N/A  | N/A  | CTTGUTCTAGATCTAC          | 26  | F | 2648 |
| 1408451 | 225772 | 225787 | N/A  | N/A  | GAGCACGGGCTCTGGA          | 108 | F | 2649 |
| 1408456 | 235412 | 235427 | N/A  | N/A  | ATTTGGTTTAATAGCA          | 12  | F | 2650 |
| 1408459 | 235352 | 235367 | N/A  | N/A  | AGCA <u>C</u> ACACAGCCTGG | 34  | F | 2651 |
| 1408461 | 235272 | 235287 | N/A  | N/A  | AGCT <u>C</u> TGTTAAATTCA | 14  | F | 2652 |
| 1408463 | 235252 | 235267 | N/A  | N/A  | TGACUGAAATAGACAA          | 48  | F | 2653 |
|         | 235325 | 235340 |      |      |                           |     |   |      |
| 1408473 | 235099 | 235114 | N/A  | N/A  | CCTGUTGGTTGTCCAA          | 15  | F | 2654 |
| 1408477 | 243434 | 243449 | N/A  | N/A  | GGCAGAGAGGGTCACG          | 30  | F | 2655 |
| 1408481 | 243344 | 243359 | N/A  | N/A  | CTTGUGGTAACCTGGA          | 58  | F | 2656 |
| 1408485 | 243294 | 243309 | N/A  | N/A  | GCCTGGATAGAAGTTG          | 53  | F | 2657 |
| 1408490 | 243224 | 243239 | N/A  | N/A  | CACTUGCCACATCTCT          | 18  | F | 2658 |
| 1408493 | 249544 | 249559 | N/A  | N/A  | ATGAGCTTTCATTTGT          | 60  | F | 2659 |
| 1408497 | 249464 | 249479 | N/A  | N/A  | TTCCAGGTTGGTCTAA          | 18  | F | 2660 |
| 1408500 | 249344 | 249359 | N/A  | N/A  | GGTTUCCCATAAACACG         | 96  | F | 2661 |
| 1408505 | 249294 | 249309 | N/A  | N/A  | GCAGUCTGACTTTAGA          | 37  | F | 2662 |
| 1408516 | 262960 | 262975 | N/A  | N/A  | ATGT <u>C</u> ACAGTTAAGAG | 71  | F | 2663 |
| 1408518 | 263149 | 263164 | N/A  | N/A  | TGTACTGTAAAGTCCTG         | 24  | F | 2664 |
| 1408520 | 263059 | 263074 | N/A  | N/A  | TCACACCAAAGTGATA          | 83  | F | 2665 |
| 1408524 | 262919 | 262934 | N/A  | N/A  | TCTCUCACTGATATCA          | 71  | F | 2666 |
| 1408530 | 271249 | 271264 | N/A  | N/A  | TCAGUTGGGAAGAAAA          | 88  | F | 2667 |
| 1408535 | 271199 | 271214 | N/A  | N/A  | GGCCUTTACATTTATA          | 76  | F | 2668 |
| 1408538 | 271119 | 271134 | N/A  | N/A  | CCTTGGA CTGATAAAT         | 109 | F | 2669 |
| 1408542 | 271029 | 271044 | N/A  | N/A  | CTGC <u>C</u> TGTTACATCAG | 73  | F | 2670 |

|         |        |        |      |      |                   |     |   |      |
|---------|--------|--------|------|------|-------------------|-----|---|------|
| 1408741 | 217801 | 217816 | 767  | 782  | CCTGAGTGTCTCCAGT  | 36  | F | 2671 |
| 1408746 | 217761 | 217776 | 727  | 742  | GATGCTCAAATAAAAA  | 64  | F | 2672 |
| 1408751 | 217671 | 217686 | 637  | 652  | GACTCTCTGTGTTT    | 10  | F | 2673 |
| 1408755 | 217601 | 217616 | 567  | 582  | GCATCTTGGTCCAGTA  | 32  | F | 2674 |
| 1408760 | 217541 | 217556 | 507  | 522  | GCTTUCAGAGCTGAAA  | 58  | F | 2675 |
| 1408769 | 218073 | 218088 | 1039 | 1054 | CTGGGTCTCTCTCTTG  | 50  | F | 2676 |
| 1408771 | 218053 | 218068 | 1019 | 1034 | CTCCUGTCCACAGTAT  | 60  | F | 2677 |
| 1408782 | 217903 | 217918 | 869  | 884  | GGCAGGTCAGTCTGA   | 84  | F | 2678 |
| 1408786 | 217853 | 217868 | 819  | 834  | TGCAACACAGACAGCCC | 57  | F | 2679 |
| 1408790 | 218132 | 218147 | 1098 | 1113 | GACTCTTTGCTGTCAG  | 37  | F | 2680 |
| 1408793 | 218112 | 218127 | 1078 | 1093 | GGCTGTTCTTTGCAGT  | 77  | F | 2681 |
| 1408799 | 218022 | 218037 | 988  | 1003 | TTCCACATGTTTGACC  | 37  | F | 2682 |
| 1408801 | 217992 | 218007 | 958  | 973  | CATGGAGCTGCTTCGA  | 35  | F | 2683 |
| 1408803 | 217962 | 217977 | 928  | 943  | GTGCUCTCTCCCAAGA  | 71  | F | 2684 |
| 1408807 | 222252 | 222267 | 1662 | 1677 | AGCCATTGGTGACGC   | 39  | F | 2685 |
| 1408811 | 222192 | 222207 | 1602 | 1617 | AGGAUATCCTGATGTC  | 69  | F | 2686 |
| 1408815 | 222132 | 222147 | 1542 | 1557 | CGCTGTTGTATCATTG  | 17  | F | 2687 |
| 1408819 | 222022 | 222037 | 1432 | 1447 | AATGGTTTCAAACCTGG | 10  | F | 2688 |
| 1408822 | 288829 | 288844 | N/A  | N/A  | GTTAUCACTAGGTAAC  | 89  | F | 2689 |
| 1408830 | 288700 | 288715 | 2095 | 2110 | ATCTGGGTTACAATAA  | 46  | F | 2690 |
| 1408831 | 288640 | 288655 | 2035 | 2050 | AGTTUCTCCACAAGA   | 52  | F | 2691 |
| 1408833 | 288560 | 288575 | N/A  | N/A  | GCTAUCACACTCTTTC  | 66  | F | 2692 |
| 1408839 | 290607 | 290622 | N/A  | N/A  | GCATGAATTCGCTTTT  | 100 | F | 2693 |
| 1408843 | 290809 | 290824 | N/A  | N/A  | GCCAUGGGAACCATGT  | 95  | F | 2694 |
| 1408846 | 290689 | 290704 | 2168 | 2183 | GGCCATGTAGATCGGT  | 64  | F | 2695 |
| 1408847 | 290669 | 290684 | 2148 | 2163 | AGAAGCATTATTGCAC  | 72  | F | 2696 |
| 1408852 | 290579 | 290594 | N/A  | N/A  | CCACCTTATTATCACT  | 75  | F | 2697 |
| 1408856 | 82340  | 82355  | N/A  | N/A  | TGAGGTTTGCCTAGGT  | 33  | F | 2698 |
| 1408860 | 82290  | 82305  | N/A  | N/A  | TCAGCACGAGGTAAGC  | 19  | F | 2699 |
| 1408864 | 82190  | 82205  | N/A  | N/A  | CATGGAAAGCAATGGT  | 40  | F | 2700 |
| 1408869 | 181382 | 181397 | N/A  | N/A  | TGTCUCCTTATGAAAG  | 124 | F | 2701 |
| 1408874 | 181332 | 181347 | N/A  | N/A  | ACAAGTCATCTGTTCA  | 27  | F | 2702 |
| 1408877 | 181232 | 181247 | N/A  | N/A  | AGTTATTATCTCCTT   | 46  | F | 2703 |
| 1408880 | 188698 | 188713 | N/A  | N/A  | GCAGGTCAAAACCTGT  | 83  | F | 2704 |
| 1408884 | 188638 | 188653 | N/A  | N/A  | TAGAGCTGGGTCATGT  | 68  | F | 2705 |
| 1408890 | 188428 | 188443 | N/A  | N/A  | GGTTUTCTGTAGCCTA  | 81  | F | 2706 |
| 1408892 | 189938 | 189953 | N/A  | N/A  | TTCTUCTCAATGATT   | 107 | F | 2707 |
| 1408896 | 189898 | 189913 | N/A  | N/A  | CTACUGCTTCTTGGCT  | 88  | F | 2708 |
| 1411023 | 94389  | 94404  | N/A  | N/A  | TCAGGCTGCTATTAAA  | 66  | F | 388  |
| 1408267 | 217663 | 217678 | 629  | 644  | GTGTUTTACGACTGGC  | 9   | G | 2709 |
| 1408270 | 217985 | 218000 | 951  | 966  | CTGCUTCATCACATC   | 22  | G | 2710 |
| 1408274 | 217981 | 217996 | 947  | 962  | TTCGATCACATCCCCC  | 29  | G | 1936 |
| 1408287 | 290681 | 290696 | 2160 | 2175 | AGATCGGTATTAAGAA  | 63  | G | 182  |

|         |        |        |      |      |                           |     |   |      |
|---------|--------|--------|------|------|---------------------------|-----|---|------|
| 1408288 | 188561 | 188576 | N/A  | N/A  | AGGGUATTATTGATAG          | 65  | G | 2711 |
| 1408403 | 218077 | 218092 | 1043 | 1058 | GATG <u>C</u> TGGGTCTCTCT | 26  | G | 381  |
| 1408406 | 222137 | 222152 | 1547 | 1562 | TAATGCGCTGTTGTAT          | 16  | G | 348  |
| 1408407 | 288674 | 288689 | 2069 | 2084 | TGGAGAAGTGTATTAA          | 4   | G | 350  |
| 1408409 | 82195  | 82210  | N/A  | N/A  | TAGCUCATGGAAAGCA          | 67  | G | 2712 |
| 1408412 | 225078 | 225093 | N/A  | N/A  | CGTGUGTATTATTGAC          | 12  | G | 2713 |
| 1408413 | 225068 | 225083 | N/A  | N/A  | ATTGACCTGGTAAATT          | 85  | G | 364  |
| 1408419 | 189778 | 189793 | N/A  | N/A  | CACCUTCCTTTTGCTT          | 78  | G | 2714 |
| 1408426 | 225173 | 225188 | N/A  | N/A  | TCAAUGTCCACTTCCT          | 31  | G | 2715 |
| 1408433 | 224963 | 224978 | N/A  | N/A  | CAGA <u>C</u> TTCCGGCTTTA | 46  | G | 2716 |
| 1408437 | 226032 | 226047 | N/A  | N/A  | CCTCUTGCACCTTTCT          | 6   | G | 2717 |
| 1408441 | 225962 | 225977 | N/A  | N/A  | ACTGUCCAATACCGCC          | 8   | G | 2718 |
| 1408445 | 225842 | 225857 | N/A  | N/A  | GATAUCTGGTCTTGTT          | 53  | G | 2719 |
| 1408450 | 225782 | 225797 | N/A  | N/A  | AGCT <u>C</u> AGTAAGAGCAC | 97  | G | 2720 |
| 1408454 | 225742 | 225757 | N/A  | N/A  | GTTTCGAGGGCTGAGTA         | 25  | G | 2721 |
| 1408455 | 235422 | 235437 | N/A  | N/A  | TTTG <u>C</u> CACTGATTGG  | 43  | G | 2722 |
| 1408465 | 235359 | 235374 | N/A  | N/A  | TTCCUACAGCACACAC          | 22  | G | 2723 |
| 1408467 | 235339 | 235354 | N/A  | N/A  | TGGT <u>C</u> CTAAAGAAATG | 66  | G | 2724 |
| 1408469 | 235259 | 235274 | N/A  | N/A  | TCACACTTGACTGAAA          | 33  | G | 2725 |
| 1408471 | 235189 | 235204 | N/A  | N/A  | AATT <u>C</u> ACACTTAATCT | 74  | G | 2726 |
| 1408475 | 243444 | 243459 | N/A  | N/A  | TTGTATTCTTGGCAGA          | 56  | G | 2727 |
| 1408480 | 243384 | 243399 | N/A  | N/A  | TCAGUACACTGACCAA          | 27  | G | 2728 |
| 1408484 | 243304 | 243319 | N/A  | N/A  | GACGGCCTCTGCCTGG          | 87  | G | 2729 |
| 1408489 | 243234 | 243249 | N/A  | N/A  | CCTTUGCCCTCACTTG          | 77  | G | 2730 |
| 1408496 | 249474 | 249489 | N/A  | N/A  | ACTT <u>C</u> CGATATTCCAG | 22  | G | 2731 |
| 1408499 | 249354 | 249369 | N/A  | N/A  | ACAGGTGCTAGGTTTC          | 12  | G | 2732 |
| 1408504 | 249304 | 249319 | N/A  | N/A  | GTGTATCCAGGCAGTC          | 45  | G | 2733 |
| 1408510 | 263150 | 263165 | N/A  | N/A  | ATGTACTGTAAGTCCT          | 11  | G | 2734 |
| 1408512 | 263060 | 263075 | N/A  | N/A  | CTCA <u>C</u> ACCAAAGTGAT | 88  | G | 2735 |
| 1408517 | 262920 | 262935 | N/A  | N/A  | TTCT <u>C</u> TCACTGATATC | 42  | G | 2736 |
| 1408521 | 262989 | 263004 | N/A  | N/A  | GGTT <u>C</u> TGACATTGTTT | 8   | G | 2737 |
| 1408527 | 262879 | 262894 | N/A  | N/A  | CCTG <u>C</u> CGGGCACCATA | 80  | G | 2738 |
| 1408529 | 271309 | 271324 | N/A  | N/A  | CTCCATACCCCCCCA           | 92  | G | 2739 |
| 1408534 | 271209 | 271224 | N/A  | N/A  | AATGUGACAAGGCCTT          | 53  | G | 2740 |
| 1408537 | 271159 | 271174 | N/A  | N/A  | CCTC <u>C</u> TAACAGATTGT | 87  | G | 2741 |
| 1408541 | 271039 | 271054 | N/A  | N/A  | CAGGGCATGTCTGCCT          | 103 | G | 2742 |
| 1408740 | 217811 | 217826 | 777  | 792  | GAAAUCTCTGCCTGAG          | 47  | G | 2743 |
| 1408745 | 217771 | 217786 | 737  | 752  | GATCUTTCTGGATGCT          | 23  | G | 2744 |
| 1408749 | 217701 | 217716 | 667  | 682  | ATTTUTTTGGCCAGCA          | 22  | G | 2745 |
| 1408754 | 217631 | 217646 | 597  | 612  | TCCA <u>C</u> CTGCTGAACTG | 12  | G | 2746 |
| 1408759 | 217551 | 217566 | 517  | 532  | GGCTUCTGTGGCTTTC          | 11  | G | 2747 |
| 1408763 | 218133 | 218148 | 1099 | 1114 | AGACUCTTTGCTGTCA          | 38  | G | 2748 |
| 1408765 | 218113 | 218128 | 1079 | 1094 | AGGCUGTTCTTTGCAG          | 60  | G | 2749 |

|         |        |        |      |      |                            |    |   |      |
|---------|--------|--------|------|------|----------------------------|----|---|------|
| 1408768 | 218093 | 218108 | 1059 | 1074 | GTCT <u>C</u> AAAATCTATAG  | 40 | G | 2750 |
| 1408772 | 218023 | 218038 | 989  | 1004 | ATTCC <u>C</u> ACATGTTTGAC | 22 | G | 2751 |
| 1408775 | 217993 | 218008 | 959  | 974  | CCATGGAGCTGCTTCG           | 49 | G | 2752 |
| 1408777 | 217963 | 217978 | 929  | 944  | GGTG <u>C</u> TCTCTCCCAAG  | 64 | G | 2753 |
| 1408779 | 217913 | 217928 | 879  | 894  | CCTG <u>C</u> AGAGTGGCAGG  | 72 | G | 2754 |
| 1408785 | 217863 | 217878 | 829  | 844  | AGATGGCTCCTGCACA           | 52 | G | 2755 |
| 1408796 | 218062 | 218077 | 1028 | 1043 | TCTTGTCTCCTCCTGT           | 16 | G | 2756 |
| 1408806 | 222262 | 222277 | 1672 | 1687 | GGCAUCATTGAGCCCA           | 57 | G | 2757 |
| 1408810 | 222202 | 222217 | 1612 | 1627 | AGACACACTCAGGATA           | 40 | G | 2758 |
| 1408814 | 222152 | 222167 | 1562 | 1577 | ACTGACCACCTTCTTT           | 10 | G | 2759 |
| 1408818 | 222052 | 222067 | 1462 | 1477 | TGCA <u>C</u> TGTAGTATAAAA | 23 | G | 2760 |
| 1408824 | 288719 | 288734 | N/A  | N/A  | TACCUTGTGAAGCAAT           | 88 | G | 2761 |
| 1408827 | 288579 | 288594 | N/A  | N/A  | CAGTGAAATTTTCGAA           | 98 | G | 2762 |
| 1408836 | 290817 | 290832 | N/A  | N/A  | ATTACCTGCCATGGG            | 65 | G | 2763 |
| 1408838 | 290647 | 290662 | 2126 | 2141 | GGCAATGGACTCCATC           | 16 | G | 2764 |
| 1408840 | 290587 | 290602 | N/A  | N/A  | GTTGGACTCCACCTTA           | 74 | G | 2765 |
| 1408845 | 290729 | 290744 | N/A  | N/A  | ACATGTTTTGGATCTA           | 59 | G | 2766 |
| 1408854 | 290529 | 290544 | N/A  | N/A  | TGTG <u>C</u> TAGGTACAATT  | 89 | G | 2767 |
| 1408855 | 82350  | 82365  | N/A  | N/A  | ACGAUCCAAGTGAGGT           | 19 | G | 2768 |
| 1408859 | 82300  | 82315  | N/A  | N/A  | TACA <u>C</u> TGAGCTCAGCA  | 8  | G | 2769 |
| 1408868 | 181402 | 181417 | N/A  | N/A  | CCTGATCATCTCAAAC           | 96 | G | 2770 |
| 1408873 | 181342 | 181357 | N/A  | N/A  | TCAG <u>C</u> ATGAAACAAGT  | 38 | G | 2771 |
| 1408876 | 181242 | 181257 | N/A  | N/A  | CTTG <u>C</u> TTGTAAGTTCA  | 9  | G | 2772 |
| 1408879 | 188708 | 188723 | N/A  | N/A  | GTGGACCTGTGCAGGT           | 68 | G | 2773 |
| 1408883 | 188648 | 188663 | N/A  | N/A  | GTAGGCAGCATAGAGC           | 64 | G | 2774 |
| 1408889 | 188438 | 188453 | N/A  | N/A  | GCAGUTTGGTGGTTTT           | 45 | G | 2775 |
| 1408891 | 189958 | 189973 | N/A  | N/A  | ACCTGCCAGGCAGATA           | 74 | G | 2776 |
| 1408895 | 189908 | 189923 | N/A  | N/A  | GGGAACCTGTCTACTG           | 78 | G | 2777 |
| 1408899 | 189858 | 189873 | N/A  | N/A  | GACAUTTTTTTAAGGCA          | 43 | G | 2778 |
| 1411022 | 94390  | 94405  | N/A  | N/A  | CTCAGGCTGCTATTAA           | 52 | G | 395  |
| 1408266 | 217664 | 217679 | 630  | 645  | TGTGUTTTACGACTGG           | 7  | H | 2779 |
| 1408269 | 217986 | 218001 | 952  | 967  | GCTG <u>C</u> TTTCGATCACAT | 40 | H | 2093 |
| 1408273 | 217982 | 217997 | 948  | 963  | CTTCGATCACATCCCC           | 20 | H | 256  |
| 1408279 | 218079 | 218094 | 1045 | 1060 | AGGAUGCTGGGTCTCT           | 20 | H | 2780 |
| 1408281 | 222144 | 222159 | 1554 | 1569 | CCTT <u>C</u> TTTAATGCGCT  | 26 | H | 2245 |
| 1408284 | 288676 | 288691 | 2071 | 2086 | ATTGGAGAAGTGATT            | 13 | H | 783  |
| 1408285 | 290682 | 290697 | 2161 | 2176 | TAGAUCGGTATTAAGA           | 75 | H | 2781 |
| 1408295 | 225070 | 225085 | N/A  | N/A  | TTATUGACCTGGTAAA           | 90 | H | 2782 |
| 1408418 | 189798 | 189813 | N/A  | N/A  | TTCT <u>C</u> CAAGTTTAGAT  | 89 | H | 2783 |
| 1408422 | 189688 | 189703 | N/A  | N/A  | CCTG <u>C</u> ATCCACATAAC  | 68 | H | 2784 |
| 1408425 | 225193 | 225208 | N/A  | N/A  | TGAAGGACAGGCTTAA           | 58 | H | 2785 |
| 1408429 | 225113 | 225128 | N/A  | N/A  | GCCAGCTCACTGATTG           | 79 | H | 2786 |
| 1408432 | 224973 | 224988 | N/A  | N/A  | CAGA <u>C</u> CATCTCAGACT  | 72 | H | 2787 |

|         |        |        |      |      |                            |    |   |      |
|---------|--------|--------|------|------|----------------------------|----|---|------|
| 1408436 | 226042 | 226057 | N/A  | N/A  | GCCTUCCCAACCTCTT           | 43 | H | 2788 |
| 1408440 | 225992 | 226007 | N/A  | N/A  | CAGTGTCATCCTGTGC           | 51 | H | 2789 |
| 1408444 | 225852 | 225867 | N/A  | N/A  | TTTTGTTGAAGATATC           | 18 | H | 2790 |
| 1408449 | 225792 | 225807 | N/A  | N/A  | AGTT <u>C</u> AGCATAGCTCA  | 6  | H | 2791 |
| 1408453 | 225752 | 225767 | N/A  | N/A  | GACTGCCTGTGTTCTGA          | 28 | H | 2792 |
| 1408458 | 235362 | 235377 | N/A  | N/A  | AATTUCCTACAGCACA           | 36 | H | 2793 |
| 1408460 | 235342 | 235357 | N/A  | N/A  | GCCTGGTCCTAAAGAA           | 88 | H | 2794 |
| 1408462 | 235262 | 235277 | N/A  | N/A  | AATT <u>C</u> ACACTTGA CTG | 38 | H | 2795 |
| 1408470 | 235199 | 235214 | N/A  | N/A  | AGCT <u>C</u> TATTAAATTCA  | 36 | H | 2796 |
| 1408479 | 243414 | 243429 | N/A  | N/A  | GCTGACAAATGATCAA           | 78 | H | 2797 |
| 1408483 | 243324 | 243339 | N/A  | N/A  | GTGCU GTGCAGAAATT          | 26 | H | 2798 |
| 1408487 | 243244 | 243259 | N/A  | N/A  | GTCT <u>C</u> AACTCCCTTTG  | 74 | H | 2799 |
| 1408492 | 243164 | 243179 | N/A  | N/A  | GTTGGTGCTGGAAAAA           | 20 | H | 2800 |
| 1408495 | 249524 | 249539 | N/A  | N/A  | ACTGUCATTCAAAGCA           | 62 | H | 2801 |
| 1408498 | 249384 | 249399 | N/A  | N/A  | TGT <u>C</u> CACCTGGCAGAT  | 89 | H | 2802 |
| 1408503 | 249314 | 249329 | N/A  | N/A  | GAGCUGGAATGTGTAT           | 45 | H | 2803 |
| 1408507 | 249244 | 249259 | N/A  | N/A  | CTGGGAGAGGTCTGTC           | 63 | H | 2804 |
| 1408509 | 263170 | 263185 | N/A  | N/A  | GTGTACTTTCTACCTT           | 32 | H | 2805 |
| 1408515 | 262990 | 263005 | N/A  | N/A  | TGGTUCTGACATTGTT           | 15 | H | 2806 |
| 1408519 | 263139 | 263154 | N/A  | N/A  | GTCCUGGGCCTTAAGT           | 86 | H | 2807 |
| 1408523 | 262949 | 262964 | N/A  | N/A  | AAGAGCAGCAGCTTAA           | 80 | H | 2808 |
| 1408526 | 262889 | 262904 | N/A  | N/A  | ATCCACACCTCCTGCC           | 76 | H | 2809 |
| 1408533 | 271219 | 271234 | N/A  | N/A  | GGCTUTCTAAAATGTG           | 91 | H | 2810 |
| 1408536 | 271169 | 271184 | N/A  | N/A  | ACAGUCAGAACCTCCT           | 51 | H | 2811 |
| 1408540 | 271069 | 271084 | N/A  | N/A  | GCCAGGGCTCACAGGT           | 93 | H | 2812 |
| 1408743 | 217781 | 217796 | 747  | 762  | AGCG <u>C</u> GGTGAGATCTT  | 20 | H | 99   |
| 1408748 | 217731 | 217746 | 697  | 712  | TACTUCAGCTGAAAGA           | 54 | H | 2813 |
| 1408753 | 217641 | 217656 | 607  | 622  | CAGCUCTTTTCCACC            | 17 | H | 2814 |
| 1408757 | 217581 | 217596 | 547  | 562  | TGTAGCCTGTAATGTT           | 6  | H | 2815 |
| 1408762 | 217511 | 217526 | 477  | 492  | GGCTGTAAACTTTGTT           | 66 | H | 2816 |
| 1408770 | 218063 | 218078 | 1029 | 1044 | CTCTUGTCTCCTCCTG           | 16 | H | 2817 |
| 1408784 | 217883 | 217898 | 849  | 864  | CCGAGGGAGGCCAAAG           | 67 | H | 2818 |
| 1408788 | 217833 | 217848 | 799  | 814  | CCTC <u>C</u> CATTATTCATT  | 52 | H | 2819 |
| 1408789 | 218222 | 218237 | 1188 | 1203 | GCTTUCCAGGATTCAT           | 12 | H | 2820 |
| 1408791 | 218122 | 218137 | 1088 | 1103 | TGTCAGGAGAGGCTGT           | 25 | H | 2821 |
| 1408794 | 218102 | 218117 | 1068 | 1083 | TGCAGTGATGTCTCAA           | 11 | H | 2822 |
| 1408798 | 218042 | 218057 | 1008 | 1023 | AGTAUTTCCACTCCTT           | 16 | H | 2823 |
| 1408800 | 218012 | 218027 | 978  | 993  | TTGA <u>C</u> CCGGCCTGGGC  | 69 | H | 2824 |
| 1408802 | 217972 | 217987 | 938  | 953  | ATCC <u>C</u> CCTGGGTGCTC  | 48 | H | 2825 |
| 1408804 | 217942 | 217957 | 908  | 923  | ACCT <u>C</u> TGCTCTTTCAA  | 41 | H | 2826 |
| 1408805 | 222272 | 222287 | 1682 | 1697 | TGGAGTCGCTGGCATC           | 8  | H | 2827 |
| 1408809 | 222212 | 222227 | 1622 | 1637 | CACCATCTGCAGACAC           | 12 | H | 2828 |
| 1408813 | 222172 | 222187 | 1582 | 1597 | CCCTGATGTCCTCTCC           | 5  | H | 2829 |

|         |        |        |      |      |                           |     |    |      |
|---------|--------|--------|------|------|---------------------------|-----|----|------|
| 1408817 | 222062 | 222077 | 1472 | 1487 | CCAGGGACTCTGCACT          | 46  | H  | 2830 |
| 1408829 | 288720 | 288735 | N/A  | N/A  | TTAC <u>C</u> TTGTGAAGCAA | 116 | H  | 2831 |
| 1408832 | 288580 | 288595 | N/A  | N/A  | ACAGUGAAATTTTCGA          | 84  | H  | 2832 |
| 1408834 | 288550 | 288565 | N/A  | N/A  | TCTTUCATAGTTAAAA          | 89  | H  | 2833 |
| 1408841 | 290537 | 290552 | N/A  | N/A  | AACAGTACTGTGCTAG          | 99  | H  | 2834 |
| 1408842 | 290819 | 290834 | N/A  | N/A  | TTATUCACCTGCCATG          | 87  | H  | 2835 |
| 1408844 | 290759 | 290774 | N/A  | N/A  | TGTTUGAACATAAAAAG         | 95  | H  | 2836 |
| 1408849 | 290649 | 290664 | 2128 | 2143 | AAGG <u>C</u> AATGGACTCCA | 14  | H  | 2837 |
| 1408851 | 290589 | 290604 | N/A  | N/A  | CTGTUGGACTCCACCT          | 91  | H  | 2838 |
| 1408858 | 82310  | 82325  | N/A  | N/A  | TTTTGGAGTGTACACT          | 12  | H  | 2839 |
| 1408862 | 82220  | 82235  | N/A  | N/A  | ACTCUGCCTTGATACT          | 32  | H  | 2840 |
| 1408867 | 181412 | 181427 | N/A  | N/A  | CCGTUCTGATCCTGAT          | 57  | H  | 2841 |
| 1408872 | 181352 | 181367 | N/A  | N/A  | TGCAGGATCTTCAGCA          | 83  | H  | 2842 |
| 1408875 | 181252 | 181267 | N/A  | N/A  | TGAAUGTTGTCTTGCT          | 40  | H  | 2843 |
| 1408882 | 188658 | 188673 | N/A  | N/A  | TGAGUTTCTTGTAGGC          | 40  | H  | 2844 |
| 1408886 | 188618 | 188633 | N/A  | N/A  | TCAT <u>C</u> CATTAGCCAG  | 25  | H  | 2845 |
| 1408888 | 188508 | 188523 | N/A  | N/A  | TGAAGTTGTTTGATA           | 79  | H  | 2846 |
| 1408894 | 189918 | 189933 | N/A  | N/A  | AATGGTGTCTGGGAAC          | 33  | H  | 2847 |
| 1408898 | 189878 | 189893 | N/A  | N/A  | GCTG <u>C</u> TTCTCCTGTTA | 82  | H  | 2848 |
| 1411021 | 94387  | 94402  | N/A  | N/A  | AGGCUGCTATTAAAGA          | 83  | H  | 2849 |
| 1411025 | 94392  | 94407  | N/A  | N/A  | TTCT <u>C</u> AGGCTGCTATT | 74  | H  | 390  |
| 1411020 | 94382  | 94397  | N/A  | N/A  | GCTAUTAAAGACATGC          | 85  | I  | 2850 |
| 1411024 | 94386  | 94401  | N/A  | N/A  | GGCTGCTATTAAAGAC          | 87  | I  | 393  |
| 1411026 | 88243  | 88258  | N/A  | N/A  | CTCAGAGAAGGAAGGT          | 57  | I  | 2048 |
| 1411027 | 88244  | 88259  | N/A  | N/A  | GCTCAGAGAAGGAAGG          | 74  | I  | 392  |
| 1411028 | 88241  | 88256  | N/A  | N/A  | CAGAGAAGGAAGGTAT          | 69  | I  | 389  |
| 1411029 | 88242  | 88257  | N/A  | N/A  | TCAGAGAAGGAAGGTA          | 61  | I  | 382  |
| 1411030 | 88248  | 88263  | N/A  | N/A  | CCGGGCTCAGAGAAGG          | 92  | I  | 394  |
| 1411031 | 88240  | 88255  | N/A  | N/A  | AGAGAAGGAAGGTATT          | 56  | I  | 391  |
| 1411032 | 88246  | 88261  | N/A  | N/A  | GGGCUCAGAGAAGGAA          | 103 | I  | 2851 |
| 1411033 | 88238  | 88253  | N/A  | N/A  | AGAAGGAAGGTATTCA          | 88  | I  | 385  |
| 1411034 | 88245  | 88260  | N/A  | N/A  | GGCT <u>C</u> AGAGAAGGAAG | 78  | I  | 384  |
| 1441462 | 288682 | 288697 | 2077 | 2092 | ATAT <u>C</u> TATTGGAGAAG | 10  | AR | 1091 |
| 1441465 | 288679 | 288694 | 2074 | 2089 | TCTAUTGGAGAAGTGT          | 5   | AR | 2852 |
| 1441470 | 217662 | 217677 | 628  | 643  | TGTTUTACGACTGGCA          | 39  | AR | 2853 |
| 1441473 | 218084 | 218099 | 1050 | 1065 | TCTAUAGGATGCTGGG          | 35  | AR | 2854 |
| 1441476 | 218078 | 218093 | 1044 | 1059 | GGATGCTGGGTCTCTC          | 37  | AR | 2855 |
| 1441477 | 235210 | 235225 | N/A  | N/A  | ATACACAATTTAGCTC          | 5   | AR | 337  |
|         | 235283 | 235298 |      |      |                           |     |    |      |
| 1441480 | 235205 | 235220 | N/A  | N/A  | CAATUTAGCTCTATTA          | 115 | AR | 2856 |
| 1441481 | 288675 | 288690 | 2070 | 2085 | TTGGAGAAGTGTATTA          | 6   | AR | 352  |
| 1441483 | 82202  | 82217  | N/A  | N/A  | CAGAUATTAGCTCATG          | 22  | AR | 2857 |
| 1441484 | 226035 | 226050 | N/A  | N/A  | CAAC <u>C</u> TCTTGACCTT  | 13  | AR | 2858 |

|         |        |        |      |      |                                   |    |    |      |
|---------|--------|--------|------|------|-----------------------------------|----|----|------|
| 1441489 | 217742 | 217757 | 708  | 723  | TCCT <u>C</u> CGTTGTTACTT         | 12 | AR | 2859 |
| 1441492 | 217738 | 217753 | 704  | 719  | CCGTUGTTACTTCAGC                  | 11 | AR | 2860 |
| 1441494 | 218105 | 218120 | 1071 | 1086 | CTTTGCAGTGATGTCT                  | 23 | AR | 2861 |
| 1441499 | 218221 | 218236 | 1187 | 1202 | CTTT <u>C</u> CAGGATTCATC         | 66 | AR | 2862 |
| 1441504 | 222154 | 222169 | 1564 | 1579 | GAACUGACCACCTTCT                  | 43 | AR | 2863 |
| 1441508 | 244766 | 244781 | N/A  | N/A  | AGGTAATTTATGAGTT                  | 8  | AR | 488  |
| 1441512 | 342926 | 342941 | N/A  | N/A  | GATAATGTGAAGCTTA                  | 4  | AR | 417  |
| 1441515 | 366242 | 366257 | N/A  | N/A  | CTAT <u>C</u> ATATGAAAGCC         | 5  | AR | 2476 |
| 1441518 | 181931 | 181946 | N/A  | N/A  | TGCAGAATTGATAACA                  | 36 | AR | 2864 |
| 1441522 | 365700 | 365715 | N/A  | N/A  | CAGTAATATTAAAGCC                  | 10 | AR | 2480 |
| 1441526 | 508289 | 508304 | N/A  | N/A  | GATTUTAAGAGTCCAC                  | 55 | AR | 2865 |
| 1441531 | 222038 | 222053 | 1448 | 1463 | AAGAAGTGTGTCCAA                   | 2  | AR | 2866 |
| 1441536 | 155902 | 155917 | N/A  | N/A  | AGTTATTATATGGCTG                  | 18 | AR | 414  |
| 1441538 | 251926 | 251941 | N/A  | N/A  | GGTTUTAAGTTATCTC                  | 33 | AR | 2867 |
| 1441541 | 229862 | 229877 | N/A  | N/A  | ATATUGTGTGTCTCAG                  | 7  | AR | 2868 |
| 1441542 | 285149 | 285164 | 1784 | 1799 | AAATUTCAGTGCTCCC                  | 10 | AR | 2869 |
| 1441545 | 285468 | 285483 | 2002 | 2017 | ATAC <u>C</u> TGAGTGACTGA         | 3  | AR | 2488 |
| 1441546 | 222162 | 222177 | 1572 | 1587 | CTCT <u>C</u> CAAGAACTGAC         | 39 | AR | 554  |
| 1441549 | 222158 | 222173 | 1568 | 1583 | CCAAGAACTGACCACC                  | 6  | AR | 2870 |
| 1441769 | 263008 | 263023 | N/A  | N/A  | GTGAUATGAATGGTAT                  | 2  | AR | 2871 |
|         | 263049 | 263064 |      |      |                                   |    |    |      |
| 1441774 | 217659 | 217674 | 625  | 640  | TTTAC <u>G</u> ACTGGCAGTG         | 26 | AR | 552  |
| 1441775 | 225077 | 225092 | N/A  | N/A  | GTGTGTATTATTGACC                  | 15 | AR | 2872 |
| 1441778 | 225072 | 225087 | N/A  | N/A  | TATTATTGACCTGGTA                  | 29 | AR | 476  |
| 1441780 | 222234 | 222249 | 1644 | 1659 | CTAGAATAGCCCATCA                  | 12 | AR | 848  |
| 1441783 | 222231 | 222246 | 1641 | 1656 | GAATAGCCCATCACGA                  | 48 | AR | 2520 |
| 1441786 | 218175 | 218190 | 1141 | 1156 | ACACAAACCAGCTGAT                  | 19 | AR | 2522 |
| 1441789 | 218172 | 218187 | 1138 | 1153 | CAA <u>A</u> <u>C</u> CAGCTGATGAG | 37 | AR | 1097 |
| 1441792 | 218169 | 218184 | 1135 | 1150 | ACCAGCTGATGAGATG                  | 8  | AR | 2873 |
| 1441794 | 263335 | 263350 | N/A  | N/A  | GTTTGAAGAATGCATG                  | 21 | AR | 2526 |
| 1441796 | 344740 | 344755 | N/A  | N/A  | TTAGUATCCTTCAATG                  | 99 | AR | 2874 |
| 1441799 | 391182 | 391197 | N/A  | N/A  | TTAGGATTAAGGAGTT                  | 7  | AR | 2530 |
| 1441802 | 391179 | 391194 | N/A  | N/A  | GGATUAAGGAGTTCTG                  | 67 | AR | 2875 |
| 1441804 | 229906 | 229921 | N/A  | N/A  | GAACATTTAGAGGCAT                  | 3  | AR | 915  |
| 1441807 | 229902 | 229917 | N/A  | N/A  | ATTTAGAGGCATTGCA                  | 62 | AR | 2498 |
| 1441809 | 222043 | 222058 | 1453 | 1468 | GTATAAAGAAGTGTTG                  | 14 | AR | 777  |
| 1441811 | 97753  | 97768  | N/A  | N/A  | TCTCATTAAATCAAGG                  | 39 | AR | 2500 |
| 1441815 | 350508 | 350523 | N/A  | N/A  | TTATUATAGGGTTGAA                  | 43 | AR | 2876 |
| 1441819 | 290652 | 290667 | 2131 | 2146 | GGTAAGGCAATGGACT                  | 17 | AR | 2505 |
| 1441823 | 82465  | 82480  | N/A  | N/A  | TGA <u>A</u> <u>C</u> AATGCTGATTC | 57 | AR | 2506 |
| 1441826 | 82461  | 82476  | N/A  | N/A  | CAATGCTGATTCAGGC                  | 40 | AR | 2877 |
| 1441829 | 368429 | 368444 | N/A  | N/A  | GTGAUATTGTATAAGG                  | 7  | AR | 2878 |
| 1441832 | 368425 | 368440 | N/A  | N/A  | TATTGTATAAGGTTAG                  | 13 | AR | 2510 |

|         |        |        |       |       |                           |    |    |      |
|---------|--------|--------|-------|-------|---------------------------|----|----|------|
| 1441834 | 242392 | 242407 | N/A   | N/A   | ACCGUCAAGTAATGAG          | 45 | AR | 2879 |
| 1441837 | 242389 | 242404 | N/A   | N/A   | GTCAAGTAATGAGTTT          | 3  | AR | 758  |
| 1441840 | 285252 | 285267 | 1887  | 1902  | CTTTUGAATCTGTCCA          | 5  | AR | 2880 |
| 1441843 | 285187 | 285202 | 1822  | 1837  | GGTAC <u>C</u> ATTACTGAGA | 56 | AR | 2881 |
| 1441846 | 217792 | 217807 | 758   | 773   | CTCCAGTTAACAGCGC          | 31 | AR | 2516 |
| 1441849 | 217788 | 217803 | 754   | 769   | AGTTAACAGCGCGGTG          | 22 | AR | 2517 |
| 1441942 | 82198  | 82213  | N/A   | N/A   | TATTAGCTCATGGAAA          | 51 | AR | 2091 |
| 1441945 | 229161 | 229176 | N/A   | N/A   | AAGTATTAACCACCAT          | 6  | AR | 1913 |
| 1441949 | 463907 | 463922 | N/A   | N/A   | AGATUTAATAGGTCTT          | 88 | AR | 2882 |
| 1441951 | 331865 | 331880 | N/A   | N/A   | ACTAUAGTATGATAGC          | 59 | AR | 2883 |
| 1441954 | 331862 | 331877 | N/A   | N/A   | ATAGUATGATAGCACA          | 2  | AR | 2884 |
| 1441957 | 331859 | 331874 | N/A   | N/A   | GTATGATAGCACAAAC          | 10 | AR | 2540 |
| 1441960 | 236801 | 236816 | N/A   | N/A   | TTGTUATACTGATGGG          | 6  | AR | 2885 |
| 1441963 | 236798 | 236813 | N/A   | N/A   | TTATACTGATGGGCTA          | 10 | AR | 2545 |
| 1441966 | 217510 | 217525 | 476   | 491   | GCTGUAAACTTTGTTC          | 72 | AR | 2886 |
| 1441968 | 217564 | 217579 | 530   | 545   | CGGAAATGATTCTGGC          | 21 | AR | 2161 |
| 1441972 | 561179 | 561194 | 10168 | 10183 | GAATUGAAGTTAGGGT          | 39 | AR | 2887 |
| 1441973 | 222019 | 222034 | 1429  | 1444  | GGTTUCAAACTGGGAG          | 35 | AR | 2888 |
| 1441976 | 222013 | 222028 | 1423  | 1438  | AAACUGGGAGCTGTAC          | 45 | AR | 2889 |
| 1442030 | 217668 | 217683 | 634   | 649   | TCTCUGTGTTTACGA           | 9  | AR | 2890 |
| 1442035 | 217746 | 217761 | 712   | 727   | ACTTUCCTCCGTTGTT          | 32 | AR | 2891 |
| 1442038 | 218098 | 218113 | 1064  | 1079  | GTGAUGTCTCAAAATC          | 16 | AR | 2892 |
| 1442040 | 222177 | 222192 | 1587  | 1602  | CCTC <u>C</u> CCCTGATGTCC | 26 | AR | 2893 |
| 1442042 | 508284 | 508299 | N/A   | N/A   | TAAGAGTCCACTAGCC          | 79 | AR | 2550 |
| 1442043 | 181922 | 181937 | N/A   | N/A   | GATAACAGGTAAATTA          | 90 | AR | 2894 |
| 1441461 | 288683 | 288698 | 2078  | 2093  | AATAUCTATTGGAGAA          | 7  | AS | 2895 |
| 1441464 | 288680 | 288695 | 2075  | 2090  | ATCTATTGGAGAAGTG          | 3  | AS | 260  |
| 1441467 | 288677 | 288692 | 2072  | 2087  | TATTGGAGAAGTGTAT          | 33 | AS | 859  |
| 1441469 | 217665 | 217680 | 631   | 646   | CTGTGTTTTACGACTG          | 12 | AS | 2896 |
| 1441472 | 217660 | 217675 | 626   | 641   | TTTTACGACTGGCAGT          | 14 | AS | 629  |
| 1441475 | 218082 | 218097 | 1048  | 1063  | TATAGGATGCTGGGTC          | 31 | AS | 100  |
| 1441479 | 235208 | 235223 | N/A   | N/A   | ACACAATTTAGCTCTA          | 2  | AS | 341  |
| 1441482 | 82207  | 82222  | N/A   | N/A   | ACTTUCAGATATTAGC          | 33 | AS | 2897 |
| 1441486 | 226033 | 226048 | N/A   | N/A   | ACCTC <u>T</u> TGCACCTTTC | 7  | AS | 2898 |
| 1441488 | 217743 | 217758 | 709   | 724   | TTCCUCCGTTGTTACT          | 19 | AS | 2899 |
| 1441491 | 217739 | 217754 | 705   | 720   | TCCGUTGTTACTTCAG          | 5  | AS | 2900 |
| 1441493 | 218106 | 218121 | 1072  | 1087  | TCTTUGCAGTGATGTC          | 10 | AS | 2901 |
| 1441496 | 218101 | 218116 | 1067  | 1082  | GCAGUGATGTCTCAAA          | 27 | AS | 2902 |
| 1441498 | 218224 | 218239 | 1190  | 1205  | GAGCUTTCCAGGATTC          | 23 | AS | 2903 |
| 1441502 | 222169 | 222184 | 1579  | 1594  | TGATGTCCTCTCCAAG          | 39 | AS | 2904 |
| 1441503 | 222155 | 222170 | 1565  | 1580  | AGAA <u>C</u> TGACCACCTTC | 8  | AS | 2905 |
| 1441507 | 244768 | 244783 | N/A   | N/A   | ATAGGTAATTTATGAG          | 81 | AS | 2492 |
| 1441511 | 342928 | 342943 | N/A   | N/A   | GAGAUAAATGTGAAGCT         | 3  | AS | 2906 |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1441514 | 366243 | 366258 | N/A  | N/A  | ACTAUCATATGAAAGC  | 32 | AS | 2907 |
| 1441517 | 181932 | 181947 | N/A  | N/A  | ATGCAGAATTGATAAC  | 57 | AS | 2478 |
| 1441520 | 181927 | 181942 | N/A  | N/A  | GAATUGATAACAGGTA  | 10 | AS | 2908 |
| 1441521 | 365701 | 365716 | N/A  | N/A  | GCAGUAATATTAAAGC  | 89 | AS | 2909 |
| 1441525 | 508291 | 508306 | N/A  | N/A  | GTGAUTTTAAGAGTCC  | 25 | AS | 2910 |
| 1441528 | 508286 | 508301 | N/A  | N/A  | TTTAAGAGTCCACTAG  | 96 | AS | 2482 |
| 1441530 | 222039 | 222054 | 1449 | 1464 | AAAGAAGTGTTGTCCA  | 2  | AS | 526  |
| 1441533 | 222036 | 222051 | 1446 | 1461 | GAAGUGTTGTCCAAAA  | 29 | AS | 2911 |
| 1441535 | 155903 | 155918 | N/A  | N/A  | AAGTUATTATATGGCT  | 45 | AS | 2912 |
| 1441540 | 229866 | 229881 | N/A  | N/A  | CTCAATATTGTGTGTC  | 21 | AS | 609  |
| 1441544 | N/A    | N/A    | 2003 | 2018 | AATACCTGAGTGACTG  | 3  | AS | 2487 |
| 1441548 | 222159 | 222174 | 1569 | 1584 | TCCAAGAAGTACCAC   | 7  | AS | 469  |
| 1441768 | 263009 | 263024 | N/A  | N/A  | AGTGATATGAATGGTA  | 4  | AS | 153  |
|         | 263050 | 263065 |      |      |                   |    |    |      |
| 1441771 | 263006 | 263021 | N/A  | N/A  | GATAUGAATGGTATGA  | 10 | AS | 2913 |
|         | 263047 | 263062 |      |      |                   |    |    |      |
| 1441773 | 218085 | 218100 | 1051 | 1066 | ATCTATAGGATGCTGG  | 43 | AS | 781  |
| 1441777 | 225073 | 225088 | N/A  | N/A  | GTATUATTGACCTGGT  | 22 | AS | 2914 |
| 1441779 | 222235 | 222250 | 1645 | 1660 | ACTAGAATAGCCCATC  | 16 | AS | 922  |
| 1441782 | 222232 | 222247 | 1642 | 1657 | AGAAUAGCCCATCACG  | 17 | AS | 2915 |
| 1441785 | 222229 | 222244 | 1639 | 1654 | ATAGCCCATCACGATG  | 38 | AS | 2916 |
| 1441788 | 218173 | 218188 | 1139 | 1154 | ACAAACCAGCTGATGA  | 14 | AS | 2524 |
| 1441791 | 218170 | 218185 | 1136 | 1151 | AACCAGCTGATGAGAT  | 10 | AS | 2525 |
| 1441793 | 263338 | 263353 | N/A  | N/A  | GAAGUTTGAAGAATGC  | 16 | AS | 2917 |
| 1441795 | 344746 | 344761 | N/A  | N/A  | CTAAATTTAGTATCCT  | 13 | AS | 2527 |
| 1441798 | 391183 | 391198 | N/A  | N/A  | ATTAGGATTAAGGAGT  | 28 | AS | 2529 |
| 1441801 | 391180 | 391195 | N/A  | N/A  | AGGAUTAAGGAGTTCT  | 77 | AS | 2918 |
| 1441806 | 229903 | 229918 | N/A  | N/A  | CATTUAGAGGCATTGC  | 52 | AS | 2919 |
| 1441808 | 222047 | 222062 | 1457 | 1472 | TGTAGTATAAAGAAGT  | 21 | AS | 2499 |
| 1441810 | 97754  | 97769  | N/A  | N/A  | GTCTCATTAATCAAG   | 36 | AS | 2920 |
| 1441813 | 97751  | 97766  | N/A  | N/A  | TCATUAAATCAAGCA   | 27 | AS | 2921 |
| 1441814 | 350509 | 350524 | N/A  | N/A  | TTTAUTATAGGGTTGA  | 14 | AS | 2922 |
| 1441818 | 290653 | 290668 | 2132 | 2147 | AGGTAAGGCAATGGAC  | 17 | AS | 2504 |
| 1441822 | 233649 | 233664 | N/A  | N/A  | GCTCATTAAGTTCCTC  | 8  | AS | 870  |
| 1441825 | 82462  | 82477  | N/A  | N/A  | ACAAUGCTGATTCAGG  | 13 | AS | 2923 |
| 1441828 | 368430 | 368445 | N/A  | N/A  | GGTGATATTGTATAAG  | 18 | AS | 2508 |
| 1441831 | 368427 | 368442 | N/A  | N/A  | GATAUTGTATAAGGTT  | 3  | AS | 2924 |
| 1441836 | 242390 | 242405 | N/A  | N/A  | CGTCAAGTAATGAGTT  | 5  | AS | 2512 |
| 1441839 | 285253 | 285268 | 1888 | 1903 | TCTTUTGAATCTGTCC  | 5  | AS | 2925 |
| 1441842 | 285188 | 285203 | 1823 | 1838 | TGGTACCATTACTGAG  | 78 | AS | 2515 |
| 1441845 | 285185 | 285200 | 1820 | 1835 | TACCATTACTGAGATT  | 5  | AS | 616  |
| 1441848 | 217789 | 217804 | 755  | 770  | CAGTUAACAGCGCGGT  | 25 | AS | 2926 |
| 1441851 | 217786 | 217801 | 752  | 767  | TTAAACAGCGCGGTGAG | 34 | AS | 2519 |

|         |        |        |       |       |                           |    |    |      |
|---------|--------|--------|-------|-------|---------------------------|----|----|------|
| 1441941 | 82200  | 82215  | N/A   | N/A   | GATAUTAGCTCATGGA          | 62 | AS | 2927 |
| 1441943 | 218034 | 218049 | 1000  | 1015  | CACT <u>C</u> CTTGAAATTCC | 5  | AS | 2928 |
| 1441944 | 229163 | 229178 | N/A   | N/A   | TAAAGTATTAACCACC          | 3  | AS | 1964 |
| 1441948 | 463910 | 463925 | N/A   | N/A   | GTCAGATTTAATAGGT          | 23 | AS | 2929 |
| 1441953 | 331863 | 331878 | N/A   | N/A   | TATAGTATGATAGCAC          | 21 | AS | 1607 |
| 1441956 | 331860 | 331875 | N/A   | N/A   | AGTAUGATAGCACAAA          | 4  | AS | 2930 |
| 1441959 | 236802 | 236817 | N/A   | N/A   | ATTGUTATACTGATGG          | 12 | AS | 2931 |
| 1441962 | 236799 | 236814 | N/A   | N/A   | GTTAUACTGATGGGCT          | 39 | AS | 2932 |
| 1441965 | 217512 | 217527 | 478   | 493   | GGGCUGTAAACTTTGT          | 34 | AS | 2933 |
| 1441967 | 217565 | 217580 | 531   | 546   | CCGGAAATGATTCTGG          | 69 | AS | 2238 |
| 1441971 | 561180 | 561195 | 10169 | 10184 | GGAAUTGAAGTTAGGG          | 20 | AS | 2934 |
| 1441975 | 222017 | 222032 | 1427  | 1442  | TTTCAAACCTGGGAGCT         | 16 | AS | 2548 |
| 1442029 | 217669 | 217684 | 635   | 650   | CTCT <u>C</u> TGTGTTTACG  | 7  | AS | 2935 |
| 1442033 | 235212 | 235227 | N/A   | N/A   | TTATACACAATTTAGC          | 62 | AS | 334  |
|         | 235285 | 235300 |       |       |                           |    |    |      |
| 1442034 | 226037 | 226052 | N/A   | N/A   | CCCAACCTCTTGCACC          | 51 | AS | 2549 |
| 1442039 | 218217 | 218232 | 1183  | 1198  | CCAGGATTCATCCCAA          | 37 | AS | 2936 |
| 1442041 | 342921 | 342936 | N/A   | N/A   | TGTGAAGCTTAGAACC          | 10 | AS | 2937 |
| 1442044 | 244760 | 244775 | N/A   | N/A   | TTTAUGAGTTAAAGGG          | 34 | AS | 2938 |
| 1441463 | 288681 | 288696 | 2076  | 2091  | TATCUATTGGAGAAGT          | 5  | AT | 2939 |
| 1441466 | 288678 | 288693 | 2073  | 2088  | CTATUGGAGAAGTGTA          | 4  | AT | 2940 |
| 1441468 | 217667 | 217682 | 633   | 648   | CTCTGTGTTTACGAC           | 10 | AT | 2941 |
| 1441471 | 217661 | 217676 | 627   | 642   | GTTTUACGACTGGCAG          | 13 | AT | 2942 |
| 1441474 | 218083 | 218098 | 1049  | 1064  | CTATAGGATGCTGGGT          | 46 | AT | 628  |
| 1441478 | 235209 | 235224 | N/A   | N/A   | TACA <u>C</u> AATTTAGCTCT | 3  | AT | 152  |
|         | 235282 | 235297 |       |       |                           |    |    |      |
| 1441485 | 226034 | 226049 | N/A   | N/A   | AACCUCTTGCACCTTT          | 8  | AT | 2943 |
| 1441487 | 217744 | 217759 | 710   | 725   | TTTC <u>C</u> TCCGTTGTAC  | 30 | AT | 2944 |
| 1441490 | 217740 | 217755 | 706   | 721   | CTCCGTTGTTACTTCA          | 5  | AT | 2945 |
| 1441495 | 218104 | 218119 | 1070  | 1085  | TTTG <u>C</u> AGTGATGTCTC | 11 | AT | 2946 |
| 1441497 | 218225 | 218240 | 1191  | 1206  | GGAG <u>C</u> TTTCCAGGATT | 25 | AT | 2947 |
| 1441500 | 218219 | 218234 | 1185  | 1200  | TTCCAGGATTCATCCC          | 24 | AT | 2948 |
| 1441501 | 222175 | 222190 | 1585  | 1600  | TCCC <u>C</u> TGATGTCCTC  | 12 | AT | 2949 |
| 1441505 | 222149 | 222164 | 1559  | 1574  | GACCACCTTCTTTAAT          | 35 | AT | 2491 |
| 1441506 | 244769 | 244784 | N/A   | N/A   | TATAGGTAATTTATGA          | 91 | AT | 653  |
| 1441509 | 244765 | 244780 | N/A   | N/A   | GGTAATTTATGAGTTA          | 7  | AT | 455  |
| 1441510 | 342929 | 342944 | N/A   | N/A   | TGAGATAATGTGAAGC          | 6  | AT | 2493 |
| 1441513 | 342925 | 342940 | N/A   | N/A   | ATAAUGTGAAGCTTAG          | 7  | AT | 2950 |
| 1441516 | 366241 | 366256 | N/A   | N/A   | TATCATATGAAAGCCA          | 6  | AT | 2477 |
| 1441519 | 181930 | 181945 | N/A   | N/A   | GCAGAATTGATAACAG          | 13 | AT | 562  |
| 1441523 | 365698 | 365713 | N/A   | N/A   | GTAUATTTAAAGCCAG          | 2  | AT | 2951 |
| 1441524 | 508292 | 508307 | N/A   | N/A   | GGTGATTTTAAGAGTC          | 22 | AT | 2952 |
| 1441527 | 508287 | 508302 | N/A   | N/A   | TTTTAAGAGTCCACTA          | 84 | AT | 2481 |

|         |        |        |      |      |                   |     |    |      |
|---------|--------|--------|------|------|-------------------|-----|----|------|
| 1441529 | 222040 | 222055 | 1450 | 1465 | TAAAGAAGTGTGTGCC  | 9   | AT | 2483 |
| 1441532 | 222037 | 222052 | 1447 | 1462 | AGAAGTGTGTCCAAA   | 2   | AT | 2953 |
| 1441534 | 155904 | 155919 | N/A  | N/A  | GAAGUTATTATATGGC  | 10  | AT | 2954 |
| 1441537 | 155901 | 155916 | N/A  | N/A  | GTTAUTATATGGCTGT  | 3   | AT | 2955 |
| 1441539 | 229868 | 229883 | N/A  | N/A  | ATCTCAATATTGTGTG  | 25  | AT | 2956 |
| 1441543 | N/A    | N/A    | 2005 | 2020 | GAAAUACCTGAGTGAC  | 7   | AT | 2957 |
| 1441547 | 222160 | 222175 | 1570 | 1585 | CTCCAAGAACTGACCA  | 7   | AT | 546  |
| 1441550 | 222157 | 222172 | 1567 | 1582 | CAAGAACTGACCACCT  | 5   | AT | 2472 |
| 1441767 | 263010 | 263025 | N/A  | N/A  | AAGTGATATGAATGGT  | 3   | AT | 1167 |
|         | 263051 | 263066 |      |      |                   |     |    |      |
| 1441770 | 263007 | 263022 | N/A  | N/A  | TGATATGAATGGTATG  | 6   | AT | 1012 |
|         | 263048 | 263063 |      |      |                   |     |    |      |
| 1441772 | 218086 | 218101 | 1052 | 1067 | AATCUATAGGATGCTG  | 27  | AT | 2958 |
| 1441776 | 225075 | 225090 | N/A  | N/A  | GTGTATTATTGACCTG  | 2   | AT | 630  |
| 1441781 | 222233 | 222248 | 1643 | 1658 | TAGAATAGCCCATCAC  | 22  | AT | 779  |
| 1441784 | 222230 | 222245 | 1640 | 1655 | AATAGCCCATCACGAT  | 21  | AT | 2521 |
| 1441787 | 218174 | 218189 | 1140 | 1155 | CACAAACCAGCTGATG  | 24  | AT | 2523 |
| 1441790 | 218171 | 218186 | 1137 | 1152 | AAACCAGCTGATGAGA  | 12  | AT | 2959 |
| 1441797 | 391184 | 391199 | N/A  | N/A  | AATTAGGATTAAGGAG  | 54  | AT | 2528 |
| 1441800 | 391181 | 391196 | N/A  | N/A  | TAGGATTAAGGAGTTC  | 9   | AT | 649  |
| 1441803 | 391178 | 391193 | N/A  | N/A  | GATTAAGGAGTTCTGT  | 24  | AT | 2533 |
| 1441805 | 229904 | 229919 | N/A  | N/A  | ACATUTAGAGGCATTG  | 70  | AT | 2960 |
| 1441812 | 97752  | 97767  | N/A  | N/A  | CTCAUTAAATCAAGGC  | 37  | AT | 2961 |
| 1441816 | 350507 | 350522 | N/A  | N/A  | TATTATAGGGTTGAAA  | 115 | AT | 2503 |
| 1441817 | 290657 | 290672 | 2136 | 2151 | GCACAGGTAAGGCAAT  | 8   | AT | 784  |
| 1441820 | 290651 | 290666 | 2130 | 2145 | GTAAGGCAATGGACTC  | 6   | AT | 2962 |
| 1441821 | 233651 | 233666 | N/A  | N/A  | CTGCUCATTAAGTTCT  | 28  | AT | 2963 |
| 1441824 | 82464  | 82479  | N/A  | N/A  | GAACAATGCTGATTCA  | 43  | AT | 955  |
| 1441827 | 82460  | 82475  | N/A  | N/A  | AATGCTGATTCAAGGCA | 72  | AT | 2964 |
| 1441830 | 368428 | 368443 | N/A  | N/A  | TGATATTGTATAAGGT  | 10  | AT | 2509 |
| 1441833 | 368424 | 368439 | N/A  | N/A  | ATTGUATAAGGTTAGG  | 10  | AT | 2965 |
| 1441835 | 242391 | 242406 | N/A  | N/A  | CCGTCAAGTAATGAGT  | 53  | AT | 2966 |
| 1441838 | 285255 | 285270 | 1890 | 1905 | GATCUTTTGAATCTGT  | 7   | AT | 2967 |
| 1441841 | 285251 | 285266 | 1886 | 1901 | TTTTGAATCTGTCCAG  | 5   | AT | 2968 |
| 1441844 | 285186 | 285201 | 1821 | 1836 | GTACCATTACTGAGAT  | 17  | AT | 2969 |
| 1441847 | 217790 | 217805 | 756  | 771  | CCAGUTAACAGCGCGG  | 43  | AT | 2970 |
| 1441850 | 217787 | 217802 | 753  | 768  | GTTAACAGCGCGGTGA  | 18  | AT | 2518 |
| 1441852 | 222236 | 222251 | 1646 | 1661 | CACTAGAATAGCCCAT  | 8   | AT | 1001 |
| 1441940 | 82201  | 82216  | N/A  | N/A  | AGATATTAGCTCATGG  | 27  | AT | 2246 |
| 1441946 | 229160 | 229175 | N/A  | N/A  | AGTAUTAACCACCATT  | 38  | AT | 2971 |
| 1441947 | 463911 | 463926 | N/A  | N/A  | TGTCAGATTTAATAGG  | 72  | AT | 2972 |
| 1441950 | 184997 | 185012 | N/A  | N/A  | GTGTATTAGGTTTTTC  | 47  | AT | 1840 |
| 1441952 | 331864 | 331879 | N/A  | N/A  | CTATAGTATGATAGCA  | 44  | AT | 2537 |

|         |        |        |       |       |                            |     |    |      |
|---------|--------|--------|-------|-------|----------------------------|-----|----|------|
| 1441955 | 331861 | 331876 | N/A   | N/A   | TAGTATGATAGCACAA           | 3   | AT | 2538 |
| 1441958 | 236803 | 236818 | N/A   | N/A   | AATTGTTATACTGATG           | 41  | AT | 2541 |
| 1441961 | 236800 | 236815 | N/A   | N/A   | TGTTATACTGATGGGC           | 33  | AT | 1304 |
| 1441964 | 236797 | 236812 | N/A   | N/A   | TATAC <u>T</u> GATGGGCTAG  | 17  | AT | 2546 |
| 1441969 | 217563 | 217578 | 529   | 544   | GGAAATGATTCTGGCT           | 12  | AT | 2973 |
| 1441970 | 561183 | 561198 | 10172 | 10187 | TCAGGAATTGAAGTTA           | 20  | AT | 2974 |
| 1441974 | 222018 | 222033 | 1428  | 1443  | GTTT <u>C</u> AAACTGGGAGC  | 27  | AT | 2975 |
| 1442031 | 217658 | 217673 | 624   | 639   | TTACGACTGGCAGTGT           | 20  | AT | 475  |
| 1442032 | 218076 | 218091 | 1042  | 1057  | ATGCUGGGTCTCTCTC           | 32  | AT | 2976 |
| 1442036 | 217736 | 217751 | 702   | 717   | GTTGUTACTTCAGCTG           | 51  | AT | 2977 |
| 1442037 | 218108 | 218123 | 1074  | 1089  | GTTCUTTGCAGTGATG           | 12  | AT | 2978 |
| 1442045 | 229860 | 229875 | N/A   | N/A   | ATTGUGTGTCTCAGGC           | 9   | AT | 2979 |
| 1442046 | 285147 | 285162 | 1782  | 1797  | ATTT <u>C</u> AGTGCTCCCA   | 8   | AT | 2980 |
| 1442047 | 285466 | 285481 | 2000  | 2015  | ACCTGAGTGACTGATC           | 10  | AU | 2981 |
| 1442101 | 263003 | 263018 | N/A   | N/A   | ATGAATGGTATGATGG           | 8   | AU | 2553 |
| 1442102 | 217657 | 217672 | 623   | 638   | TACGACTGGCAGTGTC           | 18  | AU | 2982 |
| 1442103 | 222237 | 222252 | 1647  | 1662  | CCACUAGAATAGCCCA           | 4   | AU | 2983 |
| 1442104 | 222227 | 222242 | 1637  | 1652  | AGCC <u>C</u> ATCACGATGCC  | 47  | AU | 2984 |
| 1442105 | 326723 | 326738 | N/A   | N/A   | GATTATGAGGAAACCT           | 8   | AU | 2552 |
| 1442106 | 263333 | 263348 | N/A   | N/A   | TTGAAGAATGCATGTC           | 12  | AU | 2554 |
| 1442107 | 344738 | 344753 | N/A   | N/A   | AGTAUCCTTCAATGGC           | 8   | AU | 2985 |
| 1442108 | 391186 | 391201 | N/A   | N/A   | TTAAUTAGGATTAAGG           | 85  | AU | 2986 |
| 1442109 | 391176 | 391191 | N/A   | N/A   | TTAAGGAGTTCTGTGT           | 75  | AU | 2556 |
| 1442110 | 229900 | 229915 | N/A   | N/A   | TTAGAGGCATTGCAGG           | 23  | AU | 2557 |
| 1442111 | 222051 | 222066 | 1461  | 1476  | GCACUGTAGTATAAAG           | 19  | AU | 2987 |
| 1442112 | 97747  | 97762  | N/A   | N/A   | TAAAUCAAGGCAAGTG           | 70  | AU | 2988 |
| 1442113 | 350504 | 350519 | N/A   | N/A   | TATAGGGTTGAAAATA           | 52  | AU | 2558 |
| 1442114 | 233653 | 233668 | N/A   | N/A   | AGCTGCTCATTAAGTT           | 106 | AU | 2989 |
| 1442115 | 82458  | 82473  | N/A   | N/A   | TGCTGATTCAAGGCAGT          | 66  | AU | 2990 |
| 1442116 | 368422 | 368437 | N/A   | N/A   | TGTAUAAGGTTAGGTG           | 33  | AU | 2991 |
| 1442117 | 242394 | 242409 | N/A   | N/A   | GTAC <u>C</u> GTC AAGTAATG | 73  | AU | 2992 |
| 1442118 | 285249 | 285264 | 1884  | 1899  | TTGAATCTGTCCAGCT           | 18  | AU | 2993 |
| 1442119 | 217794 | 217809 | 760   | 775   | GTCT <u>C</u> CAGTTAACAGC  | 33  | AU | 2994 |
| 1442120 | 217784 | 217799 | 750   | 765   | AACAGCGCGGTGAGAT           | 26  | AU | 2995 |
| 1442121 | 222238 | 222253 | 1648  | 1663  | GCCAC <u>T</u> AGAATAGCCC  | 31  | AU | 2560 |
| 1442122 | 222228 | 222243 | 1638  | 1653  | TAGCCCATCACGATGC           | 42  | AU | 2996 |
| 1442143 | 82196  | 82211  | N/A   | N/A   | TTAG <u>C</u> TCATGGAAAGC  | 18  | AV | 2997 |
| 1442144 | 229158 | 229173 | N/A   | N/A   | TATTAACCACCATTC            | 9   | AV | 2561 |
| 1442145 | 185002 | 185017 | N/A   | N/A   | GCACUGTGTATTAGGT           | 39  | AV | 2998 |
| 1442146 | 331857 | 331872 | N/A   | N/A   | ATGAUAGCACAAACCA           | 3   | AV | 2999 |
| 1442147 | 236795 | 236810 | N/A   | N/A   | TACTGATGGGCTAGCC           | 79  | AV | 2562 |
| 1442148 | 217514 | 217529 | 480   | 495   | ATGGGCTGTAAACTTT           | 14  | AV | 3000 |
| 1442149 | 217513 | 217528 | 479   | 494   | TGGG <u>C</u> TGTAAACTTTG  | 14  | AV | 3001 |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1442150 | 217567 | 217582 | 533  | 548  | TTCCGGAAATGATTCT  | 29 | AV | 2563 |
| 1442151 | 222021 | 222036 | 1431 | 1446 | ATGGUTTCAAACCTGGG | 17 | AV | 3002 |
| 1411019 | 94388  | 94403  | N/A  | N/A  | CAGGCTGCTATTAAAG  | 87 | E  | 386  |

The modified oligonucleotides in Table 4 below are 16 nucleosides in length. The sugar motif for the modified oligonucleotides is (from 5' to 3'): kkkkkkkkkkkekek; wherein each "d" represents a 2'-β-D-deoxyribose sugar moiety, each "k" represents a cEt modified sugar moiety, and each "e" represents a 2'-MOE sugar moiety. The internucleoside linkage motif for the modified oligonucleotides is (from 5' to 3'): sssssssssssss; wherein each "s" represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine.

**Table 4.** Reduction of PSD3 RNA by mixed cEt/MOE modified oligonucleotides with uniform phosphorothioate internucleoside linkages

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3') | DMPK (% UTC) RTS41435 | AID | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|---------------------|-----------------------|-----|-----------|
| 1441254      | 288683                  | 288698                 | 2078                    | 2093                   | AATATCTATTGGAGAA    | 12                    | AK  | 1168      |
| 1441257      | 288680                  | 288695                 | 2075                    | 2090                   | ATCTATTGGAGAAGTG    | 4                     | AK  | 260       |
| 1441260      | 288677                  | 288692                 | 2072                    | 2087                   | TATTGGAGAAGTGTAT    | 4                     | AK  | 859       |
| 1441262      | 217666                  | 217681                 | 632                     | 647                    | TCTGTGTTTTACGACT    | 9                     | AK  | 346       |
| 1441265      | 217663                  | 217678                 | 629                     | 644                    | GTGTTTTACGACTGGC    | 10                    | AK  | 782       |
| 1441268      | 217660                  | 217675                 | 626                     | 641                    | TTTTACGACTGGCAGT    | 35                    | AK  | 629       |
| 1441269      | 218084                  | 218099                 | 1050                    | 1065                   | TCTATAGGATGCTGGG    | 26                    | AK  | 704       |
| 1441272      | 218081                  | 218096                 | 1047                    | 1062                   | ATAGGATGCTGGGTCT    | 22                    | AK  | 551       |
| 1441275      | 218078                  | 218093                 | 1044                    | 1059                   | GGATGCTGGGTCTCTC    | 9                     | AK  | 2855      |
| 1441276      | 235210                  | 235225                 | N/A                     | N/A                    | ATACACAATTTAGCTC    | 18                    | AK  | 337       |
|              | 235283                  | 235298                 |                         |                        |                     |                       |     |           |
| 1441279      | 235205                  | 235220                 | N/A                     | N/A                    | CAATTTAGCTCTATTA    | 23                    | AK  | 2489      |
| 1441282      | 288674                  | 288689                 | 2069                    | 2084                   | TGGAGAAGTGTATTAA    | 5                     | AK  | 350       |
| 1441284      | 82202                   | 82217                  | N/A                     | N/A                    | CAGATATTAGCTCATG    | 6                     | AK  | 2324      |
| 1441287      | 226033                  | 226048                 | N/A                     | N/A                    | ACCTCTGCACCTTTC     | 7                     | AK  | 2898      |
| 1441291      | 217742                  | 217757                 | 708                     | 723                    | TCCTCCGTTGTTACTT    | 18                    | AK  | 2859      |
| 1441294      | 217739                  | 217754                 | 705                     | 720                    | TCCGTTGTTACTTCAG    | 6                     | AK  | 3003      |
| 1441298      | 218104                  | 218119                 | 1070                    | 1085                   | TTTGCAGTGATGTCTC    | 5                     | AK  | 2946      |
| 1441301      | 218101                  | 218116                 | 1067                    | 1082                   | GCAGTGATGTCTCAAA    | 13                    | AK  | 3004      |
| 1441304      | 218222                  | 218237                 | 1188                    | 1203                   | GCTTTCCAGGATTCAT    | 10                    | AK  | 3005      |
| 1441308      | 222169                  | 222184                 | 1579                    | 1594                   | TGATGTCCTCTCCAAG    | 8                     | AK  | 2904      |
| 1441309      | 222155                  | 222170                 | 1565                    | 1580                   | AGAAGTACCACCTTC     | 7                     | AK  | 2905      |
| 1441312      | 244769                  | 244784                 | N/A                     | N/A                    | TATAGGTAATTTATGA    | 97                    | AK  | 653       |
| 1441315      | 244765                  | 244780                 | N/A                     | N/A                    | GGTAATTTATGAGTTA    | 17                    | AK  | 455       |
| 1441316      | 342929                  | 342944                 | N/A                     | N/A                    | TGAGATAATGTGAAGC    | 4                     | AK  | 2493      |
| 1441320      | 342925                  | 342940                 | N/A                     | N/A                    | ATAATGTGAAGCTTAG    | 8                     | AK  | 2495      |

|         |        |        |      |      |                   |     |    |      |
|---------|--------|--------|------|------|-------------------|-----|----|------|
| 1441323 | 366241 | 366256 | N/A  | N/A  | TATCATATGAAAGCCA  | 24  | AK | 2477 |
| 1441324 | 181932 | 181947 | N/A  | N/A  | ATGCAGAATTGATAAC  | 46  | AK | 2478 |
| 1441327 | 181927 | 181942 | N/A  | N/A  | GAATTGATAACAGGTA  | 3   | AK | 449  |
| 1441330 | 365698 | 365713 | N/A  | N/A  | GTAATATTAAAGCCAG  | 17  | AK | 441  |
| 1441333 | 508289 | 508304 | N/A  | N/A  | GATTTTAAGAGTCCAC  | 38  | AK | 444  |
| 1441337 | 222039 | 222054 | 1449 | 1464 | AAAGAAAGTGTGTCCA  | 5   | AK | 526  |
| 1441340 | 222036 | 222051 | 1446 | 1461 | GAAGTGTGTGCCAAAA  | 3   | AK | 3006 |
| 1441343 | 155902 | 155917 | N/A  | N/A  | AGTTATTATATGGCTG  | 113 | AK | 414  |
| 1441348 | 229862 | 229877 | N/A  | N/A  | ATATTGTGTGTCTCAG  | 14  | AK | 3007 |
| 1441349 | 285149 | 285164 | 1784 | 1799 | AAATTTTCAGTGCTCCC | 25  | AK | 2278 |
| 1441352 | 285468 | 285483 | 2002 | 2017 | ATACCTGAGTGACTGA  | 4   | AK | 2488 |
| 1441355 | 222159 | 222174 | 1569 | 1584 | TCCAAGAACTGACCAC  | 31  | AK | 469  |
| 1441581 | 263010 | 263025 | N/A  | N/A  | AAGTGATATGAATGGT  | 5   | AK | 1167 |
|         | 263051 | 263066 |      |      |                   |     |    |      |
| 1441584 | 263007 | 263022 | N/A  | N/A  | TGATATGAATGGTATG  | 4   | AK | 1012 |
|         | 263048 | 263063 |      |      |                   |     |    |      |
| 1441590 | 225077 | 225092 | N/A  | N/A  | GTGTGTATTATTGACC  | 4   | AK | 2872 |
| 1441593 | 225074 | 225089 | N/A  | N/A  | TGTATTATTGACCTGG  | 62  | AK | 553  |
| 1441598 | 222233 | 222248 | 1643 | 1658 | TAGAATAGCCCATCAC  | 10  | AK | 779  |
| 1441601 | 222230 | 222245 | 1640 | 1655 | AATAGCCCATCACGAT  | 38  | AK | 2521 |
| 1441603 | 218175 | 218190 | 1141 | 1156 | ACACAAACCAGCTGAT  | 48  | AK | 2522 |
| 1441606 | 218172 | 218187 | 1138 | 1153 | CAAACCAGCTGATGAG  | 35  | AK | 1097 |
| 1441609 | 218169 | 218184 | 1135 | 1150 | ACCAGCTGATGAGATG  | 15  | AK | 2873 |
| 1441614 | 391184 | 391199 | N/A  | N/A  | AATTAGGATTAAGGAG  | 14  | AK | 2528 |
| 1441617 | 391181 | 391196 | N/A  | N/A  | TAGGATTAAGGAGTTC  | 18  | AK | 649  |
| 1441620 | 391178 | 391193 | N/A  | N/A  | GATTAAGGAGTTCTGT  | 33  | AK | 2533 |
| 1441621 | 229906 | 229921 | N/A  | N/A  | GAACATTTAGAGGCAT  | 15  | AK | 915  |
| 1441624 | 229902 | 229917 | N/A  | N/A  | ATTTAGAGGCATTGCA  | 66  | AK | 2498 |
| 1441625 | 222047 | 222062 | 1457 | 1472 | TGTAGTATAAAGAAGT  | 11  | AK | 2499 |
| 1441628 | 97753  | 97768  | N/A  | N/A  | TCTCATTAATCAAGG   | 20  | AK | 2500 |
| 1441633 | 350507 | 350522 | N/A  | N/A  | TATTATAGGGTTGAAA  | 18  | AK | 2503 |
| 1441635 | 290653 | 290668 | 2132 | 2147 | AGGTAAGGCAATGGAC  | 4   | AK | 2504 |
| 1441640 | 82465  | 82480  | N/A  | N/A  | TGAACAATGCTGATTC  | 6   | AK | 2506 |
| 1441643 | 82461  | 82476  | N/A  | N/A  | CAATGCTGATTCAGGC  | 6   | AK | 2877 |
| 1441647 | 368428 | 368443 | N/A  | N/A  | TGATATTGTATAAGGT  | 4   | AK | 2509 |
| 1441650 | 368424 | 368439 | N/A  | N/A  | ATTGTATAAGGTTAGG  | 3   | AK | 2511 |
| 1441653 | 242390 | 242405 | N/A  | N/A  | CGTCAAGTAATGAGTT  | 4   | AK | 2512 |
| 1441657 | 285252 | 285267 | 1887 | 1902 | CTTTTGAATCTGTCCA  | 5   | AK | 3008 |
| 1441660 | 285187 | 285202 | 1822 | 1837 | GGTACCATTACTGAGA  | 19  | AK | 2881 |
| 1441663 | 217792 | 217807 | 758  | 773  | CTCCAGTTAACAGCGC  | 44  | AK | 2516 |
| 1441666 | 217789 | 217804 | 755  | 770  | CAGTTAACAGCGCGGT  | 35  | AK | 1241 |
| 1441669 | 217786 | 217801 | 752  | 767  | TTAACAGCGCGGTGAG  | 40  | AK | 2519 |
| 1441670 | 222236 | 222251 | 1646 | 1661 | CACTAGAATAGCCCAT  | 17  | AK | 1001 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1441865 | 82198  | 82213  | N/A   | N/A   | TATTAGCTCATGGAAA  | 12 | AK | 2091 |
| 1441869 | 229160 | 229175 | N/A   | N/A   | AGTATTAACCACCATT  | 11 | AK | 2535 |
| 1441870 | 463911 | 463926 | N/A   | N/A   | TGTCAGATTTAATAGG  | 25 | AK | 2972 |
| 1441876 | 331863 | 331878 | N/A   | N/A   | TATAGTATGATAGCAC  | 3  | AK | 1607 |
| 1441879 | 331860 | 331875 | N/A   | N/A   | AGTATGATAGCACAAA  | 6  | AK | 2539 |
| 1441882 | 236802 | 236817 | N/A   | N/A   | ATTGTTATACTGATGG  | 6  | AK | 2542 |
| 1441885 | 236799 | 236814 | N/A   | N/A   | GTTATACTGATGGGCT  | 14 | AK | 2544 |
| 1441889 | 217511 | 217526 | 477   | 492   | GGCTGTAAACTTTGTT  | 11 | AK | 2816 |
| 1441892 | 217564 | 217579 | 530   | 545   | CGGAAATGATTCTGGC  | 24 | AK | 2161 |
| 1441896 | 561179 | 561194 | 10168 | 10183 | GAATTGAAGTTAGGGT  | 15 | AK | 134  |
| 1441899 | 222017 | 222032 | 1427  | 1442  | TTTCAAACCTGGGAGCT | 37 | AK | 2548 |
| 1441256 | 288681 | 288696 | 2076  | 2091  | TATCTATTGGAGAAGT  | 3  | AL | 1013 |
| 1441259 | 288678 | 288693 | 2073  | 2088  | CTATTGGAGAAGTGTA  | 2  | AL | 936  |
| 1441261 | 217667 | 217682 | 633   | 648   | CTCTGTGTTTTACGAC  | 9  | AL | 2941 |
| 1441264 | 217664 | 217679 | 630   | 645   | TGTGTTTTACGACTGG  | 16 | AL | 858  |
| 1441267 | 217661 | 217676 | 627   | 642   | GTTTTACGACTGGCAG  | 7  | AL | 21   |
| 1441271 | 218082 | 218097 | 1048  | 1063  | TATAGGATGCTGGGTC  | 18 | AL | 100  |
| 1441274 | 218079 | 218094 | 1045  | 1060  | AGGATGCTGGGTCTCT  | 12 | AL | 397  |
| 1441278 | 235208 | 235223 | N/A   | N/A   | ACACAATTTAGCTCTA  | 4  | AL | 341  |
| 1441281 | 288675 | 288690 | 2070  | 2085  | TTGGAGAAGTGTATTA  | 6  | AL | 352  |
| 1441283 | 82207  | 82222  | N/A   | N/A   | ACTTTCAGATATTAGC  | 4  | AL | 3009 |
| 1441286 | 226034 | 226049 | N/A   | N/A   | AACCTCTTGCACCTTT  | 18 | AL | 3010 |
| 1441290 | 217743 | 217758 | 709   | 724   | TTCTCCGTTGTTACT   | 15 | AL | 3011 |
| 1441293 | 217740 | 217755 | 706   | 721   | CTCCGTTGTTACTTCA  | 5  | AL | 2945 |
| 1441297 | 218105 | 218120 | 1071  | 1086  | CTTTGCAGTGATGTCT  | 10 | AL | 2861 |
| 1441300 | 218102 | 218117 | 1068  | 1083  | TGCAGTGATGTCTCAA  | 11 | AL | 2822 |
| 1441303 | 218224 | 218239 | 1190  | 1205  | GAGCTTTCAGGATTC   | 23 | AL | 3012 |
| 1441306 | 218219 | 218234 | 1185  | 1200  | TTCCAGGATTCATCCC  | 10 | AL | 2948 |
| 1441307 | 222175 | 222190 | 1585  | 1600  | TCCCCCTGATGTCCTC  | 16 | AL | 2949 |
| 1441311 | 222149 | 222164 | 1559  | 1574  | GACCACCTTCTTTAAT  | 12 | AL | 2491 |
| 1441314 | 244766 | 244781 | N/A   | N/A   | AGGTAATTTATGAGTT  | 13 | AL | 488  |
| 1441319 | 342926 | 342941 | N/A   | N/A   | GATAATGTGAAGCTTA  | 14 | AL | 417  |
| 1441322 | 366242 | 366257 | N/A   | N/A   | CTATCATATGAAAGCC  | 18 | AL | 2476 |
| 1441326 | 181930 | 181945 | N/A   | N/A   | GCAGAATTGATAACAG  | 12 | AL | 562  |
| 1441329 | 365700 | 365715 | N/A   | N/A   | CAGTAATATTAAAGCC  | 7  | AL | 2480 |
| 1441332 | 508291 | 508306 | N/A   | N/A   | GTGATTTTAAGAGTCC  | 44 | AL | 3013 |
| 1441335 | 508286 | 508301 | N/A   | N/A   | TTTAAGAGTCCACTAG  | 85 | AL | 2482 |
| 1441336 | 222040 | 222055 | 1450  | 1465  | TAAAGAAGTGTGTCC   | 5  | AL | 2483 |
| 1441339 | 222037 | 222052 | 1447  | 1462  | AGAAGTGTTGTCCAAA  | 3  | AL | 2953 |
| 1441342 | 155903 | 155918 | N/A   | N/A   | AAGTTATTATATGGCT  | 69 | AL | 2484 |
| 1441345 | 251926 | 251941 | N/A   | N/A   | GGTTTAAAGTTATCTC  | 7  | AL | 2486 |
| 1441347 | 229866 | 229881 | N/A   | N/A   | CTCAATATTGTGTGTC  | 23 | AL | 609  |
| 1441351 | N/A    | N/A    | 2003  | 2018  | AATACCTGAGTGACTG  | 5  | AL | 2487 |

|         |        |        |      |      |                  |     |    |      |
|---------|--------|--------|------|------|------------------|-----|----|------|
| 1441354 | 222160 | 222175 | 1570 | 1585 | CTCCAAGAACTGACCA | 6   | AL | 546  |
| 1441357 | 222157 | 222172 | 1567 | 1582 | CAAGAACTGACCACCT | 3   | AL | 2472 |
| 1441583 | 263008 | 263023 | N/A  | N/A  | GTGATATGAATGGTAT | 1   | AL | 1090 |
|         | 263049 | 263064 |      |      |                  |     |    |      |
| 1441587 | 218085 | 218100 | 1051 | 1066 | ATCTATAGGATGCTGG | 16  | AL | 781  |
| 1441589 | 225078 | 225093 | N/A  | N/A  | CGTGTGTATTATTGAC | 3   | AL | 363  |
| 1441592 | 225075 | 225090 | N/A  | N/A  | GTGTATTATTGACCTG | 6   | AL | 630  |
| 1441595 | 225072 | 225087 | N/A  | N/A  | TATTATTGACCTGGTA | 45  | AL | 476  |
| 1441597 | 222234 | 222249 | 1644 | 1659 | CTAGAATAGCCCATCA | 6   | AL | 848  |
| 1441600 | 222231 | 222246 | 1641 | 1656 | GAATAGCCCATCACGA | 5   | AL | 2520 |
| 1441605 | 218173 | 218188 | 1139 | 1154 | ACAAACCAGCTGATGA | 20  | AL | 2524 |
| 1441608 | 218170 | 218185 | 1136 | 1151 | AACCAGCTGATGAGAT | 4   | AL | 2525 |
| 1441611 | 263335 | 263350 | N/A  | N/A  | GTTTGAAGAATGCATG | 16  | AL | 2526 |
| 1441613 | 344740 | 344755 | N/A  | N/A  | TTAGTATCCTTCAATG | 3   | AL | 3014 |
| 1441616 | 391182 | 391197 | N/A  | N/A  | TTAGGATTAAGGAGTT | 6   | AL | 2530 |
| 1441619 | 391179 | 391194 | N/A  | N/A  | GGATTAAGGAGTTCTG | 33  | AL | 2532 |
| 1441623 | 229903 | 229918 | N/A  | N/A  | CATTAGAGGCATTGC  | 28  | AL | 737  |
| 1441627 | 97754  | 97769  | N/A  | N/A  | GTCTCATTAAATCAAG | 8   | AL | 2920 |
| 1441630 | 97751  | 97766  | N/A  | N/A  | TCATTAAATCAAGGCA | 14  | AL | 2501 |
| 1441632 | 350508 | 350523 | N/A  | N/A  | TTATTATAGGGTTGAA | 5   | AL | 2502 |
| 1441634 | 290657 | 290672 | 2136 | 2151 | GCACAGGTAAGGCAAT | 57  | AL | 784  |
| 1441637 | 290651 | 290666 | 2130 | 2145 | GTAAGGCAATGGACTC | 11  | AL | 2962 |
| 1441639 | 233649 | 233664 | N/A  | N/A  | GCTCATTAAGTTCTTC | 20  | AL | 870  |
| 1441642 | 82462  | 82477  | N/A  | N/A  | ACAATGCTGATTCAGG | 7   | AL | 2507 |
| 1441646 | 368429 | 368444 | N/A  | N/A  | GTGATATTGTATAAGG | 2   | AL | 3015 |
| 1441649 | 368425 | 368440 | N/A  | N/A  | TATTGTATAAGGTTAG | 2   | AL | 2510 |
| 1441652 | 242391 | 242406 | N/A  | N/A  | CCGTCAAGTAATGAGT | 29  | AL | 2966 |
| 1441656 | 285253 | 285268 | 1888 | 1903 | TCTTTTGAATCTGTCC | 4   | AL | 2514 |
| 1441659 | 285188 | 285203 | 1823 | 1838 | TGGTACCATTACTGAG | 57  | AL | 2515 |
| 1441662 | 285185 | 285200 | 1820 | 1835 | TACCATTACTGAGATT | 11  | AL | 616  |
| 1441665 | 217790 | 217805 | 756  | 771  | CCAGTTAACAGCGCGG | 69  | AL | 178  |
| 1441668 | 217787 | 217802 | 753  | 768  | GTTAACAGCGCGGTGA | 17  | AL | 2518 |
| 1441864 | 82200  | 82215  | N/A  | N/A  | GATATTAGCTCATGGA | 5   | AL | 223  |
| 1441866 | 218034 | 218049 | 1000 | 1015 | CACTCCTTGAAATTCC | 13  | AL | 2928 |
| 1441868 | 229161 | 229176 | 478  | 493  | AAGTATTAACCACCAT | 4   | AL | 1913 |
| 1441872 | 463907 | 463922 | N/A  | N/A  | AGATTTAATAGGTCTT | 100 | AL | 2536 |
| 1441873 | 184997 | 185012 | N/A  | N/A  | GTGTATTAGGTTTTTC | 18  | AL | 1840 |
| 1441875 | 331864 | 331879 | N/A  | N/A  | CTATAGTATGATAGCA | 88  | AL | 2537 |
| 1441878 | 331861 | 331876 | N/A  | N/A  | TAGTATGATAGCACAA | 2   | AL | 2538 |
| 1441881 | 236803 | 236818 | N/A  | N/A  | AATTGTTATACTGATG | 5   | AL | 2541 |
| 1441884 | 236800 | 236815 | N/A  | N/A  | TGTTATACTGATGGGC | 31  | AL | 1304 |
| 1441887 | 236797 | 236812 | N/A  | N/A  | TATACTGATGGGCTAG | 28  | AL | 2546 |
| 1441888 | 217512 | 217527 | N/A  | N/A  | GGGCTGTAACTTTGT  | 11  | AL | 3016 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1441891 | 217565 | 217580 | 531   | 546   | CCGGAATGATTCTGG   | 63 | AL | 2238 |
| 1441895 | 561180 | 561195 | 10169 | 10184 | GGAATTGAAGTTAGGG  | 20 | AL | 212  |
| 1441898 | 222018 | 222033 | 1428  | 1443  | GTTTCAAACCTGGGAGC | 59 | AL | 2975 |
| 1441255 | 288682 | 288697 | 2077  | 2092  | ATATCTATTGGAGAAG  | 5  | AM | 1091 |
| 1441258 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAGTGT  | 5  | AM | 181  |
| 1441263 | 217665 | 217680 | 631   | 646   | CTGTGTTTTACGACTG  | 9  | AM | 2896 |
| 1441266 | 217662 | 217677 | 628   | 643   | TGTTTTACGACTGGCA  | 8  | AM | 705  |
| 1441270 | 218083 | 218098 | 1049  | 1064  | CTATAGGATGCTGGGT  | 41 | AM | 628  |
| 1441273 | 218080 | 218095 | 1046  | 1061  | TAGGATGCTGGGTCTC  | 11 | AM | 474  |
| 1441277 | 235209 | 235224 | N/A   | N/A   | TACACAATTTAGCTCT  | 17 | AM | 152  |
|         | 235282 | 235297 |       |       |                   |    |    |      |
| 1441280 | 288676 | 288691 | 2071  | 2086  | ATTGGAGAAGTGATT   | 3  | AM | 783  |
| 1441285 | 226035 | 226050 | N/A   | N/A   | CAACCTCTTGCACCTT  | 45 | AM | 2858 |
| 1441288 | 226032 | 226047 | N/A   | N/A   | CCTCTTGCACCTTTCT  | 6  | AM | 3017 |
| 1441289 | 217744 | 217759 | 710   | 725   | TTTCTCCGTTGTTAC   | 18 | AM | 2944 |
| 1441292 | 217741 | 217756 | 707   | 722   | CCTCCGTTGTTACTTC  | 16 | AM | 2601 |
| 1441295 | 217738 | 217753 | 704   | 719   | CCGTTGTTACTTCAGC  | 6  | AM | 3018 |
| 1441296 | 218106 | 218121 | 1072  | 1087  | TCTTTGCAGTGATGTC  | 9  | AM | 3019 |
| 1441299 | 218103 | 218118 | 1069  | 1084  | TTGCAGTGATGTCTCA  | 11 | AM | 2606 |
| 1441302 | 218225 | 218240 | 1191  | 1206  | GGAGCTTTCCAGGATT  | 21 | AM | 2947 |
| 1441305 | 218221 | 218236 | 1187  | 1202  | CTTCCAGGATTCATC   | 7  | AM | 2862 |
| 1441310 | 222154 | 222169 | 1564  | 1579  | GAACCTGACCACCTTCT | 10 | AM | 2490 |
| 1441313 | 244768 | 244783 | N/A   | N/A   | ATAGGTAATTTATGAG  | 74 | AM | 2492 |
| 1441317 | 342928 | 342943 | N/A   | N/A   | GAGATAATGTGAAGCT  | 4  | AM | 2494 |
| 1441321 | 366243 | 366258 | N/A   | N/A   | ACTATCATATGAAAGC  | 25 | AM | 2475 |
| 1441325 | 181931 | 181946 | N/A   | N/A   | TGCAGAATTGATAACA  | 69 | AM | 2864 |
| 1441328 | 365701 | 365716 | N/A   | N/A   | GCAGTAATATTAAAGC  | 8  | AM | 2479 |
| 1441331 | 508292 | 508307 | N/A   | N/A   | GGTGATTTTAAGAGTC  | 21 | AM | 2952 |
| 1441334 | 508287 | 508302 | N/A   | N/A   | TTTTAAGAGTCCACTA  | 32 | AM | 2481 |
| 1441338 | 222038 | 222053 | 1448  | 1463  | AAGAAAGTGTGTCCAA  | 4  | AM | 2866 |
| 1441341 | 155904 | 155919 | N/A   | N/A   | GAAGTTATTATATGGC  | 6  | AM | 530  |
| 1441344 | 155901 | 155916 | N/A   | N/A   | GTTATTATATGGCTGT  | 35 | AM | 2485 |
| 1441346 | 229868 | 229883 | N/A   | N/A   | ATCTCAATATTGTGTG  | 5  | AM | 2956 |
| 1441350 | N/A    | N/A    | 2005  | 2020  | GAAATACCTGAGTGAC  | 6  | AM | 462  |
| 1441353 | 222162 | 222177 | 1572  | 1587  | CTCTCCAAGAACTGAC  | 6  | AM | 554  |
| 1441356 | 222158 | 222173 | 1568  | 1583  | CCAAGAACTGACCACC  | 14 | AM | 2870 |
| 1441582 | 263009 | 263024 | N/A   | N/A   | AGTGATATGAATGGTA  | 2  | AM | 153  |
|         | 263050 | 263065 |       |       |                   |    |    |      |
| 1441585 | 263006 | 263021 | N/A   | N/A   | GATATGAATGGTATGA  | 4  | AM | 935  |
|         | 263047 | 263062 |       |       |                   |    |    |      |
| 1441586 | 218086 | 218101 | 1052  | 1067  | AATCTATAGGATGCTG  | 27 | AM | 2496 |
| 1441588 | 217659 | 217674 | 625   | 640   | TTTACGACTGGCAGTG  | 30 | AM | 552  |
| 1441591 | 225076 | 225091 | N/A   | N/A   | TGTGTATTATTGACCT  | 2  | AM | 706  |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1441594 | 225073 | 225088 | N/A   | N/A   | GTATTATTGACCTGGT  | 28 | AM | 229  |
| 1441596 | 222235 | 222250 | 1645  | 1660  | ACTAGAATAGCCCATC  | 9  | AM | 922  |
| 1441599 | 222232 | 222247 | 1642  | 1657  | AGAATAGCCCATCACG  | 24 | AM | 631  |
| 1441602 | 222229 | 222244 | 1639  | 1654  | ATAGCCCATCACGATG  | 32 | AM | 2916 |
| 1441604 | 218174 | 218189 | 1140  | 1155  | CACAAACCAGCTGATG  | 10 | AM | 2523 |
| 1441607 | 218171 | 218186 | 1137  | 1152  | AAACCAGCTGATGAGA  | 9  | AM | 2959 |
| 1441610 | 263338 | 263353 | N/A   | N/A   | GAAGTTTGAAGAATGC  | 7  | AM | 949  |
| 1441612 | 344746 | 344761 | N/A   | N/A   | CTAAATTTAGTATCCT  | 13 | AM | 2527 |
| 1441615 | 391183 | 391198 | N/A   | N/A   | ATTAGGATTAAGGAGT  | 11 | AM | 2529 |
| 1441618 | 391180 | 391195 | N/A   | N/A   | AGGATTAAGGAGTTCT  | 50 | AM | 2531 |
| 1441622 | 229904 | 229919 | N/A   | N/A   | ACATTTAGAGGCATTG  | 2  | AM | 2497 |
| 1441626 | 222043 | 222058 | 1453  | 1468  | GTATAAAGAAGTGTTG  | 2  | AM | 777  |
| 1441629 | 97752  | 97767  | N/A   | N/A   | CTCATTAATCAAGGC   | 28 | AM | 747  |
| 1441631 | 350509 | 350524 | N/A   | N/A   | TTTATTATAGGGTTGA  | 3  | AM | 1053 |
| 1441636 | 290652 | 290667 | 2131  | 2146  | GGTAAGGCAATGGACT  | 5  | AM | 2505 |
| 1441638 | 233651 | 233666 | N/A   | N/A   | CTGCTCATTAAGTTCT  | 25 | AM | 3020 |
| 1441641 | 82464  | 82479  | N/A   | N/A   | GAACAATGCTGATTCA  | 65 | AM | 955  |
| 1441644 | 82460  | 82475  | N/A   | N/A   | AATGCTGATTCAGGCA  | 18 | AM | 2964 |
| 1441645 | 368430 | 368445 | N/A   | N/A   | GGTGATATTGTATAAG  | 4  | AM | 2508 |
| 1441648 | 368427 | 368442 | N/A   | N/A   | GATATTGTATAAGGTT  | 3  | AM | 1060 |
| 1441651 | 242392 | 242407 | N/A   | N/A   | ACCGTCAAGTAATGAG  | 43 | AM | 3021 |
| 1441654 | 242389 | 242404 | N/A   | N/A   | GTCAAGTAATGAGTTT  | 12 | AM | 758  |
| 1441655 | 285255 | 285270 | 1890  | 1905  | GATCTTTTGAATCTGT  | 21 | AM | 2513 |
| 1441658 | 285251 | 285266 | 1886  | 1901  | TTTTGAATCTGTCCAG  | 13 | AM | 2968 |
| 1441661 | 285186 | 285201 | 1821  | 1836  | GTACCATTACTGAGAT  | 14 | AM | 2969 |
| 1441664 | 217791 | 217806 | 757   | 772   | TCCAGTTAACAGCGCG  | 63 | AM | 2600 |
| 1441667 | 217788 | 217803 | 754   | 769   | AGTTAACAGCGCGGTG  | 25 | AM | 2517 |
| 1441862 | 218077 | 218092 | 1043  | 1058  | GATGCTGGGTCTCTCT  | 7  | AM | 381  |
| 1441863 | 82201  | 82216  | N/A   | N/A   | AGATATTAGCTCATGG  | 19 | AM | 2246 |
| 1441867 | 229163 | 229178 | N/A   | N/A   | TAAAGTATTAACCACC  | 8  | AM | 1964 |
| 1441871 | 463910 | 463925 | N/A   | N/A   | GTCAGATTTAATAGGT  | 26 | AM | 2929 |
| 1441874 | 331865 | 331880 | N/A   | N/A   | ACTATAGTATGATAGC  | 14 | AM | 1644 |
| 1441877 | 331862 | 331877 | N/A   | N/A   | ATAGTATGATAGCACA  | 3  | AM | 1533 |
| 1441880 | 331859 | 331874 | N/A   | N/A   | GTATGATAGCACAAAC  | 6  | AM | 2540 |
| 1441883 | 236801 | 236816 | N/A   | N/A   | TTGTTATACTGATGGG  | 4  | AM | 2543 |
| 1441886 | 236798 | 236813 | N/A   | N/A   | TTATACTGATGGGCTA  | 31 | AM | 2545 |
| 1441890 | 217510 | 217525 | 476   | 491   | GCTGTAACTTTGTTC   | 7  | AM | 2547 |
| 1441893 | 217563 | 217578 | 529   | 544   | GGAAATGATTCTGGCT  | 15 | AM | 2973 |
| 1441894 | 561183 | 561198 | 10172 | 10187 | TCAGGAATTGAAGTTA  | 49 | AM | 2974 |
| 1441897 | 222019 | 222034 | 1429  | 1444  | GGTTTCAAACCTGGGAG | 28 | AM | 3022 |
| 1441900 | 222013 | 222028 | 1423  | 1438  | AAACTGGGAGCTGTAC  | 12 | AU | 2534 |
| 1441991 | 218076 | 218091 | 1042  | 1057  | ATGCTGGGTCTCTCTC  | 19 | AU | 3023 |
| 1441992 | 235212 | 235227 | N/A   | N/A   | TTATACACAATTTAGC  | 2  | AU | 334  |

|         |        |        |      |      |                  |    |    |      |
|---------|--------|--------|------|------|------------------|----|----|------|
|         | 235285 | 235300 |      |      |                  |    |    |      |
| 1441993 | 226037 | 226052 | N/A  | N/A  | CCCAACCTCTTGCACC | 81 | AU | 2549 |
| 1441994 | 217746 | 217761 | 712  | 727  | ACTTTCCTCCGTTGTT | 32 | AU | 3024 |
| 1441995 | 217736 | 217751 | 702  | 717  | GTTGTTACTTCAGCTG | 25 | AU | 3025 |
| 1441996 | 218108 | 218123 | 1074 | 1089 | GTTCTTTGCAGTGATG | 5  | AU | 3026 |
| 1441997 | 218098 | 218113 | 1064 | 1079 | GTGATGTCTCAAAATC | 10 | AU | 3027 |
| 1441998 | 218217 | 218232 | 1183 | 1198 | CCAGGATTCATCCCAA | 22 | AU | 2936 |
| 1441999 | 222177 | 222192 | 1587 | 1602 | CCTCCCCCTGATGTCC | 53 | AU | 2893 |
| 1442000 | 222147 | 222162 | 1557 | 1572 | CCACCTTCTTTAATGC | 15 | AU | 347  |
| 1442001 | 342921 | 342936 | N/A  | N/A  | TGTGAAGCTTAGAACC | 3  | AU | 2937 |
| 1442002 | 508284 | 508299 | N/A  | N/A  | TAAGAGTCCACTAGCC | 66 | AU | 2550 |
| 1442003 | 181922 | 181937 | N/A  | N/A  | GATAACAGGTAAATTA | 73 | AU | 2894 |
| 1442004 | 244760 | 244775 | N/A  | N/A  | TTTATGAGTTAAAGGG | 13 | AU | 2447 |
| 1442005 | 229860 | 229875 | N/A  | N/A  | ATTGTGTGTCTCAGGC | 10 | AU | 3028 |
| 1442006 | 285147 | 285162 | 1782 | 1797 | ATTTCAGTGCTCCCCA | 21 | AU | 2980 |
| 1442007 | 285466 | 285481 | 2000 | 2015 | ACCTGAGTGACTGATC | 9  | AU | 2981 |
| 1442049 | 217669 | 217684 | 635  | 650  | CTCTCTGTGTTTACG  | 6  | AU | 2935 |
| 1442050 | 217668 | 217683 | 634  | 649  | TCTCTGTGTTTACGA  | 4  | AU | 3029 |
| 1442051 | 217658 | 217673 | 624  | 639  | TTACGACTGGCAGTGT | 19 | AU | 475  |
| 1442052 | 217657 | 217672 | 623  | 638  | TACGACTGGCAGTGTC | 11 | AU | 2982 |
| 1442053 | 225070 | 225085 | N/A  | N/A  | TTATTGACCTGGTAAA | 84 | AU | 2400 |
| 1442054 | 222237 | 222252 | 1647 | 1662 | CCACTAGAATAGCCCA | 19 | AU | 2551 |
| 1442055 | 222227 | 222242 | 1637 | 1652 | AGCCCATCACGATGCC | 25 | AU | 2984 |
| 1442056 | 326723 | 326738 | N/A  | N/A  | GATTATGAGGAAACCT | 28 | AU | 2552 |
| 1442057 | 263333 | 263348 | N/A  | N/A  | TTGAAGAATGCATGTC | 14 | AU | 2554 |
| 1442058 | 344738 | 344753 | N/A  | N/A  | AGTATCCTTCAATGGC | 20 | AU | 3030 |
| 1442059 | 391186 | 391201 | N/A  | N/A  | TTAATTAGGATTAAGG | 63 | AU | 2555 |
| 1442060 | 391176 | 391191 | N/A  | N/A  | TTAAGGAGTTCTGTGT | 16 | AU | 2556 |
| 1442061 | 229900 | 229915 | N/A  | N/A  | TTAGAGGCATTGCAGG | 20 | AU | 2557 |
| 1442062 | 222051 | 222066 | 1461 | 1476 | GCACTGTAGTATAAAG | 6  | AU | 3031 |
| 1442063 | 350504 | 350519 | N/A  | N/A  | TATAGGGTTGAAAATA | 95 | AU | 2558 |
| 1442064 | 290659 | 290674 | 2138 | 2153 | TTGCACAGGTAAGGCA | 16 | AU | 2622 |
| 1442065 | 290649 | 290664 | 2128 | 2143 | AAGGCAATGGACTCCA | 29 | AU | 2837 |
| 1442066 | 233653 | 233668 | N/A  | N/A  | AGCTGCTCATTAAGTT | 68 | AU | 2989 |
| 1442067 | 82458  | 82473  | N/A  | N/A  | TGCTGATTCAGGCAGT | 88 | AU | 2990 |
| 1442068 | 368422 | 368437 | N/A  | N/A  | TGTATAAGGTTAGGTG | 3  | AU | 2559 |
| 1442069 | 242394 | 242409 | N/A  | N/A  | GTACCGTCAAGTAATG | 34 | AU | 2992 |
| 1442070 | 285249 | 285264 | 1884 | 1899 | TTGAATCTGTCCAGCT | 10 | AU | 2993 |
| 1442071 | 217794 | 217809 | 760  | 775  | GTCTCCAGTTAACAGC | 30 | AU | 2994 |
| 1442072 | 217784 | 217799 | 750  | 765  | AACAGCGCGGTGAGAT | 21 | AU | 2995 |
| 1442073 | 222238 | 222253 | 1648 | 1663 | GCCACTAGAATAGCCC | 39 | AU | 2560 |
| 1442074 | 222228 | 222243 | 1638 | 1653 | TAGCCCATCACGATGC | 29 | AU | 2996 |
| 1442132 | 263003 | 263018 | N/A  | N/A  | ATGAATGGTATGATGG | 7  | AU | 2553 |

|         |        |        |      |      |                   |     |    |      |
|---------|--------|--------|------|------|-------------------|-----|----|------|
| 1442133 | 222021 | 222036 | 1431 | 1446 | ATGGTTTCAAACCTGGG | 15  | AU | 2564 |
| 1442156 | 82196  | 82211  | N/A  | N/A  | TTAGCTCATGGAAAGC  | 29  | AU | 2997 |
| 1442157 | 229158 | 229173 | N/A  | N/A  | TATTAACCACCATTCC  | 7   | AU | 2561 |
| 1442158 | 185002 | 185017 | N/A  | N/A  | GCACTGTGTATTAGGT  | 8   | AU | 3032 |
| 1442159 | 331857 | 331872 | N/A  | N/A  | ATGATAGCACAAACCA  | 5   | AU | 3033 |
| 1442160 | 236795 | 236810 | N/A  | N/A  | TACTGATGGGCTAGCC  | 105 | AU | 2562 |
| 1442161 | 217514 | 217529 | 480  | 495  | ATGGGCTGTAACTTT   | 9   | AU | 3000 |
| 1442162 | 217513 | 217528 | 479  | 494  | TGGGCTGTAACTTTG   | 6   | AU | 3001 |
| 1442163 | 217567 | 217582 | 533  | 548  | TTCCGGAATGATTCT   | 19  | AU | 2563 |

The modified oligonucleotides in the Table 5 below are 16 nucleosides in length. The sugar motif for the modified oligonucleotides is (from 5' to 3'): kkkdddddskkkk; wherein each "d" represents a 2'-β-D-deoxyribose sugar moiety, each "k" represents a cEt modified sugar moiety, and each "e" represents a 2'-MOE sugar moiety. The internucleoside linkage motif for the modified oligonucleotides is (from 5' to 3'): sssssssssssss; wherein each "s" represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine.

**Table 5.** Reduction of PSD3 RNA by mixed cEt/MOE modified oligonucleotides with uniform phosphorothioate internucleoside linkages

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3') | DMPK (% UTC) RTS41435 | AID | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|---------------------|-----------------------|-----|-----------|
| 1441358      | 288683                  | 288698                 | 2078                    | 2093                   | AATATCTATTGGAGAA    | 9                     | AN  | 1168      |
| 1441361      | 288680                  | 288695                 | 2075                    | 2090                   | ATCTATTGGAGAAGTG    | 3                     | AN  | 260       |
| 1441364      | 288677                  | 288692                 | 2072                    | 2087                   | TATTGGAGAAGTGAT     | 3                     | AN  | 859       |
| 1441366      | 217666                  | 217681                 | 632                     | 647                    | TCTGTGTTTACGACT     | 8                     | AN  | 346       |
| 1441369      | 217663                  | 217678                 | 629                     | 644                    | GTGTTTTACGACTGGC    | 4                     | AN  | 782       |
| 1441372      | 217660                  | 217675                 | 626                     | 641                    | TTTTACGACTGGCAGT    | 23                    | AN  | 629       |
| 1441373      | 218084                  | 218099                 | 1050                    | 1065                   | TCTATAGGATGCTGGG    | 15                    | AN  | 704       |
| 1441376      | 218081                  | 218096                 | 1047                    | 1062                   | ATAGGATGCTGGGTCT    | 8                     | AN  | 551       |
| 1441379      | 218078                  | 218093                 | 1044                    | 1059                   | GGATGCTGGGTCTCTC    | 5                     | AN  | 2855      |
| 1441380      | 235210                  | 235225                 | N/A                     | N/A                    | ATACACAATTAGCTC     | 13                    | AN  | 337       |
|              | 235283                  | 235298                 |                         |                        |                     |                       |     |           |
| 1441383      | 235205                  | 235220                 | N/A                     | N/A                    | CAATTTAGCTCTATTA    | 39                    | AN  | 2489      |
| 1441386      | 288674                  | 288689                 | 2069                    | 2084                   | TGGAGAAGTGATTA      | 3                     | AN  | 350       |
| 1441388      | 82202                   | 82217                  | N/A                     | N/A                    | CAGATATTAGCTCATG    | 4                     | AN  | 2324      |
| 1441391      | 226033                  | 226048                 | N/A                     | N/A                    | ACCTCTTGACCTTTC     | 5                     | AN  | 2898      |
| 1441395      | 217742                  | 217757                 | 708                     | 723                    | TCCTCCGTTGTTACTT    | 13                    | AN  | 2859      |
| 1441398      | 217739                  | 217754                 | 705                     | 720                    | TCCGTTGTTACTTCAG    | 5                     | AN  | 3003      |
| 1441402      | 218104                  | 218119                 | 1070                    | 1085                   | TTTGCA GTGATGTCTC   | 7                     | AN  | 2946      |
| 1441405      | 218101                  | 218116                 | 1067                    | 1082                   | GCAGTGATGTCTCAA     | 13                    | AN  | 3004      |
| 1441408      | 218222                  | 218237                 | 1188                    | 1203                   | GCTTCCAGGATTCAT     | 7                     | AN  | 3005      |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1441412 | 222169 | 222184 | 1579 | 1594 | TGATGTCCTCTCCAAG  | 4  | AN | 2904 |
| 1441413 | 222155 | 222170 | 1565 | 1580 | AGAACTGACCACCTTC  | 5  | AN | 2905 |
| 1441416 | 244769 | 244784 | N/A  | N/A  | TATAGGTAATTTATGA  | 85 | AN | 653  |
| 1441419 | 244765 | 244780 | N/A  | N/A  | GGTAATTTATGAGTTA  | 6  | AN | 455  |
| 1441420 | 342929 | 342944 | N/A  | N/A  | TGAGATAATGTGAAGC  | 2  | AN | 2493 |
| 1441423 | 342925 | 342940 | N/A  | N/A  | ATAATGTGAAGCTTAG  | 4  | AN | 2495 |
| 1441426 | 366241 | 366256 | N/A  | N/A  | TATCATATGAAAGCCA  | 3  | AN | 2477 |
| 1441427 | 181932 | 181947 | N/A  | N/A  | ATGCAGAATTGATAAC  | 70 | AN | 2478 |
| 1441430 | 181927 | 181942 | N/A  | N/A  | GAATTGATAACAGGTA  | 2  | AN | 449  |
| 1441433 | 365698 | 365713 | N/A  | N/A  | GTAATATTAAGCCAG   | 2  | AN | 441  |
| 1441436 | 508289 | 508304 | N/A  | N/A  | GATTTTAAGAGTCCAC  | 16 | AN | 444  |
| 1441440 | 222039 | 222054 | 1449 | 1464 | AAAGAAGTGTGTCCA   | 2  | AN | 526  |
| 1441443 | 222036 | 222051 | 1446 | 1461 | GAAGTGTGTCCAAAA   | 1  | AN | 3006 |
| 1441446 | 155902 | 155917 | N/A  | N/A  | AGTTATTATATGGCTG  | 34 | AN | 414  |
| 1441451 | 229862 | 229877 | N/A  | N/A  | ATATTGTGTGTCTCAG  | 4  | AN | 3007 |
| 1441452 | 285149 | 285164 | 1784 | 1799 | AAATTCAGTGCTCCC   | 6  | AN | 2278 |
| 1441455 | 285468 | 285483 | 2002 | 2017 | ATACCTGAGTGACTGA  | 2  | AN | 2488 |
| 1441458 | 222159 | 222174 | 1569 | 1584 | TCCAAGAACTGACCAC  | 9  | AN | 469  |
| 1441671 | 263010 | 263025 | N/A  | N/A  | AAGTGATATGAATGGT  | 2  | AN | 1167 |
|         | 263051 | 263066 |      |      |                   |    |    |      |
| 1441674 | 263007 | 263022 | N/A  | N/A  | TGATATGAATGGTATG  | 4  | AN | 1012 |
|         | 263048 | 263063 |      |      |                   |    |    |      |
| 1441680 | 225077 | 225092 | N/A  | N/A  | GTGTGTATTATTGACC  | 3  | AN | 2872 |
| 1441683 | 225074 | 225089 | N/A  | N/A  | TGTATTATTGACCTGG  | 6  | AN | 553  |
| 1441688 | 222233 | 222248 | 1643 | 1658 | TAGAATAGCCCATCAC  | 13 | AN | 779  |
| 1441691 | 222230 | 222245 | 1640 | 1655 | AATAGCCCATCACGAT  | 22 | AN | 2521 |
| 1441693 | 218175 | 218190 | 1141 | 1156 | ACACAAACCAGCTGAT  | 18 | AN | 2522 |
| 1441696 | 218172 | 218187 | 1138 | 1153 | CAAAACCAGCTGATGAG | 15 | AN | 1097 |
| 1441699 | 218169 | 218184 | 1135 | 1150 | ACCAGCTGATGAGATG  | 8  | AN | 2873 |
| 1441706 | 391184 | 391199 | N/A  | N/A  | AATTAGGATTAAGGAG  | 18 | AN | 2528 |
| 1441709 | 391181 | 391196 | N/A  | N/A  | TAGGATTAAGGAGTTC  | 23 | AN | 649  |
| 1441712 | 391178 | 391193 | N/A  | N/A  | GATTAAGGAGTTCTGT  | 20 | AN | 2533 |
| 1441713 | 229906 | 229921 | N/A  | N/A  | GAACATTTAGAGGCAT  | 2  | AN | 915  |
| 1441717 | 229902 | 229917 | N/A  | N/A  | ATTTAGAGGCATTGCA  | 34 | AN | 2498 |
| 1441719 | 222047 | 222062 | 1457 | 1472 | TGTAGTATAAAGAAAGT | 4  | AN | 2499 |
| 1441723 | 97753  | 97768  | N/A  | N/A  | TCTCATTAATCAAGG   | 24 | AN | 2500 |
| 1441728 | 350507 | 350522 | N/A  | N/A  | TATTATAGGGTTGAAA  | 16 | AN | 2503 |
| 1441730 | 290653 | 290668 | 2132 | 2147 | AGGTAAGGCAATGGAC  | 3  | AN | 2504 |
| 1441735 | 82465  | 82480  | N/A  | N/A  | TGAACAATGCTGATTC  | 20 | AN | 2506 |
| 1441739 | 82461  | 82476  | N/A  | N/A  | CAATGCTGATTCAGGC  | 3  | AN | 2877 |
| 1441743 | 368428 | 368443 | N/A  | N/A  | TGATATTGTATAAGGT  | 4  | AN | 2509 |
| 1441746 | 368424 | 368439 | N/A  | N/A  | ATTGTATAAGGTTAGG  | 3  | AN | 2511 |
| 1441749 | 242390 | 242405 | N/A  | N/A  | CGTCAAGTAATGAGTT  | 15 | AN | 2512 |

|         |        |        |       |       |                   |     |    |      |
|---------|--------|--------|-------|-------|-------------------|-----|----|------|
| 1441753 | 285252 | 285267 | 1887  | 1902  | CTTTTGAATCTGTCCA  | 5   | AN | 3008 |
| 1441756 | 285187 | 285202 | 1822  | 1837  | GGTACCATTACTGAGA  | 47  | AN | 2881 |
| 1441759 | 217792 | 217807 | 758   | 773   | CTCCAGTTAACAGCGC  | 46  | AN | 2516 |
| 1441762 | 217789 | 217804 | 755   | 770   | CAGTTAACAGCGCGGT  | 15  | AN | 1241 |
| 1441765 | 217786 | 217801 | 752   | 767   | TTAACAGCGCGGTGAG  | 17  | AN | 2519 |
| 1441766 | 222236 | 222251 | 1646  | 1661  | CACTAGAATAGCCCAT  | 4   | AN | 1001 |
| 1441904 | 82198  | 82213  | N/A   | N/A   | TATTAGCTCATGGAAA  | 23  | AN | 2091 |
| 1441908 | 229160 | 229175 | N/A   | N/A   | AGTATTAACCACCATT  | 3   | AN | 2535 |
| 1441909 | 463911 | 463926 | N/A   | N/A   | TGTCAGATTTAATAGG  | 39  | AN | 2972 |
| 1441915 | 331863 | 331878 | N/A   | N/A   | TATAGTATGATAGCAC  | 4   | AN | 1607 |
| 1441918 | 331860 | 331875 | N/A   | N/A   | AGTATGATAGCACAAA  | 7   | AN | 2539 |
| 1441921 | 236802 | 236817 | N/A   | N/A   | ATTGTTATACTGATGG  | 4   | AN | 2542 |
| 1441924 | 236799 | 236814 | N/A   | N/A   | GTTATACTGATGGGCT  | 14  | AN | 2544 |
| 1441928 | 217511 | 217526 | 477   | 492   | GGCTGTAAACTTTGTT  | 11  | AN | 2816 |
| 1441931 | 217564 | 217579 | 530   | 545   | CGGAAATGATTCTGGC  | 31  | AN | 2161 |
| 1441935 | 561179 | 561194 | 10168 | 10183 | GAATTGAAGTTAGGGT  | 10  | AN | 134  |
| 1441938 | 222017 | 222032 | 1427  | 1442  | TTTCAAAGTGGGAGCT  | 48  | AN | 2548 |
| 1441360 | 288681 | 288696 | 2076  | 2091  | TATCTATTGGAGAAGT  | 3   | AO | 1013 |
| 1441363 | 288678 | 288693 | 2073  | 2088  | CTATTGGAGAAGTGTA  | 2   | AO | 936  |
| 1441365 | 217667 | 217682 | 633   | 648   | CTCTGTGTTTTACGAC  | 8   | AO | 2941 |
| 1441368 | 217664 | 217679 | 630   | 645   | TGTGTTTTACGACTGG  | 17  | AO | 858  |
| 1441371 | 217661 | 217676 | 627   | 642   | GTTTTACGACTGGCAG  | 14  | AO | 21   |
| 1441375 | 218082 | 218097 | 1048  | 1063  | TATAGGATGCTGGGTC  | 16  | AO | 100  |
| 1441378 | 218079 | 218094 | 1045  | 1060  | AGGATGCTGGGTCTCT  | 10  | AO | 397  |
| 1441382 | 235208 | 235223 | N/A   | N/A   | ACACAATTTAGCTCTA  | 3   | AO | 341  |
| 1441385 | 288675 | 288690 | 2070  | 2085  | TTGGAGAAGTGTATTA  | 4   | AO | 352  |
| 1441387 | 82207  | 82222  | N/A   | N/A   | ACTTTCAGATATTAGC  | 8   | AO | 3009 |
| 1441390 | 226034 | 226049 | N/A   | N/A   | AACCTCTGCACCTTT   | 7   | AO | 3010 |
| 1441394 | 217743 | 217758 | 709   | 724   | TTCTCCGTTGTTACT   | 18  | AO | 3011 |
| 1441397 | 217740 | 217755 | 706   | 721   | CTCCGTGTGTTACTTCA | 6   | AO | 2945 |
| 1441401 | 218105 | 218120 | 1071  | 1086  | CTTTGCAGTGATGTCT  | 5   | AO | 2861 |
| 1441404 | 218102 | 218117 | 1068  | 1083  | TGCAGTGATGTCTCAA  | 9   | AO | 2822 |
| 1441407 | 218224 | 218239 | 1190  | 1205  | GAGCTTTCCAGGATTC  | 20  | AO | 3012 |
| 1441410 | 218219 | 218234 | 1185  | 1200  | TTCCAGGATTCATCCC  | 31  | AO | 2948 |
| 1441411 | 222175 | 222190 | 1585  | 1600  | TCCCCCTGATGTCCTC  | 14  | AO | 2949 |
| 1441415 | 222149 | 222164 | 1559  | 1574  | GACCACCTTCTTTAAT  | 51  | AO | 2491 |
| 1441418 | 244766 | 244781 | 1450  | 1465  | AGGTAATTTATGAGTT  | 8   | AO | 488  |
| 1441422 | 342926 | 342941 | 1447  | 1462  | GATAATGTGAAGCTTA  | 3   | AO | 417  |
| 1441425 | 366242 | 366257 | 2003  | 2018  | CTATCATATGAAAGCC  | 5   | AO | 2476 |
| 1441429 | 181930 | 181945 | N/A   | N/A   | GCAGAATTGATAACAG  | 9   | AO | 562  |
| 1441432 | 365700 | 365715 | N/A   | N/A   | CAGTAATATTAAAGCC  | 10  | AO | 2480 |
| 1441435 | 508291 | 508306 | N/A   | N/A   | GTGATTTTAAGAGTCC  | 46  | AO | 3013 |
| 1441438 | 508286 | 508301 | N/A   | N/A   | TTTAAGAGTCCACTAG  | 115 | AO | 2482 |

|         |        |        |      |      |                  |     |    |      |
|---------|--------|--------|------|------|------------------|-----|----|------|
| 1441439 | 222040 | 222055 | N/A  | N/A  | TAAAGAAGTGTGTGCC | 2   | AO | 2483 |
| 1441442 | 222037 | 222052 | N/A  | N/A  | AGAAAGTGTGTCCAAA | 1   | AO | 2953 |
| 1441445 | 155903 | 155918 | N/A  | N/A  | AAGTTATTATATGGCT | 36  | AO | 2484 |
| 1441448 | 251926 | 251941 | N/A  | N/A  | GGTTTTAAGTTATCTC | 6   | AO | 2486 |
| 1441450 | 229866 | 229881 | N/A  | N/A  | CTCAATATTGTGTGTC | 23  | AO | 609  |
| 1441454 | N/A    | N/A    | N/A  | N/A  | AATACCTGAGTGACTG | 2   | AO | 2487 |
| 1441457 | 222160 | 222175 | 1570 | 1585 | CTCCAAGAACTGACCA | 17  | AO | 546  |
| 1441460 | 222157 | 222172 | 1567 | 1582 | CAAGAACTGACCACCT | 3   | AO | 2472 |
| 1441673 | 263008 | 263023 | N/A  | N/A  | GTGATATGAATGGTAT | 2   | AO | 1090 |
|         | 263049 | 263064 |      |      |                  |     |    |      |
| 1441677 | 218085 | 218100 | 1051 | 1066 | ATCTATAGGATGCTGG | 16  | AO | 781  |
| 1441679 | 225078 | 225093 | N/A  | N/A  | CGTGTGTATTATTGAC | 4   | AO | 363  |
| 1441682 | 225075 | 225090 | N/A  | N/A  | GTGTATTATTGACCTG | 7   | AO | 630  |
| 1441685 | 225072 | 225087 | N/A  | N/A  | TATTATTGACCTGGTA | 17  | AO | 476  |
| 1441687 | 222234 | 222249 | 1644 | 1659 | CTAGAATAGCCCATCA | 9   | AO | 848  |
| 1441690 | 222231 | 222246 | 1641 | 1656 | GAATAGCCCATCACGA | 13  | AO | 2520 |
| 1441695 | 218173 | 218188 | 1139 | 1154 | ACAAACCAGCTGATGA | 13  | AO | 2524 |
| 1441698 | 218170 | 218185 | 1136 | 1151 | AACCAGCTGATGAGAT | 8   | AO | 2525 |
| 1441703 | 263335 | 263350 | N/A  | N/A  | GTTTGAAGAATGCATG | 12  | AO | 2526 |
| 1441705 | 344740 | 344755 | N/A  | N/A  | TTAGTATCCTTCAATG | 10  | AO | 3014 |
| 1441708 | 391182 | 391197 | N/A  | N/A  | TTAGGATTAAGGAGTT | 6   | AO | 2530 |
| 1441711 | 391179 | 391194 | N/A  | N/A  | GGATTAAGGAGTTCTG | 41  | AO | 2532 |
| 1441716 | 229903 | 229918 | N/A  | N/A  | CATTAGAGGCATTGC  | 40  | AO | 737  |
| 1441721 | 97754  | 97769  | N/A  | N/A  | GTCTCATTAATCAAG  | 15  | AO | 2920 |
| 1441725 | 97751  | 97766  | N/A  | N/A  | TCATTAAATCAAGGCA | 5   | AO | 2501 |
| 1441727 | 350508 | 350523 | N/A  | N/A  | TTATTATAGGGTTGAA | 2   | AO | 2502 |
| 1441729 | 290657 | 290672 | 2136 | 2151 | GCACAGGTAAGGCAAT | 50  | AO | 784  |
| 1441732 | 290651 | 290666 | 2130 | 2145 | GTAAGGCAATGGACTC | 6   | AO | 2962 |
| 1441734 | 233649 | 233664 | N/A  | N/A  | GCTCATTAAGTTCTTC | 5   | AO | 870  |
| 1441738 | 82462  | 82477  | N/A  | N/A  | ACAATGCTGATTCAGG | 3   | AO | 2507 |
| 1441742 | 368429 | 368444 | N/A  | N/A  | GTGATATTGTATAAGG | 2   | AO | 3015 |
| 1441745 | 368425 | 368440 | N/A  | N/A  | TATTGTATAAGGTTAG | 4   | AO | 2510 |
| 1441748 | 242391 | 242406 | N/A  | N/A  | CCGTCAAGTAATGAGT | 5   | AO | 2966 |
| 1441752 | 285253 | 285268 | 1888 | 1903 | TCTTTTGAATCTGTCC | 3   | AO | 2514 |
| 1441755 | 285188 | 285203 | 1823 | 1838 | TGGTACCATTACTGAG | 45  | AO | 2515 |
| 1441758 | 285185 | 285200 | 1820 | 1835 | TACCATTACTGAGATT | 5   | AO | 616  |
| 1441761 | 217790 | 217805 | 756  | 771  | CCAGTTAACAGCGCGG | 21  | AO | 178  |
| 1441764 | 217787 | 217802 | 753  | 768  | GTTAACAGCGCGGTGA | 28  | AO | 2518 |
| 1441903 | 82200  | 82215  | N/A  | N/A  | GATATTAGCTCATGGA | 15  | AO | 223  |
| 1441905 | 218034 | 218049 | 1000 | 1015 | CACTCCTTGAAATTCC | 9   | AO | 2928 |
| 1441907 | 229161 | 229176 | N/A  | N/A  | AAGTATTAACCACCAT | 8   | AO | 1913 |
| 1441911 | 463907 | 463922 | N/A  | N/A  | AGATTTAATAGGTCTT | 116 | AO | 2536 |
| 1441912 | 184997 | 185012 | N/A  | N/A  | GTGTATTAGGTTTTTC | 10  | AO | 1840 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1441914 | 331864 | 331879 | N/A   | N/A   | CTATAGTATGATAGCA  | 23 | AO | 2537 |
| 1441917 | 331861 | 331876 | N/A   | N/A   | TAGTATGATAGCACAA  | 2  | AO | 2538 |
| 1441920 | 236803 | 236818 | N/A   | N/A   | AATTGTTATACTGATG  | 5  | AO | 2541 |
| 1441923 | 236800 | 236815 | N/A   | N/A   | TGTTATACTGATGGGC  | 5  | AO | 1304 |
| 1441926 | 236797 | 236812 | N/A   | N/A   | TATACTGATGGGCTAG  | 36 | AO | 2546 |
| 1441927 | 217512 | 217527 | 478   | 493   | GGGCTGTAACTTTGT   | 10 | AO | 3016 |
| 1441930 | 217565 | 217580 | 531   | 546   | CCGGAATGATTCTGG   | 72 | AO | 2238 |
| 1441934 | 561180 | 561195 | 10169 | 10184 | GGAATTGAAGTTAGGG  | 11 | AO | 212  |
| 1441937 | 222018 | 222033 | 1428  | 1443  | GTTTCAAACCTGGGAGC | 33 | AO | 2975 |
| 1441359 | 288682 | 288697 | 2077  | 2092  | ATATCTATTGGAGAAG  | 5  | AP | 1091 |
| 1441362 | 288679 | 288694 | 2074  | 2089  | TCTATTGGAGAAAGTGT | 4  | AP | 181  |
| 1441367 | 217665 | 217680 | 631   | 646   | CTGTGTTTTACGACTG  | 12 | AP | 2896 |
| 1441370 | 217662 | 217677 | 628   | 643   | TGTTTTACGACTGGCA  | 5  | AP | 705  |
| 1441374 | 218083 | 218098 | 1049  | 1064  | CTATAGGATGCTGGGT  | 16 | AP | 628  |
| 1441377 | 218080 | 218095 | 1046  | 1061  | TAGGATGCTGGGTCTC  | 10 | AP | 474  |
| 1441381 | 235209 | 235224 | N/A   | N/A   | TACACAATTTAGCTCT  | 3  | AP | 152  |
|         | 235282 | 235297 |       |       |                   |    |    |      |
| 1441384 | 288676 | 288691 | 2071  | 2086  | ATTGGAGAAAGTGATT  | 8  | AP | 783  |
| 1441389 | 226035 | 226050 | N/A   | N/A   | CAACCTCTTGACCTT   | 26 | AP | 2858 |
| 1441392 | 226032 | 226047 | N/A   | N/A   | CCTCTTGACCTTTCT   | 4  | AP | 3017 |
| 1441393 | 217744 | 217759 | 710   | 725   | TTCCCTCCGTTGTTAC  | 13 | AP | 2944 |
| 1441396 | 217741 | 217756 | 707   | 722   | CCTCCGTTGTTACTTC  | 6  | AP | 2601 |
| 1441399 | 217738 | 217753 | 704   | 719   | CCGTTGTTACTTCAGC  | 4  | AP | 3018 |
| 1441400 | 218106 | 218121 | 1072  | 1087  | TCTTTGCAGTGATGTC  | 4  | AP | 3019 |
| 1441403 | 218103 | 218118 | 1069  | 1084  | TGTCAGTGATGTCTCA  | 9  | AP | 2606 |
| 1441406 | 218225 | 218240 | 1191  | 1206  | GGAGCTTTCCAGGATT  | 32 | AP | 2947 |
| 1441409 | 218221 | 218236 | 1187  | 1202  | CTTCCAGGATTCATC   | 7  | AP | 2862 |
| 1441414 | 222154 | 222169 | 1564  | 1579  | GAACTGACCACCTTCT  | 24 | AP | 2490 |
| 1441417 | 244768 | 244783 | N/A   | N/A   | ATAGGTAATTTATGAG  | 14 | AP | 2492 |
| 1441421 | 342928 | 342943 | N/A   | N/A   | GAGATAATGTGAAGCT  | 5  | AP | 2494 |
| 1441424 | 366243 | 366258 | N/A   | N/A   | ACTATCATATGAAAGC  | 27 | AP | 2475 |
| 1441428 | 181931 | 181946 | N/A   | N/A   | TGCAGAATTGATAACA  | 18 | AP | 2864 |
| 1441431 | 365701 | 365716 | N/A   | N/A   | GCAGTAATATTAAAGC  | 28 | AP | 2479 |
| 1441434 | 508292 | 508307 | N/A   | N/A   | GGTGATTTTAAGAGTC  | 34 | AP | 2952 |
| 1441437 | 508287 | 508302 | N/A   | N/A   | TTTAAAGAGTCCACTA  | 69 | AP | 2481 |
| 1441441 | 222038 | 222053 | 1448  | 1463  | AAGAAGTGTTGTCCAA  | 2  | AP | 2866 |
| 1441444 | 155904 | 155919 | N/A   | N/A   | GAAGTTATTATATGGC  | 3  | AP | 530  |
| 1441447 | 155901 | 155916 | N/A   | N/A   | GTTATTATATGGCTGT  | 5  | AP | 2485 |
| 1441449 | 229868 | 229883 | N/A   | N/A   | ATCTCAATATTGTGTG  | 5  | AP | 2956 |
| 1441453 | N/A    | N/A    | 2005  | 2020  | GAAATACCTGAGTGAC  | 5  | AP | 462  |
| 1441456 | 222162 | 222177 | 1572  | 1587  | CTCTCCAAGAACTGAC  | 8  | AP | 554  |
| 1441459 | 222158 | 222173 | 1568  | 1583  | CCAAGAACTGACCACC  | 3  | AP | 2870 |
| 1441672 | 263009 | 263024 | N/A   | N/A   | AGTGATATGAATGGTA  | 1  | AP | 153  |

|         |        |        |      |      |                  |     |    |      |
|---------|--------|--------|------|------|------------------|-----|----|------|
|         | 263050 | 263065 |      |      |                  |     |    |      |
| 1441675 | 263006 | 263021 | N/A  | N/A  | GATATGAATGGTATGA | 7   | AP | 935  |
|         | 263047 | 263062 |      |      |                  |     |    |      |
| 1441676 | 218086 | 218101 | 1052 | 1067 | AATCTATAGGATGCTG | 5   | AP | 2496 |
| 1441678 | 217659 | 217674 | 625  | 640  | TTTACGACTGGCAGTG | 10  | AP | 552  |
| 1441681 | 225076 | 225091 | N/A  | N/A  | TGTGTATTATTGACCT | 8   | AP | 706  |
| 1441684 | 225073 | 225088 | N/A  | N/A  | GTATTATTGACCTGGT | 8   | AP | 229  |
| 1441686 | 222235 | 222250 | 1645 | 1660 | ACTAGAATAGCCCATC | 4   | AP | 922  |
| 1441689 | 222232 | 222247 | 1642 | 1657 | AGAATAGCCCATCACG | 11  | AP | 631  |
| 1441692 | 222229 | 222244 | 1639 | 1654 | ATAGCCCATCACGATG | 14  | AP | 2916 |
| 1441694 | 218174 | 218189 | 1140 | 1155 | CACAAACCAGCTGATG | 9   | AP | 2523 |
| 1441697 | 218171 | 218186 | 1137 | 1152 | AAACCAGCTGATGAGA | 6   | AP | 2959 |
| 1441701 | 263338 | 263353 | N/A  | N/A  | GAAGTTTGAAGAATGC | 16  | AP | 949  |
| 1441704 | 344746 | 344761 | N/A  | N/A  | CTAAATTTAGTATCCT | 2   | AP | 2527 |
| 1441707 | 391183 | 391198 | N/A  | N/A  | ATTAGGATTAAGGAGT | 7   | AP | 2529 |
| 1441710 | 391180 | 391195 | N/A  | N/A  | AGGATTAAGGAGTTCT | 59  | AP | 2531 |
| 1441715 | 229904 | 229919 | N/A  | N/A  | ACATTTAGAGGCATTG | 2   | AP | 2497 |
| 1441720 | 222043 | 222058 | 1453 | 1468 | GTATAAAGAAGTGTTG | 6   | AP | 777  |
| 1441724 | 97752  | 97767  | N/A  | N/A  | CTCATTAATCAAGGC  | 26  | AP | 747  |
| 1441726 | 350509 | 350524 | N/A  | N/A  | TTTATTATAGGGTTGA | 5   | AP | 1053 |
| 1441731 | 290652 | 290667 | 2131 | 2146 | GGTAAGGCAATGGACT | 11  | AP | 2505 |
| 1441733 | 233651 | 233666 | N/A  | N/A  | CTGCTCATTAAGTTCT | 12  | AP | 3020 |
| 1441736 | 82464  | 82479  | N/A  | N/A  | GAACAATGCTGATTCA | 62  | AP | 955  |
| 1441740 | 82460  | 82475  | N/A  | N/A  | AATGCTGATTCAGGCA | 72  | AP | 2964 |
| 1441741 | 368430 | 368445 | N/A  | N/A  | GGTGATATTGTATAAG | 4   | AP | 2508 |
| 1441744 | 368427 | 368442 | N/A  | N/A  | GATATTGTATAAGGTT | 2   | AP | 1060 |
| 1441747 | 242392 | 242407 | N/A  | N/A  | ACCGTCAAGTAATGAG | 24  | AP | 3021 |
| 1441750 | 242389 | 242404 | N/A  | N/A  | GTCAGTAATGAGTTT  | 6   | AP | 758  |
| 1441751 | 285255 | 285270 | 1890 | 1905 | GATCTTTTGAATCTGT | 9   | AP | 2513 |
| 1441754 | 285251 | 285266 | 1886 | 1901 | TTTTGAATCTGTCCAG | 5   | AP | 2968 |
| 1441757 | 285186 | 285201 | 1821 | 1836 | GTACCATTACTGAGAT | 14  | AP | 2969 |
| 1441760 | 217791 | 217806 | 757  | 772  | TCCAGTTAACAGCGCG | 37  | AP | 2600 |
| 1441763 | 217788 | 217803 | 754  | 769  | AGTTAACAGCGCGGTG | 16  | AP | 2517 |
| 1441901 | 218077 | 218092 | 1043 | 1058 | GATGCTGGGTCTCTCT | 14  | AP | 381  |
| 1441902 | 82201  | 82216  | N/A  | N/A  | AGATATTAGCTCATGG | 6   | AP | 2246 |
| 1441906 | 229163 | 229178 | N/A  | N/A  | TAAAGTATTAACCACC | 2   | AP | 1964 |
| 1441910 | 463910 | 463925 | N/A  | N/A  | GTCAGATTTAATAGGT | 28  | AP | 2929 |
| 1441913 | 331865 | 331880 | N/A  | N/A  | ACTATAGTATGATAGC | 124 | AP | 1644 |
| 1441916 | 331862 | 331877 | N/A  | N/A  | ATAGTATGATAGCACA | 2   | AP | 1533 |
| 1441919 | 331859 | 331874 | N/A  | N/A  | GTATGATAGCACAAAC | 5   | AP | 2540 |
| 1441922 | 236801 | 236816 | N/A  | N/A  | TTGTTATACTGATGGG | 6   | AP | 2543 |
| 1441925 | 236798 | 236813 | N/A  | N/A  | TTATACTGATGGGCTA | 25  | AP | 2545 |
| 1441929 | 217510 | 217525 | 476  | 491  | GCTGTAAACTTTGTTC | 23  | AP | 2547 |

|         |        |        |       |       |                   |    |    |      |
|---------|--------|--------|-------|-------|-------------------|----|----|------|
| 1441932 | 217563 | 217578 | 529   | 544   | GGAAATGATTCTGGCT  | 13 | AP | 2973 |
| 1441933 | 561183 | 561198 | 10172 | 10187 | TCAGGAATTGAAGTTA  | 9  | AP | 2974 |
| 1441936 | 222019 | 222034 | 1429  | 1444  | GGTTTCAAACCTGGGAG | 16 | AP | 3022 |
| 1441939 | 222013 | 222028 | 1423  | 1438  | AAACTGGGAGCTGTAC  | 13 | AV | 2534 |
| 1442008 | 217669 | 217684 | 635   | 650   | CTCTCTGTGTTTTACG  | 5  | AV | 2935 |
| 1442009 | 217668 | 217683 | 634   | 649   | TCTCTGTGTTTTACGA  | 7  | AV | 3029 |
| 1442010 | 217658 | 217673 | 624   | 639   | TTACGACTGGCAGTGT  | 10 | AV | 475  |
| 1442011 | 218076 | 218091 | 1042  | 1057  | ATGCTGGGTCTCTCTC  | 13 | AV | 3023 |
| 1442012 | 235212 | 235227 | N/A   | N/A   | TTATACACAATTTAGC  | 3  | AV | 334  |
|         | 235285 | 235300 |       |       |                   |    |    |      |
| 1442013 | 226037 | 226052 | N/A   | N/A   | CCCAACCTCTTGACC   | 72 | AV | 2549 |
| 1442014 | 217746 | 217761 | 712   | 727   | ACTTTCCTCCGTTGTT  | 26 | AV | 3024 |
| 1442016 | 217736 | 217751 | 702   | 717   | GTTGTACTTCAGCTG   | 17 | AV | 3025 |
| 1442017 | 218108 | 218123 | 1074  | 1089  | GTTCTTTGCAGTGATG  | 9  | AV | 3026 |
| 1442018 | 218098 | 218113 | 1064  | 1079  | GTGATGTCTCAAAATC  | 13 | AV | 3027 |
| 1442019 | 218217 | 218232 | 1183  | 1198  | CCAGGATTCATCCCAA  | 16 | AV | 2936 |
| 1442020 | 222177 | 222192 | 1587  | 1602  | CCTCCCCCTGATGTCC  | 29 | AV | 2893 |
| 1442021 | 222147 | 222162 | 1557  | 1572  | CCACCTTCTTTAATGC  | 11 | AV | 347  |
| 1442022 | 342921 | 342936 | N/A   | N/A   | TGTGAAGCTTAGAACC  | 15 | AV | 2937 |
| 1442023 | 508284 | 508299 | N/A   | N/A   | TAAGAGTCCACTAGCC  | 57 | AV | 2550 |
| 1442024 | 181922 | 181937 | N/A   | N/A   | GATAACAGGTAAATTA  | 62 | AV | 2894 |
| 1442025 | 244760 | 244775 | N/A   | N/A   | TTTATGAGTTAAAGGG  | 26 | AV | 2447 |
| 1442026 | 229860 | 229875 | N/A   | N/A   | ATTGTGTGTCTCAGGC  | 9  | AV | 3028 |
| 1442027 | 285147 | 285162 | 1782  | 1797  | ATTTCAGTGCTCCCCA  | 5  | AV | 2980 |
| 1442028 | 285466 | 285481 | 2000  | 2015  | ACCTGAGTGACTGATC  | 7  | AV | 2981 |
| 1442075 | 263003 | 263018 | N/A   | N/A   | ATGAATGGTATGATGG  | 12 | AV | 2553 |
| 1442076 | 217657 | 217672 | 623   | 638   | TACGACTGGCAGTGTC  | 16 | AV | 2982 |
| 1442077 | 225070 | 225085 | N/A   | N/A   | TTATTGACCTGGTAAA  | 52 | AV | 2400 |
| 1442078 | 222237 | 222252 | 1647  | 1662  | CCACTAGAATAGCCCA  | 6  | AV | 2551 |
| 1442079 | 222227 | 222242 | 1637  | 1652  | AGCCCATCACGATGCC  | 53 | AV | 2984 |
| 1442080 | 326723 | 326738 | N/A   | N/A   | GATTATGAGGAAACCT  | 8  | AV | 2552 |
| 1442081 | 263333 | 263348 | N/A   | N/A   | TTGAAGAATGCATGTC  | 10 | AV | 2554 |
| 1442082 | 344738 | 344753 | N/A   | N/A   | AGTATCCTTCAATGGC  | 15 | AV | 3030 |
| 1442083 | 391186 | 391201 | N/A   | N/A   | TTAATTAGGATTAAGG  | 88 | AV | 2555 |
| 1442084 | 391176 | 391191 | N/A   | N/A   | TTAAGGAGTTCTGTGT  | 9  | AV | 2556 |
| 1442086 | 229900 | 229915 | N/A   | N/A   | TTAGAGGCATTGCAGG  | 21 | AV | 2557 |
| 1442087 | 222051 | 222066 | 1461  | 1476  | GCACTGTAGTATAAAG  | 5  | AV | 3031 |
| 1442088 | 97747  | 97762  | N/A   | N/A   | TAAATCAAGGCAAGTG  | 13 | AV | 3034 |
| 1442089 | 350504 | 350519 | N/A   | N/A   | TATAGGGTTGAAAATA  | 60 | AV | 2558 |
| 1442090 | 290659 | 290674 | 2138  | 2153  | TTGCACAGGTAAGGCA  | 56 | AV | 2622 |
| 1442091 | 290649 | 290664 | 2128  | 2143  | AAGGCAATGGACTCCA  | 6  | AV | 2837 |
| 1442092 | 233653 | 233668 | N/A   | N/A   | AGCTGCTCATTAAGTT  | 99 | AV | 2989 |
| 1442093 | 82458  | 82473  | N/A   | N/A   | TGCTGATTCAGGCAGT  | 74 | AV | 2990 |

|         |        |        |      |      |                   |    |    |      |
|---------|--------|--------|------|------|-------------------|----|----|------|
| 1442094 | 368422 | 368437 | N/A  | N/A  | TGTATAAGGTTAGGTG  | 3  | AV | 2559 |
| 1442095 | 242394 | 242409 | N/A  | N/A  | GTACCGTCAAGTAATG  | 61 | AV | 2992 |
| 1442096 | 285249 | 285264 | 1884 | 1899 | TTGAATCTGTCCAGCT  | 10 | AV | 2993 |
| 1442097 | 217794 | 217809 | 760  | 775  | GTCTCCAGTTAACAGC  | 35 | AV | 2994 |
| 1442098 | 217784 | 217799 | 750  | 765  | AACAGCGCGGTGAGAT  | 19 | AV | 2995 |
| 1442099 | 222238 | 222253 | 1648 | 1663 | GCCACTAGAATAGCCC  | 62 | AV | 2560 |
| 1442100 | 222228 | 222243 | 1638 | 1653 | TAGCCCATCACGATGC  | 22 | AV | 2996 |
| 1442134 | 82196  | 82211  | N/A  | N/A  | TTAGCTCATGGAAAGC  | 38 | AV | 2997 |
| 1442135 | 229158 | 229173 | N/A  | N/A  | TATTAACCACCATTCC  | 43 | AV | 2561 |
| 1442136 | 185002 | 185017 | N/A  | N/A  | GCACTGTGTATTAGGT  | 9  | AV | 3032 |
| 1442137 | 331857 | 331872 | N/A  | N/A  | ATGATAGCACAAACCA  | 4  | AV | 3033 |
| 1442138 | 236795 | 236810 | N/A  | N/A  | TACTGATGGGCTAGCC  | 84 | AV | 2562 |
| 1442139 | 217514 | 217529 | 480  | 495  | ATGGGCTGTAAACTTT  | 8  | AV | 3000 |
| 1442140 | 217513 | 217528 | 479  | 494  | TGGGCTGTAAACTTTG  | 11 | AV | 3001 |
| 1442141 | 217567 | 217582 | 533  | 548  | TTCCGGAATGATTCT   | 16 | AV | 2563 |
| 1442142 | 222021 | 222036 | 1431 | 1446 | ATGGTTTCAAACCTGGG | 9  | AV | 2564 |

#### Example 2: Dose-dependent inhibition of human PSD3 in A431 cells by modified oligonucleotides

Modified oligonucleotides selected from the example above were tested at various doses in A431 cells. Cells plated at a density of 10,000 cells per well were treated using free uptake with various concentrations of modified oligonucleotide as specified in the tables below. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and PSD3 RNA levels were measured by quantitative real-time RT-PCR. Either human PSD3 primer-probe set RTS41429 (described herein above) or human PSD3 primer-probe set RTS41435 (described herein above) as specified in the tables below were used to measure RNA levels. PSD3 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of PSD3 RNA is presented in the tables below as percent PSD3 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC<sub>50</sub>) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in Excel and is also presented in the tables below.

“N.C.” in the table below refers to instances where the value was Not Calculated.

**Table 6.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41429 |        |         |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|--------|---------|---------|-----------------------|
|              | 78 nM                     | 313 nM | 1250 nM | 5000 nM |                       |
| 1173386      | 37                        | 33     | 32      | 40      | N.C.                  |
| 1173390      | 51                        | 44     | 49      | 56      | N.C.                  |
| 1173391      | 43                        | 36     | 31      | 34      | <0.08                 |
| 1173396      | 40                        | 30     | 26      | 22      | <0.08                 |
| 1173403      | 12                        | 5      | 2       | 2       | <0.08                 |
| 1173404      | 19                        | 7      | 3       | 2       | <0.08                 |

|         |    |    |    |    |       |
|---------|----|----|----|----|-------|
| 1173405 | 49 | 25 | 13 | 5  | <0.08 |
| 1173406 | 59 | 45 | 26 | 19 | 0.17  |
| 1173570 | 29 | 20 | 17 | 18 | <0.08 |
| 1173586 | 52 | 36 | 24 | 21 | <0.08 |
| 1173588 | 72 | 48 | 42 | 45 | 0.80  |
| 1173589 | 91 | 65 | 45 | 32 | 1.11  |
| 1173594 | 32 | 23 | 19 | 18 | <0.08 |
| 1173595 | 64 | 43 | 30 | 24 | 0.23  |
| 1173597 | 41 | 23 | 18 | 25 | <0.08 |
| 1173598 | 48 | 29 | 22 | 20 | <0.08 |
| 1173599 | 39 | 26 | 20 | 22 | <0.08 |
| 1173601 | 28 | 20 | 18 | 26 | <0.08 |
| 1173603 | 57 | 40 | 27 | 21 | 0.13  |

**Table 7.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |        |         |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|--------|---------|---------|-----------------------|
|              | 78 nM                     | 313 nM | 1250 nM | 5000 nM |                       |
| 1173386      | 13                        | 14     | 12      | 10      | <0.08                 |
| 1173390      | 25                        | 21     | 21      | 17      | <0.08                 |
| 1173391      | 20                        | 14     | 13      | 15      | <0.08                 |
| 1173396      | 22                        | 13     | 12      | 10      | <0.08                 |
| 1173403      | 15                        | 8      | 7       | 8       | <0.08                 |
| 1173404      | 25                        | 10     | 9       | 8       | <0.08                 |
| 1173405      | 83                        | 44     | 22      | 14      | 0.36                  |
| 1173406      | 89                        | 66     | 44      | 33      | 1.13                  |
| 1173570      | 24                        | 13     | 11      | 15      | <0.08                 |
| 1173586      | 56                        | 22     | 12      | 11      | <0.08                 |
| 1173588      | 55                        | 46     | 30      | 17      | 0.16                  |
| 1173589      | 81                        | 57     | 27      | 13      | 0.46                  |
| 1173594      | 16                        | 13     | 10      | 8       | <0.08                 |
| 1173595      | 63                        | 37     | 21      | 16      | 0.15                  |
| 1173597      | 34                        | 11     | 7       | 5       | <0.08                 |
| 1173598      | 61                        | 26     | 13      | 10      | 0.09                  |
| 1173599      | 34                        | 14     | 9       | 7       | <0.08                 |
| 1173601      | 20                        | 9      | 6       | 5       | <0.08                 |
| 1173603      | 53                        | 33     | 19      | 11      | 0.08                  |

**Table 8.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 89                        | 44    | 23     | 7      | 8       | 0.04                  |
| 1408277      | 72                        | 36    | 17     | 16     | 15      | 0.02                  |
| 1408278      | 92                        | 28    | 14     | 9      | 9       | 0.03                  |
| 1408291      | 71                        | 70    | 27     | 15     | 8       | 0.05                  |
| 1408294      | 80                        | 60    | 29     | 13     | 10      | 0.05                  |
| 1408299      | 70                        | 48    | 26     | 13     | 8       | 0.03                  |
| 1408400      | 68                        | 63    | 23     | 17     | 13      | 0.04                  |
| 1408456      | 73                        | 57    | 44     | 17     | 10      | 0.05                  |
| 1408461      | 95                        | 77    | 54     | 31     | 31      | 0.23                  |
| 1408747      | 66                        | 34    | 16     | 16     | 11      | 0.01                  |
| 1408751      | 77                        | 46    | 21     | 15     | 9       | 0.03                  |
| 1408767      | 71                        | 33    | 26     | 14     | 14      | 0.02                  |
| 1408797      | 89                        | 60    | 35     | 30     | 22      | 0.10                  |
| 1408808      | 96                        | 121   | 50     | 20     | 16      | 0.22                  |
| 1408819      | 121                       | 43    | 24     | 10     | 12      | 0.08                  |

**Table 9.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 60                        | 40    | 15     | 8      | 7       | 0.01                  |
| 1408267      | 68                        | 26    | 24     | 12     | 16      | 0.01                  |
| 1408407      | 117                       | 41    | 25     | 9      | 6       | 0.07                  |
| 1408412      | 74                        | 77    | 69     | 39     | 21      | 0.23                  |
| 1408437      | 102                       | 69    | 27     | 9      | 1       | 0.08                  |
| 1408441      | 127                       | 68    | 41     | 12     | N.C.    | 0.09                  |
| 1408473      | 71                        | 72    | 36     | 20     | 11      | 0.07                  |
| 1408497      | 90                        | 54    | 30     | 21     | 16      | 0.07                  |
| 1408510      | 74                        | 73    | 63     | 37     | 19      | 0.17                  |
| 1408521      | 99                        | 76    | 41     | 26     | 18      | 0.14                  |
| 1408759      | 72                        | 56    | 27     | 20     | 18      | 0.04                  |
| 1408814      | 63                        | 35    | 24     | 22     | 12      | 0.01                  |
| 1408815      | 92                        | 48    | 18     | 10     | 9       | 0.05                  |
| 1408859      | 137                       | 64    | 44     | 26     | 12      | 0.17                  |
| 1408876      | 82                        | 62    | 25     | 22     | 10      | 0.06                  |

**Table 10.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 68                        | 26    | 14     | 6      | 6       | 0.01                  |
| 1173404      | 106                       | 40    | 14     | 8      | 5       | 0.05                  |
| 1408266      | 51                        | 21    | 10     | 8      | 6       | <0.008                |
| 1408357      | 100                       | 61    | 20     | 6      | 5       | 0.06                  |
| 1408360      | 86                        | 50    | 19     | 8      | 5       | 0.04                  |
| 1408370      | 66                        | 28    | 6      | 3      | 4       | 0.01                  |
| 1408372      | 93                        | 42    | 17     | 9      | 6       | 0.04                  |
| 1408449      | 73                        | 66    | 46     | 14     | 4       | 0.06                  |
| 1408757      | 66                        | 54    | 27     | 8      | 6       | 0.03                  |
| 1408789      | 57                        | 41    | 18     | 10     | 9       | 0.01                  |
| 1408794      | 50                        | 43    | 11     | 12     | 9       | 0.01                  |
| 1408805      | 93                        | 66    | 32     | 11     | 7       | 0.08                  |
| 1408809      | 76                        | 53    | 27     | 17     | 10      | 0.04                  |
| 1408813      | 62                        | 35    | 14     | 6      | 5       | 0.01                  |
| 1408858      | 63                        | 55    | 23     | 11     | 7       | 0.03                  |

**Table 11.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |       |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|-------|--------|---------|-----------------------|
|              | 3 nM                      | 16 nM | 80 nM | 400 nM | 2000 nM |                       |
| 1173403      | 95                        | 40    | 12    | 4      | 4       | 0.02                  |
| 1408296      | 59                        | 34    | 11    | 8      | 5       | 0.003                 |
| 1408356      | 78                        | 58    | 32    | 11     | 4       | 0.03                  |
| 1408361      | 61                        | 41    | 18    | 6      | 4       | 0.01                  |
| 1408365      | 59                        | 23    | 10    | 5      | 5       | <0.003                |
| 1408366      | 81                        | 46    | 22    | 12     | 6       | 0.02                  |
| 1408375      | 61                        | 39    | 16    | 6      | 4       | 0.01                  |
| 1408383      | 55                        | 46    | 10    | 3      | 4       | 0.004                 |
| 1409326      | 60                        | 41    | 13    | 4      | 5       | 0.01                  |
| 1409614      | 79                        | 60    | 22    | 10     | 4       | 0.02                  |
| 1410093      | 73                        | 51    | 14    | 5      | 3       | 0.01                  |
| 1410193      | 67                        | 46    | 33    | 16     | 6       | 0.01                  |
| 1410297      | 74                        | 46    | 13    | 4      | 3       | 0.01                  |
| 1411145      | 86                        | 23    | 7     | 3      | 4       | 0.01                  |
| 1411362      | 94                        | 70    | 15    | 7      | 6       | 0.04                  |

**Table 12.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 74                        | 34    | 7      | 6      | 6       | 0.02                  |
| 1408704      | 87                        | 52    | 30     | 17     | 7       | 0.06                  |
| 1409345      | 64                        | 50    | 24     | 16     | 5       | 0.02                  |
| 1409495      | 50                        | 25    | 12     | 7      | 9       | <0.008                |
| 1409923      | 86                        | 58    | 26     | 13     | 7       | 0.06                  |
| 1409946      | 65                        | 48    | 19     | 5      | 5       | 0.02                  |
| 1410071      | 60                        | 18    | 6      | 5      | 5       | <0.008                |
| 1410215      | 63                        | 68    | 36     | 10     | 6       | 0.04                  |
| 1410225      | 70                        | 60    | 16     | 4      | 1       | 0.03                  |
| 1410233      | 45                        | 14    | 5      | 4      | 4       | <0.008                |
| 1410352      | 82                        | 43    | 8      | 5      | 2       | 0.03                  |
| 1410363      | 84                        | 40    | 16     | 3      | 4       | 0.03                  |
| 1410436      | 62                        | 28    | 21     | 9      | 5       | 0.01                  |
| 1411113      | 50                        | 34    | 16     | 8      | 6       | <0.008                |
| 1411146      | 51                        | 49    | 26     | 11     | 12      | 0.01                  |

**Table 13.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 79                        | 32    | 14     | 5      | 5       | 0.02                  |
| 1408328      | 86                        | 56    | 26     | 11     | 6       | 0.05                  |
| 1408344      | 57                        | 32    | 10     | 5      | 4       | <0.008                |
| 1409091      | 74                        | 34    | 12     | 4      | 4       | 0.02                  |
| 1409215      | 62                        | 45    | 28     | 9      | 4       | 0.02                  |
| 1409384      | 59                        | 65    | 20     | 7      | 4       | 0.03                  |
| 1409393      | 92                        | 32    | 26     | 4      | 3       | 0.04                  |
| 1409953      | 79                        | 62    | 31     | 13     | 10      | 0.06                  |
| 1410129      | 91                        | 80    | 37     | 12     | 3       | 0.09                  |
| 1410391      | 100                       | 61    | 24     | 12     | 8       | 0.07                  |
| 1410423      | 56                        | 21    | 8      | 4      | 5       | <0.008                |
| 1410497      | 58                        | 48    | 22     | 10     | 6       | 0.02                  |
| 1411157      | 71                        | 29    | 12     | 7      | 5       | 0.01                  |
| 1411192      | 68                        | 62    | 23     | 11     | 6       | 0.04                  |
| 1411386      | 48                        | 47    | 18     | 10     | 6       | 0.008                 |

**Table 14.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 98                        | 44    | 12     | 8      | 6       | 0.04                  |
| 1408286      | 48                        | 31    | 12     | 7      | 7       | <0.008                |
| 1408304      | 48                        | 39    | 8      | 4      | 4       | <0.008                |
| 1408342      | 65                        | 56    | 26     | 10     | 5       | 0.03                  |
| 1408343      | 55                        | 37    | 12     | 3      | 3       | <0.008                |
| 1408415      | 63                        | 45    | 19     | 11     | 6       | 0.02                  |
| 1409194      | 83                        | 52    | 29     | 9      | 5       | 0.05                  |
| 1409255      | 80                        | 86    | 32     | 17     | 7       | 0.09                  |
| 1409396      | 81                        | 84    | 35     | 14     | 6       | 0.09                  |
| 1409418      | 104                       | 79    | 26     | 7      | 4       | 0.09                  |
| 1409420      | 58                        | 38    | 15     | 6      | 4       | 0.01                  |
| 1409457      | 94                        | 72    | 41     | 14     | 5       | 0.09                  |
| 1409827      | 134                       | 54    | 27     | 8      | 6       | 0.10                  |
| 1410063      | 74                        | 28    | 8      | 3      | 2       | 0.01                  |
| 1410348      | 77                        | 52    | 18     | 8      | 4       | 0.03                  |

**Table 15.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 79                        | 24    | 10     | 5      | 4       | 0.02                  |
| 1408282      | 79                        | 39    | 11     | 9      | 6       | 0.02                  |
| 1408292      | 44                        | 10    | 4      | 3      | 4       | <0.008                |
| 1408308      | 80                        | 74    | 38     | 16     | 6       | 0.08                  |
| 1409419      | 55                        | 61    | 28     | 13     | 5       | 0.02                  |
| 1409469      | 57                        | 45    | 21     | 7      | 4       | 0.01                  |
| 1409636      | 61                        | 32    | 11     | 6      | 4       | 0.01                  |
| 1409945      | 134                       | 72    | 23     | 14     | 8       | 0.13                  |
| 1409970      | 55                        | 47    | 31     | 12     | 6       | 0.02                  |
| 1410113      | 123                       | 85    | 46     | 23     | 10      | 0.18                  |
| 1410131      | 48                        | 33    | 14     | 8      | 3       | <0.008                |
| 1410142      | 86                        | 34    | 19     | 4      | 4       | 0.03                  |
| 1410176      | 114                       | 37    | 18     | 8      | 5       | 0.06                  |
| 1410506      | 68                        | 68    | 16     | 4      | 1       | 0.03                  |
| 1411403      | 59                        | 52    | 22     | 10     | 6       | 0.02                  |

**Table 16.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 84                        | 59    | 23     | 11     | 10      | 0.05                  |
| 1408242      | 98                        | 49    | 18     | 13     | 10      | 0.06                  |
| 1408259      | 81                        | 61    | 32     | 11     | 6       | 0.06                  |
| 1408633      | 84                        | 62    | 34     | 15     | 10      | 0.07                  |
| 1409097      | 86                        | 83    | 46     | 21     | 9       | 0.12                  |
| 1409293      | 100                       | 51    | 21     | 12     | 8       | 0.06                  |
| 1409302      | 101                       | 85    | 44     | 22     | 11      | 0.15                  |
| 1409833      | 107                       | 81    | 62     | 18     | 7       | 0.16                  |
| 1409922      | 136                       | 101   | 45     | 22     | 13      | 0.22                  |
| 1409940      | 93                        | 100   | 39     | 19     | 8       | 0.14                  |
| 1410181      | 90                        | 62    | 34     | 15     | 13      | 0.08                  |
| 1410211      | 79                        | 89    | 25     | 12     | 8       | 0.08                  |
| 1410341      | 110                       | 74    | 49     | 14     | 7       | 0.13                  |
| 1410521      | 105                       | 70    | 62     | 17     | 11      | 0.15                  |
| 1411118      | 77                        | 74    | 32     | 19     | 11      | 0.07                  |

**Table 17.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 85                        | 48    | 17     | 5      | 7       | 0.04                  |
| 1408305      | 82                        | 54    | 24     | 8      | 5       | 0.04                  |
| 1408306      | 67                        | 43    | 11     | 6      | 4       | 0.02                  |
| 1408414      | 79                        | 54    | 28     | 13     | 8       | 0.04                  |
| 1408632      | 74                        | 65    | 35     | 13     | 6       | 0.05                  |
| 1409264      | 72                        | 54    | 20     | 6      | 6       | 0.03                  |
| 1409534      | 92                        | 79    | 25     | 16     | 9       | 0.09                  |
| 1409824      | 73                        | 38    | 14     | 7      | 5       | 0.02                  |
| 1409883      | 79                        | 62    | 23     | 10     | 6       | 0.05                  |
| 1409977      | 69                        | 24    | 7      | 3      | 3       | 0.01                  |
| 1410167      | 84                        | 69    | 36     | 10     | 4       | 0.07                  |
| 1410220      | 102                       | 84    | 39     | 18     | 10      | 0.13                  |
| 1410390      | 85                        | 64    | 25     | 10     | 6       | 0.06                  |
| 1411136      | 88                        | 67    | 56     | 16     | 8       | 0.10                  |
| 1411395      | 79                        | 75    | 26     | 12     | 11      | 0.07                  |

**Table 18.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |       |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|-------|--------|---------|-----------------------|
|              | 3 nM                      | 16 nM | 80 nM | 400 nM | 2000 nM |                       |
| 1173403      | 87                        | 42    | 9     | 6      | 6       | 0.02                  |
| 1408257      | 112                       | 49    | 15    | 5      | 4       | 0.04                  |
| 1408258      | 97                        | 96    | 57    | 19     | 9       | 0.12                  |
| 1408774      | 77                        | 45    | 19    | 10     | 8       | 0.02                  |
| 1408780      | 95                        | 57    | 22    | 12     | 7       | 0.04                  |
| 1408781      | 86                        | 52    | 20    | 9      | 5       | 0.02                  |
| 1409410      | 109                       | 80    | 47    | 17     | 7       | 0.09                  |
| 1409519      | 88                        | 80    | 56    | 22     | 10      | 0.09                  |
| 1410042      | 104                       | 83    | 52    | 16     | 6       | 0.09                  |
| 1410119      | 96                        | 73    | 26    | 7      | 6       | 0.05                  |
| 1410156      | 95                        | 43    | 9     | 5      | 4       | 0.02                  |
| 1410248      | 88                        | 68    | 16    | 7      | 4       | 0.03                  |
| 1410456      | 105                       | 100   | 47    | 14     | 4       | 0.10                  |
| 1410458      | 81                        | 67    | 27    | 9      | 4       | 0.03                  |
| 1410546      | 107                       | 75    | 34    | 12     | 5       | 0.07                  |

**Table 19.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 91                        | 57    | 14     | 4      | 5       | 0.05                  |
| 1408256      | 91                        | 53    | 16     | 4      | 2       | 0.05                  |
| 1408309      | 96                        | 86    | 48     | 22     | 8       | 0.14                  |
| 1408605      | 92                        | 61    | 20     | 7      | 5       | 0.06                  |
| 1408630      | 123                       | 75    | 55     | 18     | 6       | 0.16                  |
| 1408766      | 94                        | 60    | 20     | 7      | 5       | 0.06                  |
| 1409295      | 657                       | 74    | 34     | 11     | 9       | 0.37                  |
| 1409374      | 98                        | 79    | 44     | 16     | 8       | 0.12                  |
| 1409684      | 99                        | 61    | 31     | 14     | 8       | 0.08                  |
| 1409814      | 88                        | 76    | 41     | 17     | 7       | 0.10                  |
| 1409930      | 122                       | 98    | 35     | 18     | 12      | 0.17                  |
| 1410024      | 97                        | 70    | 41     | 16     | 9       | 0.10                  |
| 1410152      | 87                        | 57    | 19     | 8      | 4       | 0.05                  |
| 1410575      | 90                        | 88    | 35     | 12     | 5       | 0.10                  |
| 1411317      | 92                        | 55    | 19     | 11     | 6       | 0.05                  |

**Table 20.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 83                        | 40    | 12     | 6      | 7       | 0.03                  |
| 1408255      | 98                        | 70    | 27     | 8      | 6       | 0.08                  |
| 1408312      | 89                        | 79    | 37     | 16     | 8       | 0.10                  |
| 1409092      | 65                        | 22    | 5      | 6      | 8       | 0.01                  |
| 1409299      | 94                        | 53    | 19     | 8      | 6       | 0.05                  |
| 1409381      | 99                        | 92    | 50     | 19     | 9       | 0.15                  |
| 1409405      | 94                        | 77    | 31     | 13     | 7       | 0.09                  |
| 1410036      | 94                        | 79    | 36     | 10     | 3       | 0.09                  |
| 1410041      | 90                        | 63    | 22     | 13     | 9       | 0.06                  |
| 1410069      | 99                        | 71    | 33     | 13     | 9       | 0.09                  |
| 1410101      | 90                        | 74    | 33     | 13     | 8       | 0.08                  |
| 1410509      | 99                        | 76    | 42     | 17     | 8       | 0.11                  |
| 1410545      | 92                        | 45    | 12     | 7      | 7       | 0.04                  |
| 1410560      | 86                        | 56    | 29     | 15     | 11      | 0.06                  |
| 1411095      | 82                        | 44    | 17     | 10     | 7       | 0.03                  |

**Table 21.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 75                        | 39    | 11     | 7      | 7       | 0.02                  |
| 1408560      | 95                        | 88    | 51     | 28     | 16      | 0.18                  |
| 1409113      | 102                       | 93    | 62     | 29     | 17      | 0.23                  |
| 1409394      | 92                        | 76    | 38     | 21     | 13      | 0.11                  |
| 1409412      | 99                        | 73    | 52     | 25     | 13      | 0.14                  |
| 1409450      | 92                        | 83    | 56     | 23     | 14      | 0.16                  |
| 1409465      | 90                        | 75    | 51     | 22     | 9       | 0.12                  |
| 1409500      | 94                        | 70    | 36     | 14     | 8       | 0.09                  |
| 1410016      | 85                        | 71    | 32     | 13     | 9       | 0.07                  |
| 1410155      | 89                        | 81    | 38     | 16     | 8       | 0.10                  |
| 1410169      | 80                        | 43    | 14     | 6      | 6       | 0.03                  |
| 1410190      | 104                       | 88    | 57     | 27     | 13      | 0.19                  |
| 1410242      | 93                        | 75    | 48     | 17     | 8       | 0.11                  |
| 1410339      | 89                        | 74    | 38     | 17     | 11      | 0.10                  |
| 1411127      | 70                        | 38    | 14     | 10     | 7       | 0.02                  |

**Table 22.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 85                        | 45    | 12     | 6      | 6       | 0.03                  |
| 1408248      | 78                        | 40    | 12     | 6      | 5       | 0.02                  |
| 1408625      | 97                        | 61    | 23     | 11     | 7       | 0.07                  |
| 1409278      | 82                        | 59    | 23     | 10     | 6       | 0.05                  |
| 1409375      | 88                        | 71    | 34     | 13     | 6       | 0.08                  |
| 1409473      | 83                        | 52    | 17     | 7      | 5       | 0.04                  |
| 1409481      | 78                        | 52    | 17     | 8      | 4       | 0.03                  |
| 1409859      | 72                        | 51    | 17     | 6      | 3       | 0.03                  |
| 1409909      | 105                       | 78    | 39     | 15     | 7       | 0.12                  |
| 1410141      | 92                        | 63    | 21     | 6      | 4       | 0.06                  |
| 1410195      | 79                        | 58    | 21     | 10     | 6       | 0.04                  |
| 1410405      | 93                        | 66    | 34     | 13     | 7       | 0.08                  |
| 1410533      | 77                        | 43    | 9      | 4      | 4       | 0.02                  |
| 1411117      | 71                        | 37    | 17     | 13     | 9       | 0.02                  |
| 1411379      | 82                        | 66    | 25     | 10     | 7       | 0.06                  |

**Table 23.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 88                        | 46    | 13     | 6      | 6       | 0.04                  |
| 1408331      | 83                        | 58    | 27     | 10     | 5       | 0.05                  |
| 1409147      | 85                        | 43    | 12     | 5      | 4       | 0.03                  |
| 1409207      | 82                        | 50    | 19     | 7      | 4       | 0.04                  |
| 1409391      | 85                        | 60    | 22     | 8      | 4       | 0.05                  |
| 1409408      | 89                        | 62    | 31     | 12     | 5       | 0.06                  |
| 1409546      | 96                        | 59    | 21     | 8      | 4       | 0.06                  |
| 1409751      | 97                        | 75    | 40     | 14     | 6       | 0.10                  |
| 1409881      | 92                        | 75    | 40     | 15     | 10      | 0.10                  |
| 1409906      | 86                        | 53    | 18     | 7      | 6       | 0.04                  |
| 1410066      | 85                        | 72    | 44     | 16     | 8       | 0.09                  |
| 1410087      | 95                        | 58    | 21     | 8      | 5       | 0.06                  |
| 1410556      | 90                        | 80    | 44     | 16     | 6       | 0.11                  |
| 1411195      | 94                        | 62    | 33     | 15     | 10      | 0.08                  |
| 1411204      | 78                        | 34    | 15     | 12     | 11      | 0.02                  |

**Table 24.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 79                        | 45    | 13     | 6      | 7       | 0.03                  |
| 1408573      | 90                        | 55    | 20     | 9      | 7       | 0.05                  |
| 1409305      | 95                        | 78    | 44     | 18     | 11      | 0.12                  |
| 1409336      | 95                        | 89    | 60     | 25     | 11      | 0.18                  |
| 1409342      | 89                        | 67    | 33     | 14     | 7       | 0.08                  |
| 1409668      | 83                        | 52    | 20     | 8      | 5       | 0.04                  |
| 1409767      | 78                        | 48    | 16     | 8      | 8       | 0.03                  |
| 1409854      | 86                        | 48    | 19     | 6      | 6       | 0.04                  |
| 1410028      | 95                        | 85    | 50     | 25     | 13      | 0.16                  |
| 1410116      | 98                        | 72    | 38     | 16     | 7       | 0.10                  |
| 1410139      | 86                        | 58    | 22     | 8      | 6       | 0.05                  |
| 1410201      | 102                       | 79    | 52     | 30     | 15      | 0.18                  |
| 1411251      | 92                        | 68    | 33     | 17     | 12      | 0.09                  |
| 1411302      | 87                        | 52    | 22     | 11     | 9       | 0.05                  |
| 1411443      | 71                        | 43    | 25     | 17     | 13      | 0.03                  |

**Table 25.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 86                        | 48    | 12     | 7      | 7       | 0.04                  |
| 1408325      | 82                        | 54    | 18     | 7      | 5       | 0.04                  |
| 1408326      | 95                        | 83    | 53     | 25     | 12      | 0.16                  |
| 1409179      | 95                        | 86    | 41     | 18     | 9       | 0.12                  |
| 1409200      | 102                       | 83    | 53     | 25     | 13      | 0.17                  |
| 1409243      | 97                        | 89    | 64     | 27     | 17      | 0.22                  |
| 1409480      | 84                        | 54    | 15     | 6      | 5       | 0.04                  |
| 1409621      | 88                        | 69    | 37     | 18     | 12      | 0.09                  |
| 1409752      | 95                        | 78    | 40     | 17     | 7       | 0.11                  |
| 1409807      | 92                        | 69    | 30     | 10     | 6       | 0.07                  |
| 1410097      | 92                        | 77    | 45     | 22     | 10      | 0.12                  |
| 1410132      | 89                        | 72    | 38     | 16     | 9       | 0.09                  |
| 1410387      | 80                        | 38    | 11     | 6      | 6       | 0.02                  |
| 1411295      | 104                       | 85    | 56     | 30     | 16      | 0.21                  |
| 1411358      | 103                       | 87    | 58     | 33     | 22      | 0.25                  |

**Table 26.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 79                        | 48    | 14     | 8      | 7       | 0.03                  |
| 1408622      | 99                        | 86    | 52     | 25     | 12      | 0.17                  |
| 1409127      | 90                        | 60    | 29     | 10     | 6       | 0.06                  |
| 1409170      | 85                        | 61    | 22     | 8      | 6       | 0.05                  |
| 1409284      | 89                        | 73    | 37     | 13     | 7       | 0.09                  |
| 1409528      | 108                       | 85    | 64     | 37     | 15      | 0.25                  |
| 1409555      | 94                        | 101   | 41     | 15     | 8       | 0.14                  |
| 1409719      | 91                        | 63    | 21     | 7      | 6       | 0.06                  |
| 1409829      | 77                        | 61    | 27     | 13     | 12      | 0.05                  |
| 1409893      | 90                        | 71    | 31     | 13     | 8       | 0.08                  |
| 1410094      | 94                        | 55    | 18     | 9      | 8       | 0.05                  |
| 1410267      | 101                       | 88    | 49     | 21     | 10      | 0.16                  |
| 1410342      | 99                        | 70    | 53     | 22     | 9       | 0.13                  |
| 1410392      | 91                        | 80    | 47     | 22     | 10      | 0.13                  |
| 1410467      | 99                        | 63    | 22     | 8      | 6       | 0.07                  |

**Table 27.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 85                        | 44    | 13     | 6      | 6       | 0.03                  |
| 1408597      | 106                       | 87    | 24     | 11     | 8       | 0.11                  |
| 1409109      | 87                        | 56    | 17     | 8      | 7       | 0.05                  |
| 1409499      | 75                        | 37    | 10     | 6      | 5       | 0.02                  |
| 1409549      | 90                        | 82    | 52     | 23     | 8       | 0.13                  |
| 1409563      | 88                        | 84    | 49     | 19     | 10      | 0.13                  |
| 1409842      | 104                       | 73    | 34     | 11     | 3       | 0.10                  |
| 1410088      | 92                        | 84    | 39     | 14     | 6       | 0.11                  |
| 1410314      | 90                        | 61    | 30     | 13     | 8       | 0.07                  |
| 1410327      | 99                        | 91    | 49     | 20     | 9       | 0.15                  |
| 1410407      | 92                        | 61    | 25     | 8      | 5       | 0.06                  |
| 1410495      | 100                       | 90    | 59     | 19     | 9       | 0.17                  |
| 1410515      | 101                       | 84    | 50     | 23     | 9       | 0.15                  |
| 1411300      | 103                       | 76    | 40     | 20     | 10      | 0.12                  |
| 1411348      | 93                        | 72    | 37     | 14     | 9       | 0.09                  |

**Table 28.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 83                        | 48    | 14     | 7      | 7       | 0.03                  |
| 1408301      | 85                        | 54    | 24     | 11     | 8       | 0.05                  |
| 1408302      | 98                        | 58    | 20     | 9      | 8       | 0.06                  |
| 1409107      | 98                        | 87    | 49     | 22     | 9       | 0.15                  |
| 1409206      | 94                        | 85    | 59     | 31     | 13      | 0.19                  |
| 1409327      | 101                       | 71    | 32     | 9      | 3       | 0.09                  |
| 1409599      | 99                        | 84    | 44     | 14     | 6       | 0.12                  |
| 1409617      | 91                        | 70    | 26     | 12     | 10      | 0.07                  |
| 1409913      | 96                        | 80    | 34     | 16     | 8       | 0.10                  |
| 1410218      | 95                        | 91    | 37     | 14     | 7       | 0.12                  |
| 1410324      | 86                        | 82    | 46     | 15     | 7       | 0.10                  |
| 1410537      | 93                        | 84    | 52     | 22     | 10      | 0.14                  |
| 1410549      | 82                        | 56    | 25     | 13     | 7       | 0.05                  |
| 1410572      | 102                       | 82    | 38     | 10     | 6       | 0.11                  |
| 1411197      | 76                        | 35    | 14     | 8      | 5       | 0.02                  |

**Table 29.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 81                        | 47    | 16     | 8      | 7       | 0.03                  |
| 1408300      | 91                        | 64    | 22     | 10     | 7       | 0.06                  |
| 1408835      | 63                        | 25    | 11     | 9      | 9       | 0.01                  |
| 1409115      | 98                        | 67    | 32     | 10     | 7       | 0.08                  |
| 1409180      | 91                        | 88    | 57     | 27     | 11      | 0.17                  |
| 1409213      | 85                        | 56    | 16     | 5      | 5       | 0.04                  |
| 1409461      | 102                       | 73    | 39     | 14     | 7       | 0.11                  |
| 1409769      | 87                        | 72    | 45     | 18     | 11      | 0.10                  |
| 1409872      | 104                       | 76    | 46     | 16     | 5       | 0.12                  |
| 1409971      | 95                        | 90    | 59     | 32     | 16      | 0.22                  |
| 1410032      | 98                        | 69    | 32     | 11     | 5       | 0.08                  |
| 1410209      | 97                        | 89    | 63     | 25     | 10      | 0.18                  |
| 1410442      | 102                       | 82    | 58     | 27     | 12      | 0.18                  |
| 1410585      | 87                        | 60    | 20     | 7      | 5       | 0.05                  |
| 1411429      | 104                       | 63    | 29     | 12     | 8       | 0.09                  |

**Table 30.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 88                        | 47    | 17     | 8      | 8       | 0.04                  |
| 1408265      | 105                       | 77    | 46     | 20     | 11      | 0.14                  |
| 1408317      | 99                        | 65    | 33     | 16     | 10      | 0.09                  |
| 1408318      | 78                        | 42    | 13     | 10     | 9       | 0.03                  |
| 1408592      | 79                        | 45    | 19     | 11     | 9       | 0.03                  |
| 1408636      | 96                        | 89    | 62     | 28     | 14      | 0.20                  |
| 1408648      | 70                        | 30    | 13     | 10     | 9       | 0.01                  |
| 1409347      | 101                       | 63    | 34     | 17     | 10      | 0.09                  |
| 1409604      | 91                        | 75    | 45     | 17     | 9       | 0.11                  |
| 1409606      | 99                        | 74    | 36     | 16     | 8       | 0.10                  |
| 1409707      | 86                        | 80    | 37     | 13     | 7       | 0.09                  |
| 1409729      | 95                        | 60    | 27     | 13     | 9       | 0.07                  |
| 1409984      | 111                       | 86    | 54     | 24     | 12      | 0.19                  |
| 1410223      | 95                        | 62    | 20     | 8      | 6       | 0.06                  |
| 1411365      | 87                        | 59    | 21     | 10     | 7       | 0.05                  |

**Table 31.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|--------|--------|---------|-----------------------|
|              | 8 nM                      | 31 nM | 125 nM | 500 nM | 2000 nM |                       |
| 1173403      | 81                        | 47    | 12     | 7      | 8       | 0.03                  |
| 1408264      | 103                       | 83    | 45     | 17     | 10      | 0.14                  |
| 1408316      | 79                        | 35    | 8      | 7      | 6       | 0.02                  |
| 1408514      | 96                        | 77    | 40     | 18     | 13      | 0.12                  |
| 1408644      | 77                        | 40    | 12     | 9      | 9       | 0.02                  |
| 1408723      | 97                        | 74    | 49     | 15     | 8       | 0.11                  |
| 1409139      | 98                        | 86    | 59     | 26     | 11      | 0.18                  |
| 1409189      | 86                        | 240   | 53     | 21     | 10      | 0.41                  |
| 1409340      | 89                        | 77    | 44     | 14     | 7       | 0.10                  |
| 1409863      | 101                       | 76    | 57     | 22     | 9       | 0.15                  |
| 1410419      | 92                        | 68    | 40     | 13     | 8       | 0.09                  |
| 1410534      | 94                        | 89    | 55     | 22     | 11      | 0.16                  |
| 1411286      | 88                        | 64    | 38     | 16     | 10      | 0.08                  |
| 1411398      | 66                        | 30    | 12     | 8      | 8       | 0.01                  |
| 1411402      | 93                        | 70    | 34     | 15     | 7       | 0.09                  |

**Example 3: Dose-dependent inhibition of human PSD3 in A431 cells by modified oligonucleotides**

Modified oligonucleotides selected from the example above were tested at various doses in A431 cells. Cells plated at a density of 20,000 cells per well were treated using free uptake with various concentrations of modified oligonucleotide as specified in the tables below. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and PSD3 RNA levels were measured by quantitative real-time RTPCR. Human PSD3 primer-probe set RTS41435 (described herein above) was used to measure RNA levels. PSD3 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of PSD3 RNA is presented in the table below as percent PSD3 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC<sub>50</sub>) of each modified oligonucleotide was calculated using a linear regression on a log/linear plot of the data in Excel and is also presented in the table below.

**Table 32.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441256      | 110              | 79   | 58    | 61    | 26     | 9      | 4      | 2       | 2       | 2        | 0.05                  |
| 1441259      | 76               | 108  | 40    | 10    | 2      | 2      | 2      | 2       | 2       | 3        | 0.02                  |
| 1441340      | 82               | 47   | 19    | 8     | 3      | 2      | 2      | 2       | 2       | 2        | <0.003                |
| 1441646      | 63               | 79   | 28    | 7     | 3      | 2      | 2      | 2       | 3       | 3        | 0.003                 |
| 1441649      | 90               | 89   | 73    | 43    | 12     | 4      | 2      | 2       | 2       | 2        | 0.04                  |
| 1441650      | 79               | 75   | 30    | 10    | 2      | 1      | 2      | 2       | 27      | 3        | 0.01                  |
| 1441878      | 126              | 110  | 65    | 22    | 6      | 2      | 8      | 2       | 24      | 3        | 0.06                  |

**Table 33.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441582      | 100              | 69   | 54    | 18    | 3      | 3      | 2      | 2       | 2       | 2        | 0.02                  |
| 1441583      | 79               | 68   | 55    | 23    | 7      | 2      | 1      | 2       | 1       | 1        | 0.01                  |
| 1441589      | 76               | 62   | 39    | 16    | 4      | 2      | 1      | 2       | 2       | 2        | 0.01                  |
| 1441591      | 78               | 111  | 70    | 35    | 17     | 5      | 2      | 2       | 2       | 2        | 0.04                  |
| 1441622      | 105              | 79   | 65    | 20    | 5      | 1      | 2      | 2       | 2       | 2        | 0.03                  |
| 1441626      | 109              | 60   | 34    | 11    | 7      | 4      | 3      | 2       | 3       | 2        | 0.01                  |
| 1441631      | 97               | 65   | 31    | 6     | 2      | 1      | 1      | 1       | 2       | 1        | 0.01                  |

**Table 34.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441382      | 110              | 75   | 60    | 26    | 6      | 4      | 2      | 3       | 5       | 4        | 0.03                  |

|         |     |     |     |    |    |   |   |   |   |    |      |
|---------|-----|-----|-----|----|----|---|---|---|---|----|------|
| 1441422 | 70  | 139 | 151 | 24 | 14 | 5 | 3 | 3 | 3 | 6  | 0.09 |
| 1441439 | 108 | 65  | 47  | 18 | 5  | 5 | 4 | 4 | 3 | 3  | 0.02 |
| 1441460 | 40  | 130 | 103 | 33 | 11 | 9 | 5 | 3 | 3 | 3  | 0.04 |
| 1441727 | 153 | 83  | 72  | 35 | 6  | 4 | 4 | 3 | 6 | 6  | 0.08 |
| 1441742 | 108 | 100 | 50  | 22 | 4  | 3 | 2 | 3 | 4 | 3  | 0.03 |
| 1441917 | 153 | 123 | 107 | 41 | 17 | 4 | 3 | 3 | 3 | 35 | 0.15 |

**Table 35.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441454      | 153              | 119  | 99    | 36    | 20     | 6      | 4      | 4       | 5       | 7        | 0.12                  |
| 1441459      | 116              | 84   | 71    | 45    | 17     | 9      | 6      | 5       | 7       | 9        | 0.06                  |
| 1441672      | 120              | 67   | 71    | 18    | 4      | 2      | 1      | 2       | 1       | 1        | 0.03                  |
| 1441704      | 67               | 135  | 63    | 40    | 8      | 4      | 2      | 3       | 3       | 6        | 0.04                  |
| 1441738      | 86               | 114  | 105   | 41    | 13     | 4      | 2      | 3       | 3       | 2        | 0.07                  |
| 1441744      | 100              | 69   | 45    | 11    | 4      | 3      | 3      | 3       | 7       | 7        | 0.01                  |
| 1441916      | 110              | 92   | 84    | 39    | 15     | 3      | 3      | 2       | 3       | 5        | 0.06                  |

**Table 36.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441381      | 201              | 123  | 51    | 24    | 16     | 6      | 4      | 4       | 3       | 6        | 0.12                  |
| 1441441      | 101              | 68   | 32    | 16    | 8      | 3      | 4      | 2       | 4       | 4        | 0.01                  |
| 1441444      | 132              | 92   | 81    | 28    | 17     | 6      | 4      | 4       | 5       | 4        | 0.07                  |
| 1441554      | 99               | 109  | 67    | 12    | 4      | 3      | 3      | 2       | 2       | 2        | 0.04                  |
| 1441555      | 104              | 106  | 50    | 28    | 7      | 3      | 2      | 2       | 2       | 2        | 0.04                  |
| 1441715      | 119              | 124  | 80    | 28    | 15     | 4      | 3      | 3       | 4       | 4        | 0.08                  |
| 1441906      | 81               | 73   | 65    | 47    | 16     | 5      | 3      | 4       | 3       | 4        | 0.03                  |

5

**Table 37.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441251      | 124              | 105  | 46    | 12    | 4      | 2      | 4      | 4       | 5       | 6        | 0.04                  |
| 1441530      | 81               | 52   | 25    | 13    | 7      | 5      | 5      | 4       | 2       | 3        | 0.00                  |
| 1441531      | 94               | 52   | 37    | 10    | 8      | 3      | 2      | 3       | 3       | 3        | 0.01                  |
| 1441769      | 160              | 57   | 83    | 31    | 10     | 4      | 3      | 3       | 2       | 2        | 0.06                  |
| 1441804      | 126              | 132  | 74    | 35    | 28     | 9      | 3      | 3       | 3       | 3        | 0.10                  |
| 1441954      | 106              | 111  | 79    | 46    | 13     | 5      | 4      | 3       | 4       | 6        | 0.07                  |
| 1441981      | 126              | 125  | 107   | 77    | 24     | 6      | 5      | 5       | 4       | 6        | 0.15                  |

**Table 38.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441479      | 108              | 92   | 37    | 7     | 3      | 3      | 2      | 2       | 2       | 3        | 0.02                  |
| 1441523      | 157              | 102  | 64    | 25    | 12     | 4      | 3      | 3       | 3       | 4        | 0.08                  |
| 1441532      | 90               | 86   | 106   | 15    | 4      | 4      | 3      | 3       | 3       | 3        | 0.04                  |
| 1441544      | 148              | 77   | 59    | 15    | 8      | 5      | 4      | 5       | 5       | 5        | 0.05                  |
| 1441767      | 113              | 109  | 39    | 36    | 17     | 6      | 4      | 3       | 3       | 4        | 0.05                  |
| 1441776      | 140              | 126  | 61    | 30    | 6      | 3      | 4      | 3       | 4       | 5        | 0.08                  |
| 1441992      | 113              | 106  | 93    | 69    | 29     | 7      | 3      | 2       | 3       | 4        | 0.10                  |
| 1442130      | 88               | 70   | 41    | 16    | 8      | 4      | 4      | 2       | 3       | 28       | 0.01                  |

**Table 39.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441386      | 75               | 79   | 46    | 23    | 13     | 2      | 2      | 2       | 2       | 2        | 0.01                  |
| 1441420      | 92               | 96   | 46    | 22    | 5      | 3      | 2      | 1       | 1       | 1        | 0.02                  |
| 1441430      | 83               | 72   | 42    | 16    | 5      | 2      | 1      | 2       | 2       | 2        | 0.01                  |
| 1441433      | 121              | 70   | 64    | 48    | 24     | 9      | 4      | 2       | 2       | 2        | 0.05                  |
| 1441440      | 88               | 52   | 27    | 13    | 6      | 4      | 2      | 2       | 2       | 2        | 0.01                  |
| 1441443      | 81               | 67   | 38    | 14    | 5      | 2      | 2      | 1       | 1       | 1        | 0.01                  |
| 1441671      | 124              | 78   | 56    | 30    | 8      | 3      | 2      | 2       | 1       | 1        | 0.04                  |

5

**Table 40.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) |      |       |       |        |        |        |         |         |          | IC <sub>50</sub> (μM) |
|--------------|------------------|------|-------|-------|--------|--------|--------|---------|---------|----------|-----------------------|
|              | 3 nM             | 7 nM | 16 nM | 41 nM | 102 nM | 256 nM | 640 nM | 1600 nM | 4000 nM | 10000 nM |                       |
| 1441363      | 80               | 91   | 47    | 13    | 4      | 2      | 2      | 1       | 2       | 2        | 0.01                  |
| 1441442      | 90               | 49   | 19    | 9     | 3      | 1      | 2      | 1       | 1       | 1        | 0.003                 |
| 1441455      | 108              | 88   | 28    | 9     | 3      | 2      | 2      | 3       | 3       | 4        | 0.02                  |
| 1441673      | 88               | 130  | 45    | 21    | 7      | 2      | 1      | 1       | 1       | 1        | 0.03                  |
| 1441713      | 87               | 78   | 63    | 45    | 22     | 7      | 3      | 2       | 2       | 2        | 0.03                  |
| 1441730      | 104              | 62   | 51    | 29    | 9      | 4      | 3      | 2       | 3       | 2        | 0.02                  |
| 1441908      | 111              | 81   | 70    | 44    | 30     | 10     | 4      | 3       | 3       | 3        | 0.06                  |

**Example 4: Design of modified oligonucleotides complementary to a human PSD3 nucleic acid**

Modified oligonucleotides complementary to a human PSD3 nucleic acid were designed and synthesized.

10 “Start site” indicates the 5’-most nucleoside to which the modified oligonucleotide is complementary in the target nucleic acid sequence. “Stop site” indicates the 3’-most nucleoside to which the modified oligonucleotide is

complementary in the target nucleic acid sequence. Each modified oligonucleotide listed in the table below is 100% complementary to SEQ ID NO: 1 (described herein above), to SEQ ID NO: 2 (described herein above), or to both. “N/A” indicates that the modified oligonucleotide is not 100% complementary to that particular target nucleic acid sequence.

5           The modified oligonucleotides in Table 41 below are 3-10-3 cEt modified oligonucleotides with uniform phosphorothioate internucleoside linkages. The modified oligonucleotides are 16 nucleosides in length, wherein the central gap segment consists of ten 2'-β-D-deoxynucleosides, and wherein the 5' and 3' wing segments each consist of three cEt nucleosides. The sugar motif for the modified oligonucleotides is (from 5' to 3'): kkkdddddcccckkk; wherein each “d” represents a 2'-β-D-deoxyribose sugar moiety, and each “k” represents a cEt modified sugar moiety. The  
10 internucleoside linkage motif for the modified oligonucleotides is (from 5' to 3'): sssssssssssss; wherein each “s” represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine.

The modified oligonucleotides in the table below are all conjugated to a THA-C6-GalNAc<sub>3</sub> conjugate (designated as [THA-GalNAc-]) at the 5' end of the modified oligonucleotide. THA-GalNAc is represented by the structure below, wherein the phosphate group is attached to the 5'-oxygen atom of the 5'-nucleoside:

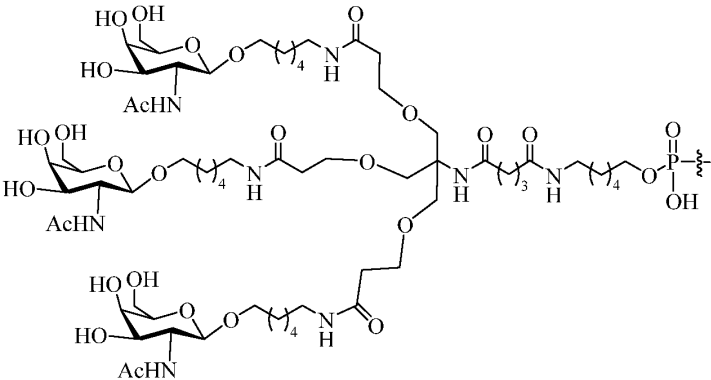


**Table 41.** GalNAc conjugated 3-10-3 cEt modified oligonucleotides with uniform phosphorothioate internucleoside linkages complementary to human PSD3

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3')          | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|------------------------------|-----------|
| 1436573      | 288680                  | 288695                 | 2075                    | 2090                   | THA-GalNAc-ATCTATTGGAGAAGTG  | 260       |
| 1454924      | 222028                  | 222043                 | 1438                    | 1453                   | THA-GalNAc-GTCCAAAATGGTTTCA  | 423       |
| 1454925      | 285152                  | 285167                 | 1787                    | 1802                   | THA-GalNAc-CCAAAATTTCAGTGCT  | 461       |
| 1454928      | 285254                  | 285269                 | 1889                    | 1904                   | THA-GalNAc-ATCTTTTGAATCTGTC  | 686       |
| 1454933      | 330574                  | 330589                 | N/A                     | N/A                    | THA-GalNAc-GCAAATTGTGTTTCAGT | 1252      |
| 1454937      | 82205                   | 82220                  | N/A                     | N/A                    | THA-GalNAc-TTTCAGATATTAGCTC  | 355       |

|         |        |        |      |      |                                  |      |
|---------|--------|--------|------|------|----------------------------------|------|
| 1454942 | 244765 | 244780 | N/A  | N/A  | THA-GalNAc-<br>GGTAATTTATGAGTTA  | 455  |
| 1454944 | 222016 | 222031 | 1426 | 1441 | THA-GalNAc-<br>TTCAAACCTGGGAGCTG | 2471 |
| 1454945 | 181927 | 181942 | N/A  | N/A  | THA-GalNAc-<br>GAATTGATAACAGGTA  | 449  |
| 1454969 | 184997 | 185012 | N/A  | N/A  | THA-GalNAc-<br>GTGTATTAGGTTTTTC  | 1840 |
| 1454970 | 218085 | 218100 | 1051 | 1066 | THA-GalNAc-<br>ATCTATAGGATGCTGG  | 781  |
| 1454972 | 463909 | 463924 | N/A  | N/A  | THA-GalNAc-<br>TCAGATTTAATAGGTC  | 1510 |
| 1454974 | 291274 | 291289 | N/A  | N/A  | THA-GalNAc-<br>GAGTATTATGAAGAGT  | 1519 |
| 1454980 | 344743 | 344758 | N/A  | N/A  | THA-GalNAc-<br>AATTTAGTATCCTTCA  | 648  |
| 1454984 | 288681 | 288696 | 2076 | 2091 | THA-GalNAc-<br>TATCTATTGGAGAAGT  | 1013 |
| 1454987 | 222044 | 222059 | 1454 | 1469 | THA-GalNAc-<br>AGTATAAAGAAGTGTT  | 832  |

The modified oligonucleotides in Table 42 below are mixed cEt/MOE modified oligonucleotides with uniform phosphorothioate internucleoside linkages. The modified oligonucleotides are 16 nucleosides in length. The sugar motifs for the modified oligonucleotides are described in the column labeled “Sugar Motif (5’ to 3’)” in Table 42 below; wherein each “d” represents a 2’-β-D-deoxyribose sugar moiety, each “k” represents a cEt modified sugar moiety, each “y” represents a 2’-O-methylribose sugar moiety, and each “e” represents a 2’-MOE sugar moiety. The internucleoside linkage motif for the modified oligonucleotides is (from 5’ to 3’): sssssssssssss; wherein each “s” represents a phosphorothioate internucleoside linkage. Each cytosine residue is a 5-methylcytosine. Each “U” represents an Uracil.

The modified oligonucleotides in the table below are all conjugated to a THA-C6-GalNAc<sub>3</sub> conjugate (designated as [THA-GalNAc-]) at the 5’ end of the modified oligonucleotide. THA-GalNAc is represented by the structure below, wherein the phosphate group is attached to the 5’-oxygen atom of the 5’-nucleoside:

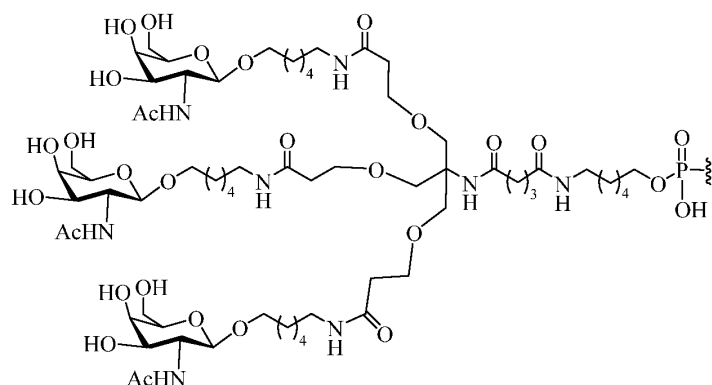


**Table 42.** GalNAc conjugated modified oligonucleotides with uniform phosphorothioate internucleoside linkages complementary to human PSD3

| Compound No. | SEQ ID NO: 1 Start Site | SEQ ID NO: 1 Stop Site | SEQ ID NO: 2 Start Site | SEQ ID NO: 2 Stop Site | Sequence (5' to 3')         | Sugar Motif (5' to 3') | SEQ ID NO |
|--------------|-------------------------|------------------------|-------------------------|------------------------|-----------------------------|------------------------|-----------|
| 1454999      | 218081                  | 218096                 | 1047                    | 1062                   | THA-GalNAc-ATAGGATGCTGGGTCT | kkkdydddddddkkk        | 551       |
| 1455000      | 217663                  | 217678                 | 629                     | 644                    | THA-GalNAc-GTGTUTTACGACTGGC | kkkdydddddddkkk        | 2709      |
| 1545962      | 288678                  | 288693                 | 2073                    | 2088                   | THA-GalNAc-CTATTGGAGAAGTGTA | kkdddddddekek          | 936       |

### 5 Example 5: Effect of modified oligonucleotides on human PSD3 *in vitro*, multiple doses

Modified oligonucleotides selected from the example above were tested at various doses in HepatoPac (donor LLT) cells (BioIVT; Catalog #: HUMAN00032-96). HepatoPac cells are cultured following the manufacturers Maintenance Kit instructions. Upon arrival, the HepatoPac system medium is replaced with supplemented Maintenance medium (64ul/well) and allowed to incubate for 72 hours. After 24 hours, the medium is replaced with new media and the modified oligonucleotides in water are added at the indicated concentrations and allowed to incubate at 37°C, 10% CO<sub>2</sub> for 48 hours. The medium is changed one more and allowed to incubate for an additional 48 hours after which the cells are lysed for total RNA purification and analysis. PSD3 RNA levels were measured by quantitative real-time RT-PCR. Human PSD3 primer-probe set LTS48177 (forward sequence GATCTGAAGGGAAAGCTCCA, designated herein as SEQ ID NO: 9; reverse sequence CCTCACCATCAAATTCCAGAGA, designated herein as SEQ ID NO: 10; probe sequence TAGGCCTTCTCCACCTTCCTCCA, designated herein as SEQ ID NO: 11) was used to measure RNA levels. PSD3 RNA levels were normalized to total RNA content, as measured by RIBOGREEN®. Reduction of PSD3 RNA is presented in the table below as percent PSD3 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC<sub>50</sub>) of each modified oligonucleotide was calculated using Graphpad Prism (log(inhibitor) vs. normalized response -- Variable slope) and is also presented in the table below.

20 **Table 43.** Dose-dependent reduction of human PSD3 RNA in HepatoPac cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) LTS48177 |      |      |       |       |        |        |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|------|------|-------|-------|--------|--------|---------|-----------------------|
|              | 0.7 nM                    | 2 nM | 6 nM | 19 nM | 56 nM | 167 nM | 500 nM | 1500 nM |                       |
| 1436573      | 66                        | 40   | 64   | 38    | 38    | 19     | 13     | 11      | 0.09                  |
| 1454924      | 39                        | 52   | 33   | 24    | 19    | 8      | 6      | 4       | 0.01                  |
| 1454925      | 56                        | 54   | 44   | 43    | 32    | 28     | 20     | 16      | 0.20                  |
| 1454928      | 57                        | 48   | 42   | 36    | 29    | 20     | 14     | 16      | 0.08                  |
| 1454933      | 41                        | 31   | 39   | 32    | 16    | 12     | 10     | 12      | 0.02                  |
| 1454937      | 73                        | 55   | 69   | 37    | 29    | 25     | 19     | 7       | 0.05                  |
| 1454942      | 61                        | 61   | 55   | 75    | 44    | 22     | 16     | 9       | 0.16                  |
| 1454944      | 50                        | 68   | 52   | 41    | 21    | 9      | 5      | 6       | 0.04                  |
| 1454945      | 52                        | 40   | 35   | 29    | 17    | 7      | 4      | 3       | 0.02                  |

|         |    |    |    |    |    |    |    |    |      |
|---------|----|----|----|----|----|----|----|----|------|
| 1454969 | 64 | 49 | 40 | 30 | 13 | 3  | 5  | 2  | 0.02 |
| 1454970 | 98 | 53 | 44 | 34 | 33 | 13 | 4  | 3  | 0.04 |
| 1454972 | 58 | 60 | 65 | 52 | 32 | 18 | 13 | 12 | 0.11 |
| 1454974 | 64 | 60 | 55 | 37 | 30 | 21 | 13 | 12 | 0.10 |
| 1454980 | 48 | 52 | 57 | 52 | 34 | 16 | 13 | 14 | 0.10 |
| 1454984 | 50 | 48 | 55 | 37 | 28 | 14 | 10 | 14 | 0.06 |
| 1454987 | 52 | 45 | 40 | 38 | 34 | 17 | 10 | 8  | 0.05 |
| 1454999 | 52 | 60 | 61 | 57 | 41 | 42 | 13 | 11 | 0.20 |
| 1455000 | 37 | 45 | 65 | 45 | 35 | 14 | 9  | 10 | 0.06 |
| 1545962 | 47 | 47 | 46 | 32 | 29 | 16 | 15 | 16 | 0.05 |

**Example 6: Effect of modified oligonucleotides on human PSD3 *in vitro*, multiple doses**

Modified oligonucleotides selected from the example above were tested at various doses in SH-SY5Y cells. Cells plated at a density of 20,000 cells per well were treated using electroporation with various concentrations of modified oligonucleotide as specified in the table below. After a treatment period of approximately 24 hours, total RNA was isolated from the cells and PSD3 RNA levels were measured by quantitative real-time RTPCR. Human PSD3 primer-probe set RTS41435 (described herein above) was used to measure RNA levels. PSD3 RNA levels were normalized to total RNA content, as measured by GAPDH. Human GAPDH was measured using the human primer-probe set RTS104 (forward sequence GAAGGTGAAGGTCGGAGTC, designated herein as SEQ ID NO: 12; reverse sequence GAAGATGGTGATGGGATTTC, designated herein as SEQ ID NO: 13; probe sequence CAAGCTTCCCCTTCTCAGCC, designated herein as SEQ ID NO: 14). Reduction of PSD3 RNA is presented in the table below as percent PSD3 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC<sub>50</sub>) of each modified oligonucleotide was calculated using Graphpad Prism (log(inhibitor) vs. normalized response -- Variable slope) and is also presented in the table below.

**Table 44.** Dose-dependent reduction of human PSD3 RNA in SH-SY5Y cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |       |       |       |        |        |         |         |         |          | IC <sub>50</sub> (μM) |
|--------------|---------------------------|-------|-------|-------|--------|--------|---------|---------|---------|----------|-----------------------|
|              | 5 nM                      | 13 nM | 33 nM | 82 nM | 205 nM | 512 nM | 1280 nM | 3200 nM | 8000 nM | 20000 nM |                       |
| 1173404      | 93                        | 89    | 84    | 61    | 46     | 34     | 19      | 14      | 10      | 4        | 0.19                  |
| 1410176      | 134                       | 80    | 88    | 72    | 69     | 39     | 19      | 10      | 4       | 4        | 0.33                  |
| 1408282      | 112                       | 109   | 114   | 78    | 63     | 30     | 31      | 18      | 12      | 10       | 0.38                  |
| 1410297      | 76                        | 84    | 79    | 71    | 56     | 58     | 25      | 15      | 12      | 10       | 0.32                  |
| 1408305      | 91                        | 101   | 94    | 75    | 66     | 58     | 27      | 23      | 14      | 5        | 0.55                  |
| 1410387      | 121                       | 110   | 95    | 92    | 71     | 46     | 19      | 19      | 13      | 6        | 0.48                  |
| 1408375      | 84                        | 103   | 86    | 90    | 75     | 50     | 36      | 31      | 17      | 8        | 0.74                  |
| 1410423      | 95                        | 103   | 75    | 78    | 52     | 35     | 16      | 6       | 4       | 2        | 0.24                  |
| 1409092      | 108                       | 100   | 79    | 62    | 32     | 30     | 14      | 5       | 4       | 2        | 0.14                  |
| 1410436      | 110                       | 107   | 94    | 96    | 77     | 60     | 40      | 15      | 3       | 3        | 0.76                  |
| 1409495      | 92                        | 98    | 80    | 67    | 58     | 42     | 36      | 16      | 11      | 6        | 0.33                  |
| 1411113      | 102                       | 97    | 90    | 81    | 77     | 49     | 24      | 24      | 7       | 1        | 0.52                  |

|         |    |    |     |    |    |    |    |    |    |   |      |
|---------|----|----|-----|----|----|----|----|----|----|---|------|
| 1409859 | 81 | 92 | 116 | 98 | 70 | 46 | 27 | 23 | 16 | 4 | 0.58 |
| 1411398 | 92 | 97 | 96  | 84 | 55 | 29 | 15 | 6  | 4  | 4 | 0.26 |

**Example 7: Effect of modified oligonucleotides on human PSD3 *in vitro*, multiple doses**

Modified oligonucleotides selected from the example above were tested at various doses in A431 cells. Cells plated at a density of 10,000 cells per well were treated using free uptake with various concentrations of modified oligonucleotide as specified in the tables below. After a treatment period of approximately 48 hours, total RNA was isolated from the cells and PSD3 RNA levels were measured by quantitative real-time RTPCR. Human PSD3 primer-probe set RTS41435 (described herein above) was used to measure RNA levels. PSD3 RNA levels were normalized to total RNA content, as measured by GAPDH. Human GAPDH was measured using the human primer-probe set RTS104 (described herein above). Reduction of PSD3 RNA is presented in the tables below as percent PSD3 RNA, relative to untreated control cells (% UTC).

The half maximal inhibitory concentration (IC<sub>50</sub>) of each modified oligonucleotide was calculated using Graphpad Prism (log(inhibitor) vs. normalized response -- Variable slope) and is also presented in the tables below.

**Table 45.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |      |        |       |       |       |        |        |         |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|------|--------|-------|-------|-------|--------|--------|---------|---------|-----------------------|
|              | 0.4 nM                    | 1 nM | 3.7 nM | 11 nM | 33 nM | 99 nM | 296 nM | 889 nM | 2667 nM | 8000 nM |                       |
| 1173404      | 103                       | 122  | 102    | 66    | 25    | 11    | 5      | 6      | 3       | 4       | 0.02                  |
| 1408282      | 102                       | 101  | 91     | 52    | 20    | 15    | 10     | 9      | 8       | 6       | 0.01                  |
| 1408305      | 83                        | 84   | 81     | 69    | 34    | 12    | 6      | 4      | 4       | 3       | 0.02                  |
| 1408375      | 119                       | 115  | 95     | 94    | 33    | 12    | 6      | 5      | 6       | 6       | 0.03                  |
| 1409092      | 103                       | 109  | 66     | 19    | 4     | 4     | 5      | 4      | 2       | 3       | 0.01                  |
| 1409495      | 88                        | 80   | 65     | 36    | 18    | 8     | 6      | 5      | 4       | 4       | 0.01                  |
| 1409859      | 100                       | 73   | 74     | 44    | 21    | 9     | 7      | 4      | 3       | 2       | 0.01                  |
| 1410176      | 79                        | 70   | 72     | 38    | 15    | 9     | 7      | 5      | 2       | 4       | 0.01                  |
| 1410297      | 83                        | 91   | 70     | 60    | 21    | 7     | 2      | 3      | 2       | 2       | 0.01                  |
| 1410387      | 84                        | 65   | 50     | 20    | 8     | 3     | 4      | 3      | 2       | 3       | 0.003                 |
| 1410423      | 105                       | 67   | 44     | 25    | 9     | 6     | 6      | 6      | 2       | 5       | 0.003                 |
| 1410436      | 109                       | 90   | 76     | 62    | 20    | 11    | 8      | 6      | 4       | 3       | 0.01                  |
| 1411113      | 97                        | 96   | 90     | 69    | 29    | 13    | 6      | 6      | 4       | 4       | 0.02                  |
| 1411398      | 95                        | 84   | 58     | 34    | 13    | 7     | 6      | 3      | 5       | 3       | 0.01                  |

**Table 46.** Dose-dependent reduction of human PSD3 RNA in A431 cells by modified oligonucleotides

| Compound No. | PSD3 RNA (% UTC) RTS41435 |      |        |       |       |       |        |        |         |         | IC <sub>50</sub> (μM) |
|--------------|---------------------------|------|--------|-------|-------|-------|--------|--------|---------|---------|-----------------------|
|              | 0.4 nM                    | 1 nM | 3.7 nM | 11 nM | 33 nM | 99 nM | 296 nM | 889 nM | 2667 nM | 8000 nM |                       |
| 1441259      | 107                       | 96   | 76     | 52    | 15    | 9     | 9      | 5      | 6       | 5       | 0.01                  |
| 1441363      | 96                        | 87   | 63     | 38    | 17    | 6     | 6      | 6      | 5       | 5       | 0.01                  |
| 1441430      | 85                        | 82   | 78     | 56    | 21    | 10    | 7      | 5      | 4       | 4       | 0.01                  |
| 1441439      | 95                        | 86   | 61     | 35    | 18    | 8     | 9      | 6      | 8       | 8       | 0.01                  |
| 1441589      | 96                        | 99   | 84     | 44    | 16    | 5     | 7      | 6      | 6       | 5       | 0.01                  |
| 1441591      | 97                        | 80   | 76     | 64    | 40    | 17    | 8      | 4      | 4       | 9       | 0.02                  |
| 1441649      | 102                       | 85   | 90     | 65    | 34    | 12    | 13     | 5      | 4       | 5       | 0.02                  |
| 1441727      | 91                        | 95   | 90     | 46    | 20    | 6     | 4      | 4      | 4       | 4       | 0.01                  |
| 1442130      | 115                       | 111  | 92     | 78    | 32    | 8     | 5      | 4      | 3       | 3       | 0.02                  |

**Example 8: Activity of modified oligonucleotides complementary to human PSD3 in humanized mice, multiple dose**

Humanized FRG® KO mice (Yecuris Tualatin, OR) were used to determine activity of modified oligonucleotides complementary to human PSD3. The FRG KO mouse are severely immunocompromised, fumarylacetoacetate hydrolase (FAH)-deficient mice that allows for engraftment of human primary hepatocytes (up to 90%) into the mouse liver. The humanized liver of this mouse model allows for in vivo activity characterization for ASOs targeting human transcripts.

*Treatment*

Humanized FRG® KO mice were divided into groups of three mice each. Each mouse received subcutaneous injections of modified oligonucleotide at various doses indicated in the tables below twice a week for two and a half weeks (a total of 5 treatments). One group of seven mice received subcutaneous injections of PBS twice a week for two and a half weeks (a total of 5 treatments). The PBS-injected group served as the control group to which oligonucleotide-treated groups were compared.

*RNA analysis*

48 hours post the final treatment, mice were sacrificed, and RNA was extracted from mouse liver, for real-time RTPCR analysis of PSD3 RNA expression. Human PSD3 primer probe set LTS48178 (forward sequence TGAATGATGCCAGCGACTC, designated herein as SEQ ID NO: 15; reverse sequence CTTCTAGCCGTGTTGTTTCAC, designated herein as SEQ ID NO: 16; probe sequence AAAGCAATCTCCGGGTGCCT, designated herein as SEQ ID NO: 17) was used to measure human PSD3 RNA levels as indicated in the table below. PSD3 RNA levels were normalized to total RNA content, as measured by GAPDH. Human GAPDH was measured using the human primer-probe set Hs99999905\_m1 (Thermo Fisher Scientific). Results are presented as percent PSD3 RNA, relative to PBS control (%control). ED50s were calculated in

Prism using nonlinear fit with variable slope (four parameter), top constrained to 100% (or 1), bottom constrained to 0.  
 $Y = \text{Bottom} + (\text{Top} - \text{Bottom}) / (1 + (\text{IC}_{50}/X)^{\text{HillSlope}})$ .

**Table 47.** Reduction of human PSD3 in transgenic mice

| Compound No. | Dose (mpk) | Liver                |            |
|--------------|------------|----------------------|------------|
|              |            | PSD3 RNA (% control) | ED50 (mpk) |
| PBS          | 0          | 100                  | -          |
| 1436573      | 0.04       | 96                   | 0.35       |
|              | 0.15       | 77                   |            |
|              | 0.60       | 31                   |            |
|              | 2.40       | 8                    |            |
| 1454945      | 0.04       | 101                  | 0.42       |
|              | 0.15       | 89                   |            |
|              | 0.60       | 32                   |            |
|              | 2.40       | 8                    |            |
| 1454987      | 0.04       | 98                   | 0.52       |
|              | 0.15       | 86                   |            |
|              | 0.60       | 40                   |            |
|              | 2.40       | 20                   |            |
| 1545962      | 0.15       | 85                   | 0.37       |
|              | 0.60       | 27                   |            |
|              | 2.40       | 12                   |            |

**CLAIMS:**

1. An oligomeric compound comprising a modified oligonucleotide consisting of 8 to 80 linked nucleosides, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion of a PSD3 nucleic acid, and wherein the modified oligonucleotide has at least one modification selected from a modified sugar moiety and a modified internucleoside linkage.

2. The oligomeric compound of claim 1, wherein the PSD3 nucleic acid has the nucleobase sequence of any of SEQ ID NOs: 1 or 2.

3. The oligomeric compound of claim 1 or 2, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 82205-82220, 181927-181942, 184997-185012, 217663-217678, 218081-218096, 218085-218100, 222016-222031, 222028-222043, 222044-222059, 244765-244780, 285152-285167, 285254-285269, 288678-288693, 288680-288695, 288681-288696, 291274-291289, 330574-330589, 344743-344758, or 463909-463924 of SEQ ID NO: 1.

4. The oligomeric compound of any of claims 1-3, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 629-644, 1047-1062, 1051-1066, 1426-1441, 1438-1453, 1454-1469, 1787-1802, 1889-1904, 2073-2088, 2075-2090, or 2076-2091 of SEQ ID NO: 2.

5. The oligomeric compound of any of claims 1-4, wherein the nucleobase sequence of the modified oligonucleotide is at least 80% complementary to an equal length portion within nucleobases 222044-222059, 288678-288693, or 288680-288695 of SEQ ID NO: 1.

6. The oligomeric compound of any of claims 1-5, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of the PSD3 nucleic acid.

7. An oligomeric compound comprising a modified oligonucleotide consisting of 8 to 80 linked nucleosides and having a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 contiguous nucleobases of any of the nucleobase sequences of any of SEQ ID NOs: 20-3034.

8. The oligomeric compound of claim 7, wherein the modified oligonucleotide has a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 20-3034.

9. The oligomeric compound of claim 8, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any of SEQ ID NOs: 20-3034.

10. The oligomeric compound of any of claims 7-9, wherein the modified oligonucleotide has a nucleobase sequence comprising at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 contiguous nucleobases of any of the nucleobase sequences of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

11. The oligomeric compound of claim 10, wherein the modified oligonucleotide consists of 16 to 80 linked nucleosides and has a nucleobase sequence comprising the nucleobase sequence of any of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

12. The oligomeric compound of claim 11, wherein the modified oligonucleotide has a nucleobase sequence consisting of the nucleobase sequence of any one of SEQ ID NOs: 260, 355, 423, 449, 455, 461, 551, 648, 686, 781, 832, 936, 1252, 1510, 1519, 1840, 2471, 2709, or 2939.

13. The oligomeric compound of any of claims 7-11, wherein the nucleobase sequence of the modified oligonucleotide is at least 85%, at least 90%, at least 95%, or 100% complementary to an equal length portion of a PSD3 nucleic acid, wherein the PSD3 nucleic acid has the nucleobase sequence of SEQ ID NOs: 1 or 2.

14. The oligomeric compound of any of claims 1-13, wherein the modified oligonucleotide consists of 10 to 25, 10 to 30, 10 to 50, 12 to 20, 12 to 25, 12 to 30, 12 to 50, 13 to 20, 13 to 25, 13 to 30, 13 to 50, 14 to 20, 14 to 25, 14 to 30, 14 to 50, 15 to 20, 15 to 25, 15 to 30, 15 to 50, 16 to 18, 16 to 20, 16 to 25, 16 to 30, 16 to 50, 17 to 20, 17 to 25, 17 to 30, 17 to 50, 18 to 20, 18 to 25, 18 to 30, 18 to 50, 19 to 20, 19 to 25, 19 to 30, 19 to 50, 20 to 25, 20 to 30, 20 to 50, 21 to 25, 21 to 30, 21 to 50, 22 to 25, 22 to 30, 22 to 50, 23 to 25, 23 to 30, or 23 to 50 linked nucleosides.

15. The oligomeric compound of any of claims 1-14, wherein at least one nucleoside of the modified oligonucleotide comprises a modified sugar moiety.

16. The oligomeric compound of claim 15, wherein the modified sugar moiety comprises a bicyclic sugar moiety.

17. The oligomeric compound of claim 16, wherein the bicyclic sugar moiety comprises a 2'-4' bridge selected from -O-CH<sub>2</sub>-; and -O-CH(CH<sub>3</sub>)-

18. The oligomeric compound of claim 15, wherein the modified sugar moiety comprises a non-bicyclic modified sugar moiety.

19. The oligomeric compound of claim 18, wherein the non-bicyclic modified sugar moiety is a 2'-MOE sugar moiety or 2'-OMe sugar moiety.

20. The oligomeric compound of any of claims 1-19, wherein at least one nucleoside of the modified oligonucleotide compound comprises a sugar surrogate.

21. The oligomeric compound of any of claims 1-20, wherein the modified oligonucleotide comprises at least one modified internucleoside linkage.

22. The oligomeric compound of claim 21, wherein at least one modified internucleoside linkage is a phosphorothioate internucleoside linkage.

23. The oligomeric compound of claim 21 or 22, wherein each internucleoside linkage is a modified internucleoside linkage.

24. The oligomeric compound of claim 24, wherein each internucleoside linkage is a phosphorothioate internucleoside linkage.

25. The oligomeric compound of any of claims 21-23, wherein at least one internucleoside linkage of the modified oligonucleotide is a phosphodiester internucleoside linkage.

26. The oligomeric compound of any of claims 1-21, wherein each internucleoside linkage of the modified oligonucleotide is independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

27. The oligomeric compound of any of claims 1-21, wherein each internucleoside linkage of the modified oligonucleotide is independently selected from a phosphodiester internucleoside linkage, a phosphorothioate internucleoside linkage, or a mesyl phosphoramidate internucleoside linkage.

28. The oligomeric compound of any of claims 1-23 or 25-27, wherein at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, or at least 16 internucleoside linkages of the modified oligonucleotide are phosphorothioate internucleoside linkages.

29. The oligomeric compound of any of claims 1-28, wherein the modified oligonucleotide comprises at least one modified nucleobase.

30. The oligomeric compound of claim 29, wherein the modified nucleobase is 5-methylcytosine.

31. The oligomeric compound of claim 29, wherein each cytosine is a 5-methylcytosine.

32. The oligomeric compound of any of claims 31, wherein the modified oligonucleotide comprises a deoxy region comprising of 5-12 contiguous 2'-deoxynucleosides.

33. The oligomeric compound of claim 32, wherein the deoxy region consists of 6, 7, 8, 9, 10, or 6-10 linked nucleosides.

34. The oligomeric compound of claim 32 or 33, wherein each nucleoside of the deoxy region is a 2'-β-D-deoxynucleoside.

35. The oligomeric compound of claim 32 or 33, wherein one nucleoside of the deoxy region comprises a 2'-OMe sugar moiety.

36. The oligomeric compound of any of claims 32-35, wherein each nucleoside immediately adjacent to the deoxy region comprises a modified sugar moiety.

37. The oligomeric compound of any of claims 32-36, wherein the deoxy region is flanked on the 5'-side by a 5'-region consisting of 1-6 linked 5'-region nucleosides and on the 3'-side by a 3'-region consisting of 1-6 linked 3'-region nucleosides; wherein

the 3'-most nucleoside of the 5' external region comprises a modified sugar moiety; and

the 5'-most nucleoside of the 3' external region comprises a modified sugar moiety.

38. The oligomeric compound of claim 37, wherein each nucleoside of the 3' external region comprises a modified sugar moiety.

39. The oligomeric compound of claim 37 or 38, wherein each nucleoside of the 5' external region comprises a modified sugar moiety.

40. The oligomeric compound of claim 39, wherein the modified oligonucleotide has:

a 5' external region consisting of 3 linked nucleosides;

a deoxy region consisting of 10 linked nucleosides; and

a 3' external region consisting of 3 linked nucleosides;

wherein each of the 5'-region nucleosides and each of the 3'-region nucleosides is a cEt nucleoside.

41. The oligomeric compound of claim 39, wherein the modified oligonucleotide has:

a 5' external region consisting of 1-6 linked nucleosides;

a deoxy region consisting of 6-10 linked nucleosides; and

a 3' external region consisting of 1-6 linked nucleosides;

wherein each of the 5' external region nucleosides and each of the 3' external region nucleosides is a cEt nucleoside or a 2'-MOE nucleoside; and each of the deoxy region nucleosides is a 2'-β-D-deoxynucleoside.

42. An oligomeric compound of any of claims 1-32, wherein the modified oligonucleotide has a sugar motif (5' to 3') selected from: kkkkkkkkkkkkk, kkkdykkkkkkkkk, kkkkkkkkkkkekek, and kkkkkkkkkkkkke.

43. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation:  $A_{ks}T_{ks}^mC_{ks}T_{ds}A_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ks}T_{ks}G_k$  (SEQ ID NO: 3036), wherein

A = an adenine nucleobase,  
 $^mC$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

44. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation:  $A_{ks}G_{ks}T_{ks}A_{ds}T_{ds}A_{ds}A_{ds}A_{ds}G_{ds}A_{ds}A_{ds}G_{ds}T_{ds}G_{ks}T_{ks}T_k$  (SEQ ID NO: 3038), wherein

A = an adenine nucleobase,  
 $^mC$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

45. An oligomeric compound comprising a modified oligonucleotide according to the following chemical notation:  $^mC_{ks}T_{ks}A_{ds}T_{ds}T_{ds}G_{ds}G_{ds}A_{ds}G_{ds}A_{ds}G_{ks}T_{es}G_{ks}T_{es}A_k$  (SEQ ID NO: 3040), wherein

A = an adenine nucleobase,  
 $^mC$  = a 5-methyl cytosine nucleobase,  
 G = a guanine nucleobase,  
 T = a thymine nucleobase,  
 e = a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> modified ribosyl sugar moiety,  
 k = a cEt sugar moiety,  
 d = a 2'-β-D-deoxyribosyl sugar moiety, and  
 s = a phosphorothioate internucleoside linkage.

46. The oligomeric compound of any of claims 1-45, wherein the oligomeric compound comprises a conjugate group.

47. The oligomeric compound of claim 46, wherein the conjugate group comprises a conjugate linker and a conjugate moiety.

48. The oligomeric compound of claim 46 or 47, wherein the conjugate linker consists of a single bond.

49. The oligomeric compound of any of claims 46-48, wherein the conjugate linker is cleavable.

50. The oligomeric compound of any of claims 46-49, wherein the conjugate linker comprises 1-3 linker-nucleosides.

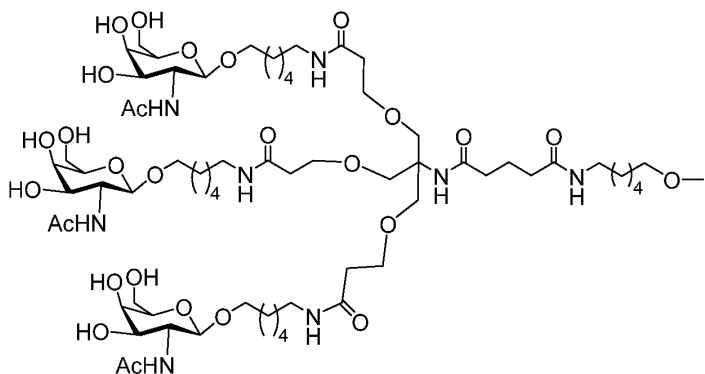
51. The oligomeric compound of any of claims 46-49, wherein the conjugate linker is a phosphate.

52. The oligomeric compound of any of claims 46-51, wherein the conjugate group is attached to the modified oligonucleotide at the 5'-end of the modified oligonucleotide.

53. The oligomeric compound of any of claims 46-51, wherein the conjugate group is attached to the modified oligonucleotide at the 3'-end of the modified oligonucleotide.

54. The oligomeric compound of any of claims 46-53, wherein the conjugate group comprises N-acetyl galactosamine.

55. The oligomeric compound of claim 54, wherein the conjugate group has the following structure:



56. The oligomeric compound of any of claims 46-55, wherein the conjugate group comprises a cell-targeting moiety.

57. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation:  $\text{THA-GalNAc-}_o\text{A}_{ks}\text{T}_{ks}{}^m\text{C}_{ks}\text{T}_{ds}\text{A}_{ds}\text{T}_{ds}\text{T}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ds}\text{A}_{ds}\text{G}_{ks}\text{T}_{ks}\text{G}_k$  (SEQ ID NO: 3037), wherein

A = an adenine nucleobase,

${}^m\text{C}$  = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

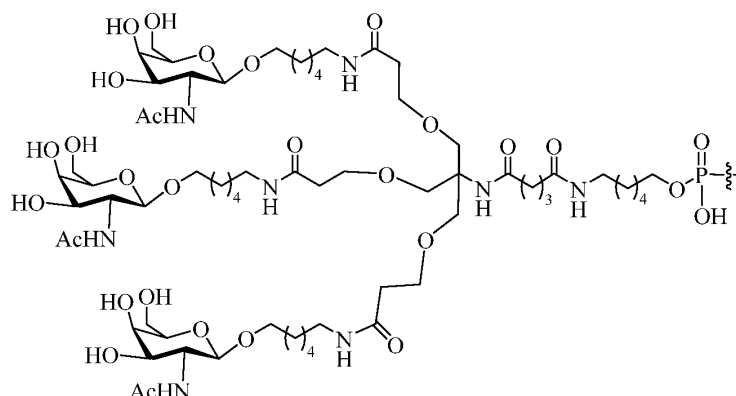
T = a thymine nucleobase,

k = a cEt sugar moiety,

d = a 2'- $\beta$ -D-deoxyribose sugar moiety,

s = a phosphorothioate internucleoside linkage, and

THA-GalNAc- $_o$  =



58. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation: THA-GalNAc-<sub>o</sub>A<sub>ks</sub>G<sub>ks</sub>T<sub>ks</sub>A<sub>ds</sub>T<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>T<sub>ds</sub>G<sub>ks</sub>T<sub>ks</sub>T<sub>k</sub> (SEQ ID NO: 3039), wherein

A = an adenine nucleobase,

G = a guanine nucleobase,

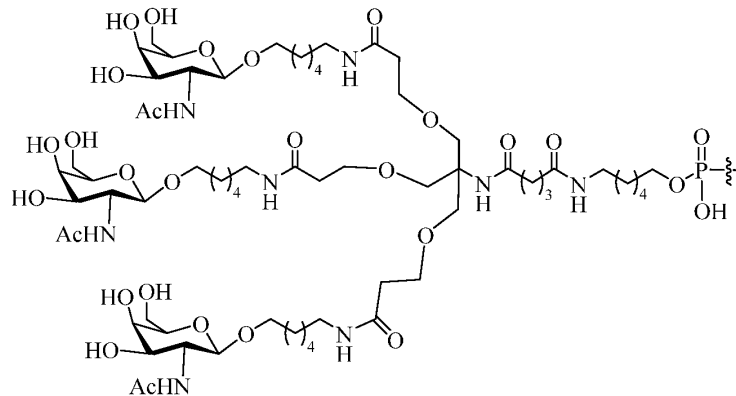
T = a thymine nucleobase,

k = a cEt sugar moiety,

d = a 2'-β-D-deoxyribsyl sugar moiety,

s = a phosphorothioate internucleoside linkage, and

THA-GalNAc-<sub>o</sub> =



59. An oligomeric compound comprising a modified oligonucleotide and a conjugate group according to the following chemical notation: THA-GalNAc-<sub>o</sub><sup>m</sup>C<sub>ks</sub>T<sub>ks</sub>A<sub>ds</sub>T<sub>ds</sub>T<sub>ds</sub>G<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>G<sub>ds</sub>A<sub>ds</sub>A<sub>ds</sub>G<sub>ks</sub>T<sub>es</sub>G<sub>ks</sub>T<sub>es</sub>A<sub>k</sub> (SEQ ID NO: 3041), wherein

A = an adenine nucleobase,

<sup>m</sup>C = a 5-methyl cytosine nucleobase,

G = a guanine nucleobase,

T = a thymine nucleobase,

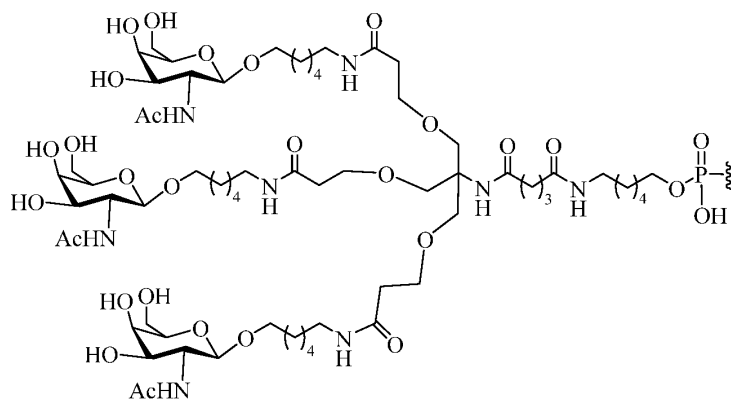
e = a 2'-OCH<sub>2</sub>CH<sub>2</sub>OCH<sub>3</sub> modified ribosyl sugar moiety,

k = a cEt sugar moiety

d = a 2'-β-D-deoxyribose sugar moiety

s = a phosphorothioate internucleoside linkage, and

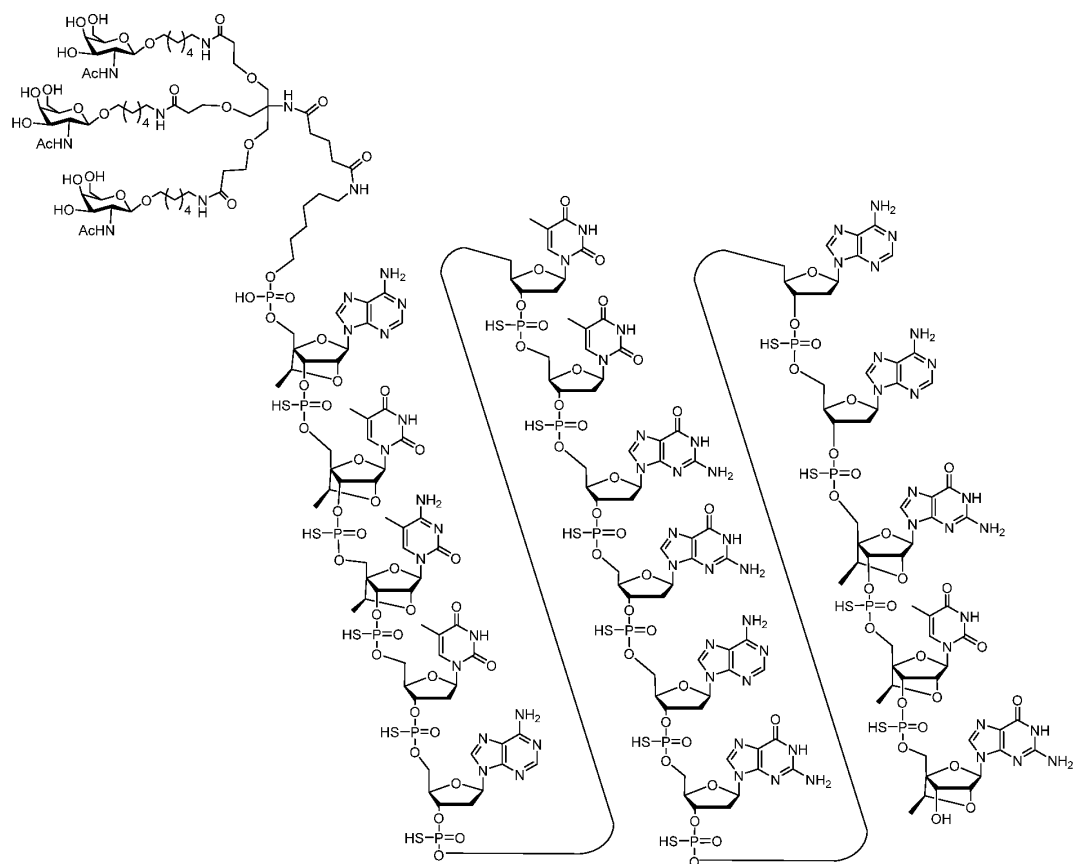
THA-GalNAc-o =



60. The oligomeric compound of any of claims 1 to 59, wherein the oligomeric compound comprises a terminal group.

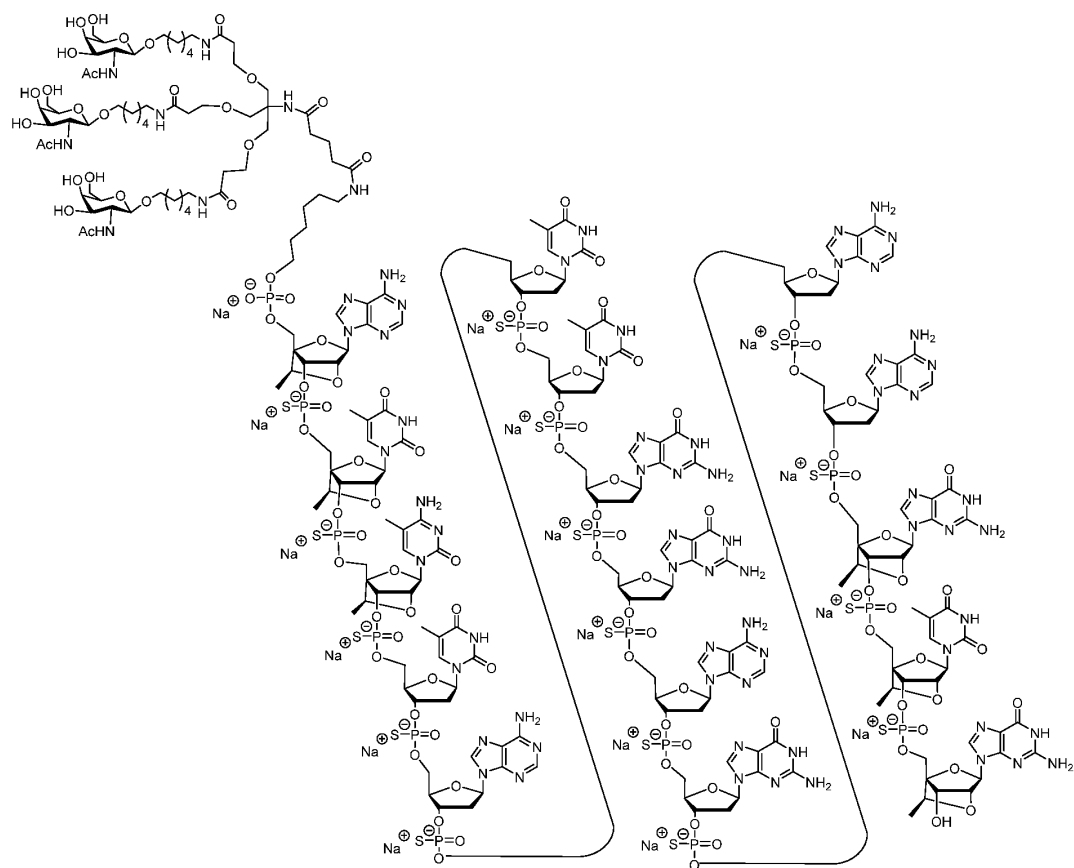
61. The oligomeric compound of claim 60, wherein the terminal group is an abasic sugar moiety.

62. An oligomeric compound according to the following chemical structure:



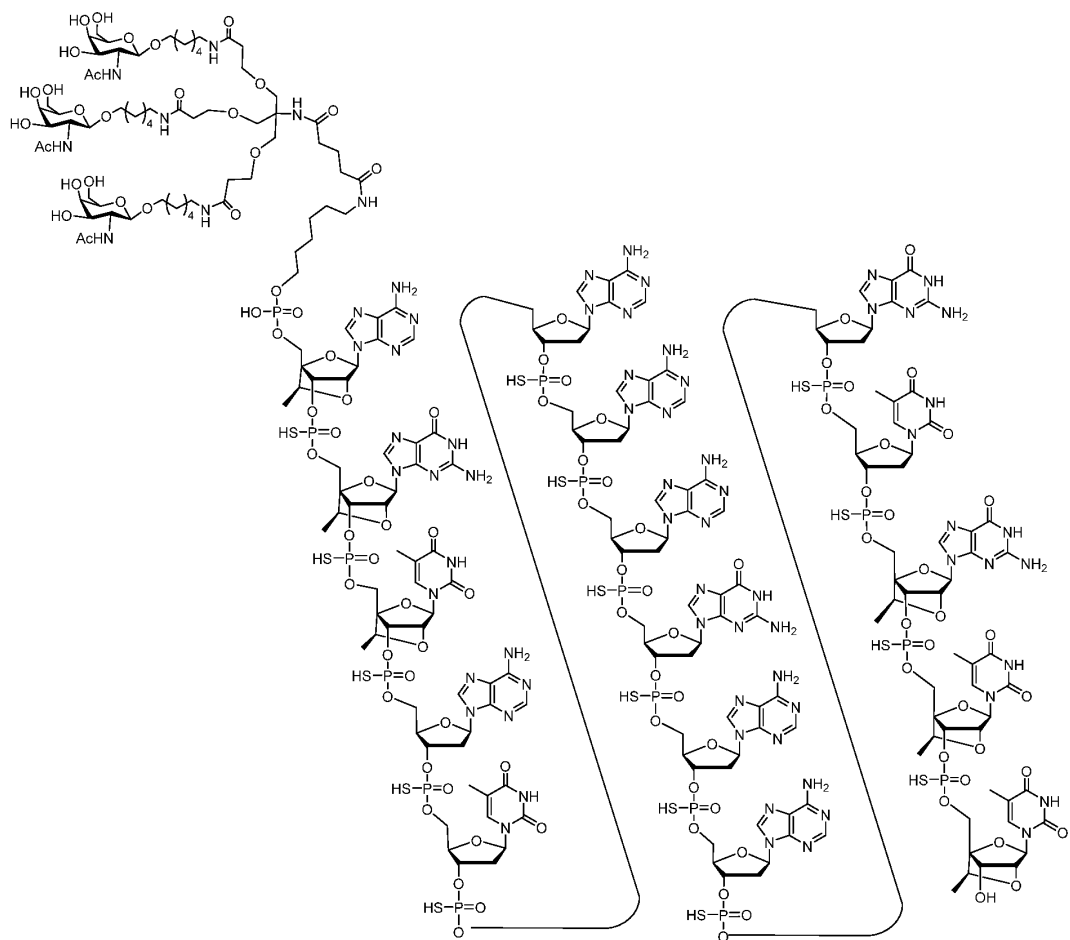
(SEQ ID NO: 3037), or a salt thereof.

63. The oligomeric compound of claim 62, which is the sodium salt or the potassium salt.
64. An oligomeric compound according to the following chemical structure:



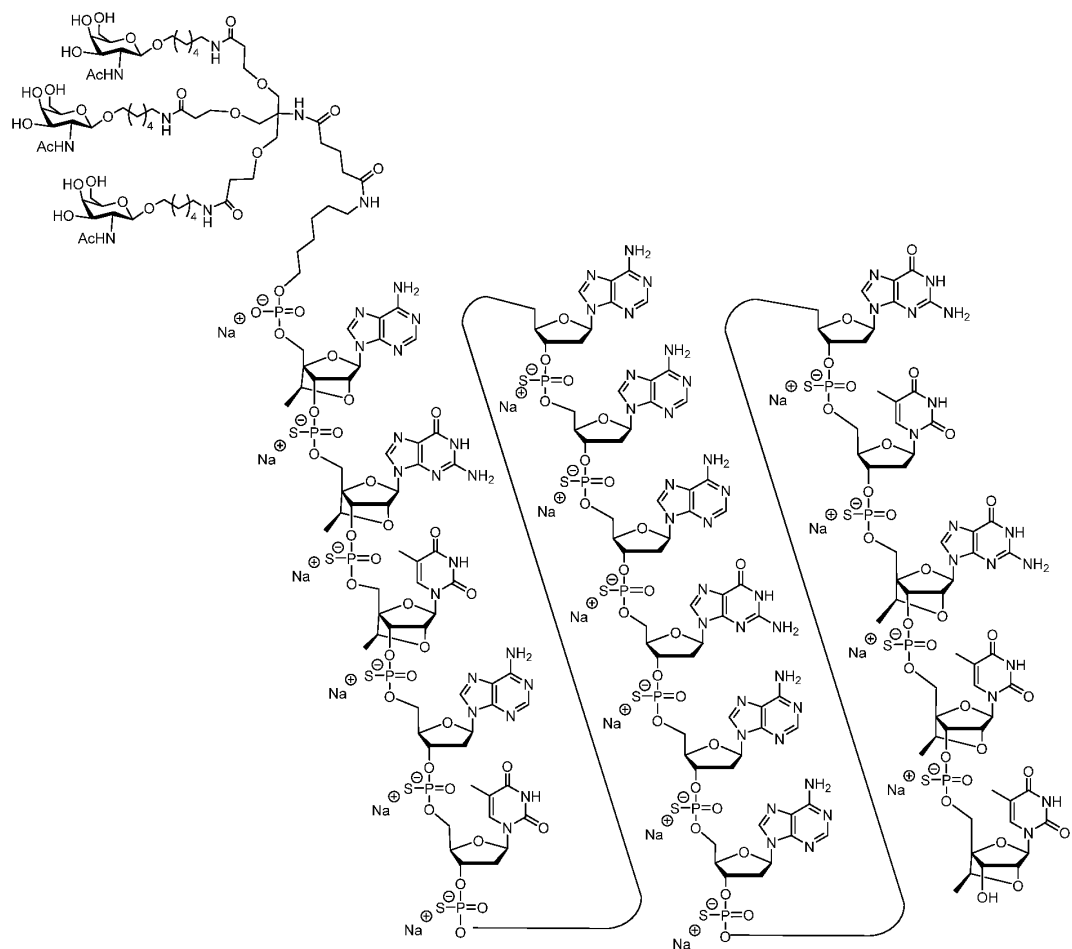
(SEQ ID NO: 3037).

65. An oligomeric compound according to the following chemical structure:



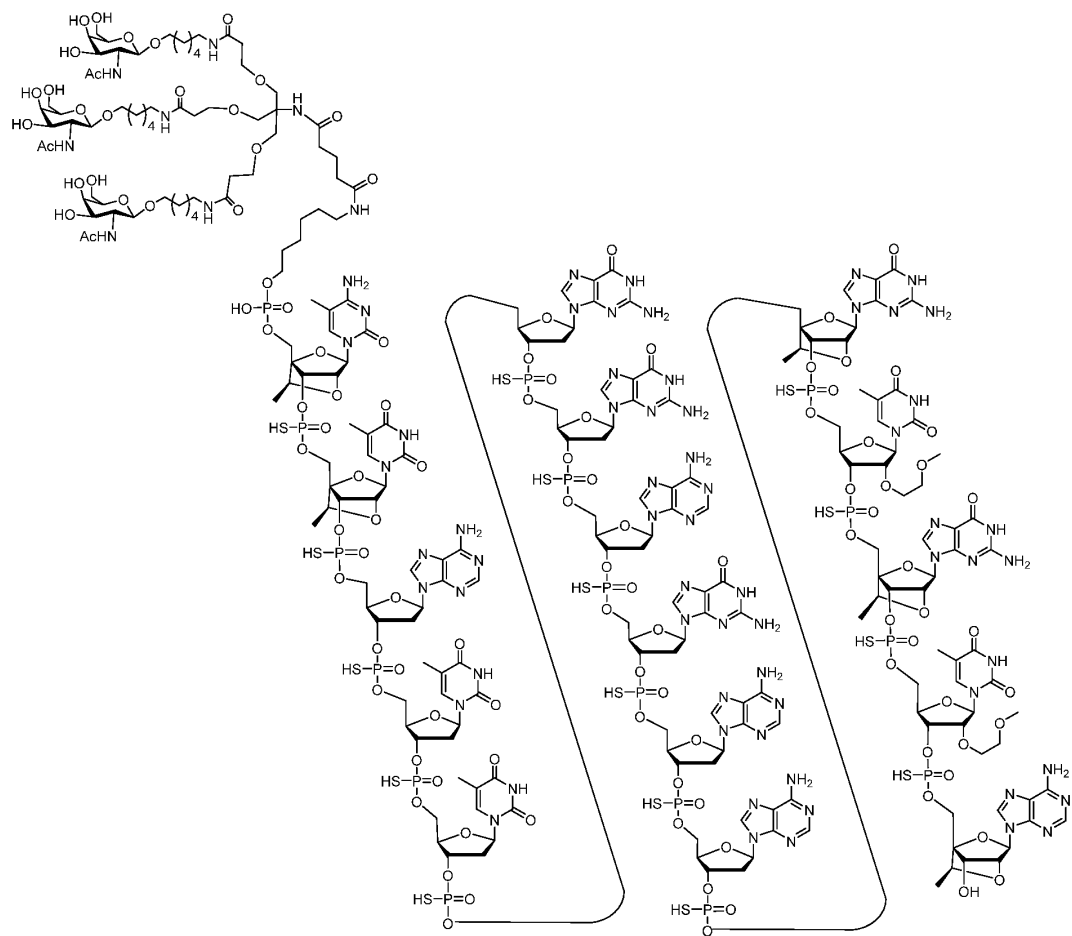
(SEQ ID NO: 3039), or a salt thereof.

66. The oligomeric compound of claim 65, which is the sodium salt or the potassium salt.
67. An oligomeric compound according to the following chemical structure:



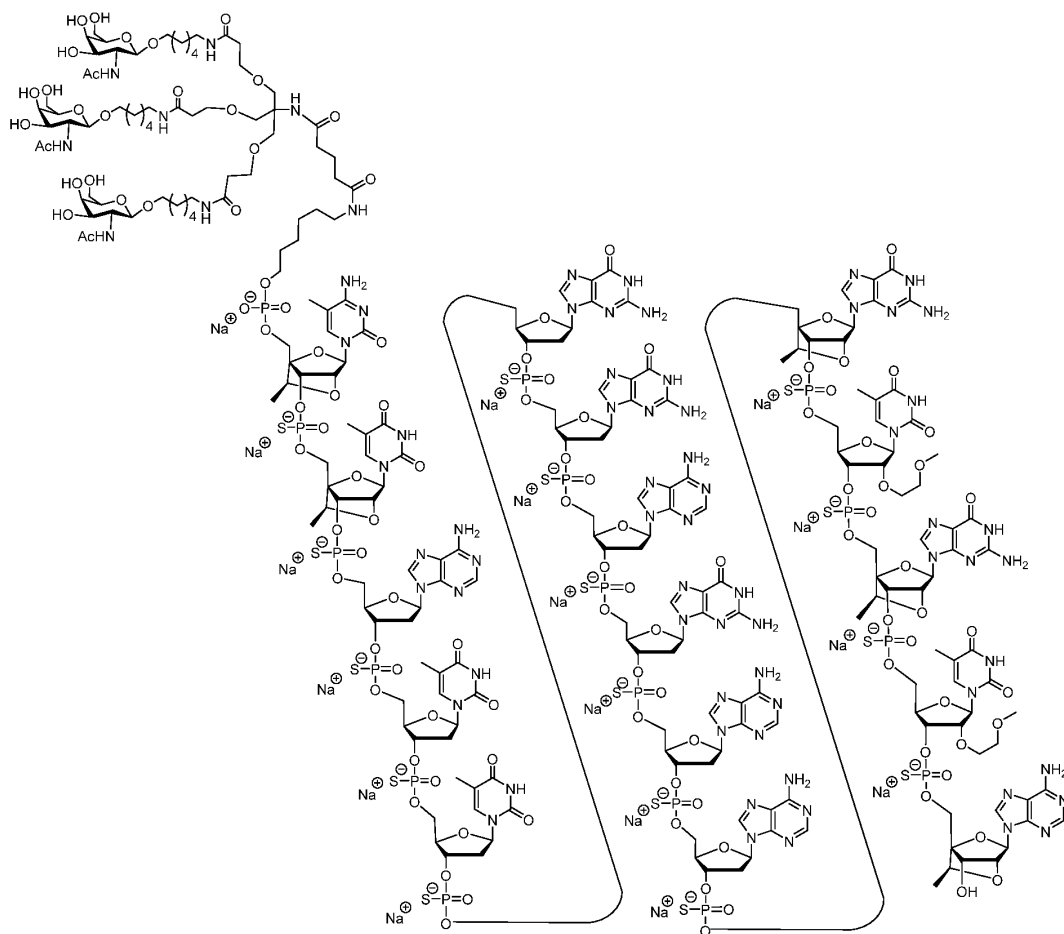
(SEQ ID NO: 3039).

68. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3041), or a salt thereof.

69. The oligomeric compound of claim 68, which is the sodium salt or the potassium salt.
70. An oligomeric compound according to the following chemical structure:



(SEQ ID NO: 3041).

71. A chirally enriched population of oligomeric compounds of any of claims 1-70, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having a particular stereochemical configuration.

72. The chirally enriched population of claim 71, wherein the population is enriched for modified oligonucleotides comprising at least one particular phosphorothioate internucleoside linkage having the (*Sp*) or (*Rp*) configuration.

73. The chirally enriched population of claim 71, wherein the population is enriched for modified oligonucleotides having a particular, independently selected stereochemical configuration at each phosphorothioate internucleoside linkage.

74. The chirally enriched population of claim 71, wherein the population is enriched for modified oligonucleotides having the (*Rp*) configuration at one particular phosphorothioate internucleoside linkage and the (*Sp*) configuration at each of the remaining phosphorothioate internucleoside linkages.

75. The chirally enriched population of claim 71, wherein the population is enriched for modified oligonucleotides having at least 3 contiguous phosphorothioate internucleoside linkages in the *Sp*, *Sp*, and *Rp* configurations, in the 5' to 3' direction.

76. A population of oligomeric compounds comprising modified oligonucleotides of any of claims 1-70 wherein all of the phosphorothioate internucleoside linkages of the modified oligonucleotide are stereorandom.

77. An oligomeric duplex, comprising a first oligomeric compound and a second oligomeric compound comprising a second modified oligonucleotide, wherein the first oligomeric compound is an oligomeric compound of any of claims 1-70.

78. The oligomeric duplex of claim 77, wherein the second oligomeric compound comprises a second modified oligonucleotide consisting of 8 to 80 linked nucleosides, and wherein the nucleobase sequence of the second modified oligonucleotide comprises a complementary region of at least 8 nucleobases that is at least 90% complementary to an equal length portion of the first modified oligonucleotide.

79. The oligomeric duplex of claim 77 or 78, wherein the modified oligonucleotide of the first oligomeric compound comprises a 5'-stabilized phosphate group.

80. The oligomeric duplex of claim 79, wherein the stabilized phosphate group comprises a cyclopropyl phosphonate or a vinyl phosphonate.

81. The oligomeric duplex of any of claims 77-80, wherein the modified oligonucleotide of the first oligomeric compound comprises a glycol nucleic acid (GNA) sugar surrogate.

82. The oligomeric duplex of any of claims 77-80, wherein the modified oligonucleotide of the first oligomeric compound comprises a 2'-NMA sugar moiety.

83. The oligomeric duplex of any of claims 77-82, wherein at least one nucleoside of the second modified oligonucleotide comprises a modified sugar moiety.

84. The oligomeric duplex of claim 83, wherein the modified sugar moiety of the second modified oligonucleotide comprises a bicyclic sugar moiety.

85. The oligomeric duplex of claim 84, wherein the bicyclic sugar moiety of the second modified oligonucleotide comprises a 2'-4' bridge selected from -O-CH<sub>2</sub>-; and -O-CH(CH<sub>3</sub>)-

86. The oligomeric duplex of claim 83, wherein the modified sugar moiety of the second modified oligonucleotide comprises a non-bicyclic modified sugar moiety.

87. The oligomeric duplex of claim 86, wherein the non-bicyclic modified sugar moiety of the second modified oligonucleotide is a 2'-MOE sugar moiety, a 2'-F sugar moiety, or 2'-OMe sugar moiety.

88. The oligomeric duplex of any of claims 77-87, wherein at least one nucleoside of the second modified oligonucleotide comprises a sugar surrogate.

89. The oligomeric duplex of any of claims 77-88, wherein at least one internucleoside linkage of the second modified oligonucleotide is a modified internucleoside linkage.

90. The oligomeric duplex of claim 89, wherein at least one modified internucleoside linkage of the second modified oligonucleotide is a phosphorothioate internucleoside linkage.

91. The oligomeric duplex of claim 89 or 90, wherein at least one modified internucleoside linkage of the second modified oligonucleotide is a mesyl phosphoramidate internucleoside linkage.

92. The oligomeric duplex of any of claims 77-91, wherein at least one internucleoside linkage of the second modified oligonucleotide is a phosphodiester internucleoside linkage.

93. The oligomeric duplex of any of claims 77-90 or 92, wherein each internucleoside linkage of the second modified oligonucleotide is independently selected from a phosphodiester or a phosphorothioate internucleoside linkage.

94. The oligomeric duplex of any of claims 77-92, wherein each internucleoside linkage of the second modified oligonucleotide is independently selected from a phosphodiester internucleoside linkage, a phosphorothioate internucleoside linkage, or a mesyl phosphoramidate internucleoside linkage.

95. The oligomeric duplex of any of claims 77-94, wherein the second modified oligonucleotide comprises at least one modified nucleobase.

96. The oligomeric duplex of claim 95, wherein the modified nucleobase of the second modified oligonucleotide is 5-methylcytosine.

97. The oligomeric duplex of any of claims 77-96, wherein the second modified oligonucleotide comprises a conjugate group.

98. The oligomeric duplex of claim 97, wherein the conjugate group comprises a conjugate linker and a conjugate moiety.

99. The oligomeric duplex of claim 97 or 98, wherein the conjugate group is attached to the second modified oligonucleotide at the 5'-end of the second modified oligonucleotide.

100. The oligomeric duplex of claim 97 or 98, wherein the conjugate group is attached to the second modified oligonucleotide at the 3'-end of the modified oligonucleotide.

101. The oligomeric duplex of any of claims 97-100, wherein the conjugate group comprises N-acetyl galactosamine.

102. The oligomeric duplex of any of claims 97-101, wherein the second modified oligonucleotide comprises a terminal group.

103. The oligomeric duplex of claim 102, wherein the terminal group is an abasic sugar moiety.

104. The oligomeric duplex of any of claims 77-103, wherein the second modified oligonucleotide consists of 10 to 25, 10 to 30, 10 to 50, 12 to 20, 12 to 25, 12 to 30, 12 to 50, 13 to 20, 13 to 25, 13 to 30, 13 to 50, 14 to 20, 14 to 25, 14 to 30, 14 to 50, 15 to 20, 15 to 25, 15 to 30, 15 to 50, 16 to 18, 16 to 20, 16 to 25, 16 to 30, 16 to 50, 17 to 20, 17 to 25, 17 to 30, 17 to 50, 18 to 20, 18 to 25, 18 to 30, 18 to 50, 19 to 20, 19 to 25, 19 to 30, 19 to 50, 20 to 25, 20 to 30, 20 to 50, 21 to 25, 21 to 30, 21 to 50, 22 to 25, 22 to 30, 22 to 50, 23 to 25, 23 to 30, or 23 to 50 linked nucleosides.

105. An antisense agent comprising an antisense compound, wherein the antisense compound is the oligomeric compound of any of claims 1-70.

106. The antisense agent of claim 105, wherein the antisense agent is the oligomeric duplex of any of claims 77-104.

107. The antisense agent of claim 105 or 106, wherein the antisense agent is:

- iii. an RNase H agent capable of reducing the amount of PSD3 nucleic acid through the activation of RNase H; or
- iv. an RNAi agent capable of reducing the amount of PSD3 nucleic acid through the activation of RISC/Ago2.

108. The antisense agent of any of claims 105-107, wherein the conjugate group is a cell-targeting moiety.
109. A pharmaceutical composition comprising the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, or the antisense agent of any of claims 105-108, and a pharmaceutically acceptable diluent or carrier.
110. The pharmaceutical composition of claim 109, wherein the pharmaceutically acceptable diluent is water or phosphate-buffered saline.
111. The pharmaceutical composition of claim 110, wherein the pharmaceutical composition consists essentially of the oligomeric compound, the modified oligonucleotide, the oligomeric duplex, or the antisense agent, and water or phosphate-buffered saline.
112. A method comprising administering to a subject the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111.
113. A method of treating a disease associated with PSD3 comprising administering to a subject having a disease associated with PSD3 a therapeutically effective amount of the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111; thereby treating the disease associated with PSD3.
114. The method of claim 113, wherein the disease associated with PSD3 is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH), liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.
115. The method of claim 114, wherein administering the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111 reduces liver damage, steatosis, liver fibrosis, liver inflammation, liver scarring or cirrhosis, liver failure, liver enlargement, elevated transaminases, or hepatic fat accumulation in the subject.
116. A method of reducing expression of PSD3 in a cell comprising contacting the cell with the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111.
117. The method of claim 116, wherein the cell is a liver cell.
118. Use of the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111 for treating a disease associated with PSD3.
119. Use of the oligomeric compound of any of claims 1-70, the population of any of claims 71-76, the oligomeric duplex of any of claims 77-104, the antisense agent of any of claims 105-108, or the pharmaceutical composition of any of claims 109-111 in the manufacture of a medicament for treating a disease associated with PSD3.
120. The use of claim 118 or 119, wherein the disease associated with PSD3 is liver disease, fatty liver disease (FLD), nonalcoholic fatty liver disease (NAFLD), hepatic steatosis, non-alcoholic steatohepatitis (NASH),

liver cirrhosis, hepatocellular carcinoma, alcoholic liver disease, alcoholic steatohepatitis (ASH), HCV hepatitis, chronic hepatitis, hereditary hemochromatosis, or primary sclerosing cholangitis.