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(57) Abrégé/Abstract:

The present invention relates to oligonucleotides that are complementary to and modulate the expression of TMEM106B. The present invention further relates to conjugates of the oligonucleotide and pharmaceutical compositions and methods for treatment of neurological disorders using the oligonucleotide.

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(54) Title: OLIGONUCLEOTIDES FOR MODULATING TMEM106B EXPRESSION

(57) Abstract: The present invention relates to oligonucleotides that are complementary to and modulate the expression of TMEM106B. The present invention further relates to conjugates of the oligonucleotide and pharmaceutical compositions and methods for treatment of neurological disorders using the oligonucleotide.



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OLIGONUCLEOTIDES FOR MODULATING TMEM106B EXPRESSION

FIELD OF INVENTION

The present invention relates to oligonucleotides complementary to Transmembrane protein 106B (TMEM106B), which are capable of modulation of the expression of TMEM106B.

- 5 Modulation of TMEM106B expression is beneficial for a range of medical disorders, such as neurological disorders, in particular neurodegenerative disorders, such as frontotemporal lobar degeneration.

BACKGROUND

- Transmembrane protein 106B (TMEM106B) is a single-pass, type 2 integral membrane glycoprotein predominantly located in the membranes of endosomes and lysosomes. It is expressed in neurons as well as glial and endothelial cells. It is believed to be involved in dendrite morphogenesis, such as dendrite branching as well as in lysosomal functioning. TMEM106B has been associated with several common neurodegenerative disorders including frontotemporal lobar degeneration (FTLD) (Nicholson and Rademakers, *Acta Neuropathol.* 2016 November; 132(5): 639–651).

Klein et al., 2017, *Neuron* 95, 281–296 reports that the loss of TMEM106B ameliorates lysosomal and frontotemporal dementia-related phenotypes in progranulin-deficient mice.

Rostgaard et al., *Neurobiology of Aging* 59 (2017) 221.e1e221.e7 reports on TMEM106B and ApoE polymorphisms in CHMP2B-mediated frontotemporal dementia (FTD-3).

- 20 Hu et al., *Journal of the Neurological Sciences* 377 (2017) 65–71 reports on the association of certain polymorphisms in the TMEM106B genes in Parkinson's disease, amyotrophic lateral sclerosis (ALS) and multiple system atrophy (MSA).

- Gallagher et al., *The American Journal of Human Genetics* 101, 643–663, November 2, 2017 reports on a dementia-associated risk variant near TMEM106B which alters chromatin architecture and gene expression.

Simons et al., *Brain* 2017; 140; 3105-3111 reports that a recurrent de novo mutation in TMEM106B causes hypomyelinating leukodystrophy.

- Holler et al. *eNeuro.* 2017 Jul-Aug; 4(4): ENEURO.0100-17.2017 show that lysosome dysfunction induced by e.g. alkalinizing agents or increased expression of TMEM106B inhibits processing of progranulin (PGRN) into granulins (GRNs). They also show that multiple GRNs are haploinsufficient in primary fibroblasts and cortical brain tissue from FTD-GRN patients. This may apply to Neuronal Ceroid Lipofuscinosis (NCL) as homozygous or heterozygous mutations

in the *GRN* gene, encoding progranulin (PGRN), cause neuronal ceroid lipofuscinosis (NCL) or frontotemporal dementia (FTD), respectively.

Gotzl et al. Acta Neuropathol.127(6):845-60. reports elevations in TMEM106b and GRN proteins in cathepsin D knock out mice, a model of NCL.

- 5 Schwenk et al., EMBO J. 2014 Mar 3;33(5):450-67 reports on FTLT-TDP risk factor TMEM106B and its functional interaction with MAP6 to control dendritic trafficking of lysosomes. siRNAs against TMEM106B was transfected into HeLa cells showing reduction TMEM106B protein expression resulting in lysosomal clustering near the nucleus. Furthermore TMEM106B knock down using shRNA transfected into hippocampal neurons impaired dendrite branching. The
- 10 changes caused in dendritic morphology by TMEM106B knock down may cause impaired synaptic strength and plasticity which are common attributes of neurodegenerative diseases. This implies that knock down of TMEM106B may cause neurodegenerative disease.

- WO2015/127037 reports on compounds and method for the treatment of neurodegenerative diseases, including small molecule compounds which are reported as being effective in
- 15 modulating the expression of a range of genes, including TMEM106B. There does not appear to be any data indicating TMEM106B inhibition by the disclosed compounds.

- Neurodegenerative disorders represent a major unmet medical need, and there is clear genetic and experimental evidence which indicates TMEM106B expression, and specific TMEM106B allele with neurodegenerative disorders. There is therefore a need for inhibitors of TMEM106B
- 20 for use in research and therapeutic applications.

OBJECTIVE OF THE INVENTION

The present invention provides nucleic acid inhibitors of TMEM106B which may be used both *in vivo* and *in vitro* for down-regulation of TMEM106B expression, and for the therapeutic intervention in neurological disorders.

25 SUMMARY OF INVENTION

The present invention relates to oligonucleotides that are complementary to and modulate the expression of TMEM106B. The present invention further relates to conjugates of the oligonucleotide and pharmaceutical compositions and methods for treatment of neurological disorders using the oligonucleotide.

- 30 The present invention provides oligonucleotide inhibitors of TMEM106B for decreasing the expression of TMEM106B in cells, and which may be used for the treatment of neurological disorders, such as neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and

multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

The present invention provides oligonucleotide inhibitors of TMEM106B for decreasing the expression of TMEM106B in cells, and which may be used for the treatment of frontotemporal lobar degeneration (FTLD).

The present invention relates to oligonucleotides targeting a nucleic acid capable of inhibiting the expression of TMEM106B and to treat or prevent diseases related to the functioning of the TMEM106B.

The invention provides for an oligonucleotide targeting TMEM106B, which comprises a contiguous nucleotide sequence of 10 – 30 nucleotides in length with at least 90% complementary, such as fully complementary, to a mammalian TMEM106B target nucleic acid.

The invention provides for an oligonucleotide, 10 – 40 nucleotides in length, targeting TMEM106B, which comprises a contiguous nucleotide sequence of 10 – 30 nucleotides in length with at least 90% complementary, such as fully complementary, to a mammalian TMEM106B target nucleic acid.

The oligonucleotide of the invention may for example be an antisense oligonucleotide (ASO), which is capable of inhibiting the expression of TMEM106B in a cell which is expressing TMEM106B.

The oligonucleotide of the invention may for example be a siRNA (or the antisense strand of a siRNA), which is capable of inhibiting the expression of TMEM106B in a cell which is expressing TMEM106B.

The invention provides an oligonucleotide which comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementarity to a mammalian TMEM106B target nucleic acid, wherein the oligonucleotide is capable of inhibiting the expression of TMEM106B in a cell which is expressing the TMEM106B target nucleic acid.

The invention provides an antisense oligonucleotide which comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementarity to a mammalian TMEM106B target nucleic acid, wherein the antisense oligonucleotide is capable of inhibiting the expression of TMEM106B in a cell which is expressing the TMEM106B target nucleic acid. Advantageously, the oligonucleotide may be an antisense oligonucleotide which is capable of recruiting RNaseH, such as human RNaseH1, such as a gapmer oligonucleotide.

The invention provides for a conjugate comprising the oligonucleotide, such as the antisense oligonucleotide or siRNA, according to the invention, and at least one conjugate moiety covalently attached to said oligonucleotide.

The invention provides for a pharmaceutically acceptable salt of the oligonucleotide of the invention, such as the antisense oligonucleotide or siRNA of the invention, or conjugate thereof.

The invention provides for a pharmaceutical composition comprising the oligonucleotide of the invention, such as the antisense oligonucleotide or siRNA of the invention, or conjugate thereof, and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

The invention provides for a method for modulating TMEM106B expression in a target cell which is expressing TMEM106B, said method comprising administering an oligonucleotide of the invention, such as the antisense oligonucleotide or siRNA of the invention, or conjugate or the pharmaceutical salt or pharmaceutical composition, in an effective amount to said cell. The method may, for example, be an *in vitro* method or an *in vivo* method.

The invention provides for a method for treating or preventing a disease comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide of the invention, such as the antisense oligonucleotide or siRNA of the invention, or conjugate thereof, or the pharmaceutical salt or pharmaceutical composition of the invention, to a subject suffering from or susceptible to the disease.

In some embodiments, the method is for treating a neurodegenerative disease in a subject who has been diagnosed with, or is suffering from, a neurodegenerative disease, such as a neurodegenerative disease selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

In some embodiments the compounds of the invention are used for the treatment of age associated changes in frontal cortex.

The method for treating or preventing a disease may, for example be for treating or preventing a neurodegenerative disease, such as a disease selected from the list consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

The invention provides for the oligonucleotide, such as the antisense oligonucleotide or siRNA of the invention, or conjugate thereof, or the pharmaceutical salt or pharmaceutical composition of the invention, for use in medicine.

The invention provides for the oligonucleotide, such as the antisense oligonucleotide or siRNA of the invention, or conjugate thereof, or pharmaceutical salt or pharmaceutical composition of the invention, for use in the treatment of a neurodegenerative disease such as a disease selected from the group consisting of prevention of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal Ceroid Lipofuscinosis (NCL).

The invention provides for the use of the oligonucleotide of the invention, such as the antisense oligonucleotide or siRNA of the invention, or the conjugate thereof, or pharmaceutical salt or pharmaceutical composition of the invention, for the preparation of a medicament for treatment or prevention of a neurodegenerative disease such as a disease selected from the group consisting of prevention of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal Ceroid Lipofuscinosis (NCL).

BRIEF DESCRIPTION OF FIGURES

Figure 1: Target inhibition after 3 days of incubation in mouse Neuro-2a cells at 5 μ M vs 25 μ M compared to PBS-treated control (mean of two biological replicates).

Figure 2: Target inhibition after 6 days of incubation in mouse Neuro-2a cells at 5 μ M vs 25 μ M compared to PBS-treated control (mean of two biological replicates).

Figure 3: Caspase activation 24 hours after transfection of gapmers compared to PBS-treated controls (mean of biological replicates).

Figure 4: Target inhibition after 3 days of incubation in human SK-N-BE(2) cells at 5 μ M vs 25 μ M (mean of two biological replicates).

Figure 5: Target inhibition after 6 days of incubation in human SK-N-BE(2) cells at 5 μ M vs 25 μ M (mean of two biological replicates).

Figure 6: Target inhibition after 3 days of incubation in human SK-N-BE(2) cells at 5 μ M, illustrated vs. the position of the target sequence on Chromosome 7.

Figure 7A: Target inhibition after continuous 10 days treatment with ASOs in human iPSC neurons and astrocytes mix culture at increasing concentration for five human ASOs.

Figure 7B: Target inhibition after 10 days with 24 hrs pulse treatment with ASOs in human iPSC neurons and astrocytes mix culture at increasing concentration for five human ASOs.

Figure 7C: Automated western blot on reduction in TMEM106b protein level after continuous 10 days treatment with ASOs in human iPSC neurons and astrocytes mix culture.

Figure 8A: Time course for *in vivo* TMEM106b mRNA reduction after a single ICV injection of 100 µg LNA oligonucleotides in a volume of 5 µl saline into the right lateral ventricle (normalized to GAPDH).

Figure 8B: *In vivo* time course for *in vivo* TMEM106b protein reduction after a single ICV injection of 100 µg LNA oligonucleotides in a volume of 5 µl saline into the right lateral ventricle (normalized to beta-Tubulin).

Figure 9: Structural formula of CMP ID NO: 65_1. Pharmaceutical salts thereof include monovalent or divalent cations, such as Na⁺, K⁺, and Ca²⁺ or a mixture of these being associated with the compound.

Figure 10: Structural formula of CMP ID NO: 66_1. Pharmaceutical salts thereof include monovalent or divalent cations, such as Na⁺, K⁺, and Ca²⁺ or a mixture of these being associated with the compound.

Figure 11: Structural formula of CMP ID NO: 71_1. Pharmaceutical salts thereof include monovalent or divalent cations, such as Na⁺, K⁺, and Ca²⁺ or a mixture of these being associated with the compound.

Figure 12: Structural formula of CMP ID NO: 74_1. Pharmaceutical salts thereof include monovalent or divalent cations, such as Na⁺, K⁺, and Ca²⁺ or a mixture of these being associated with the compound.

Figure 13: Structural formula of CMP ID NO: 75_1. Pharmaceutical salts thereof include monovalent or divalent cations, such as Na⁺, K⁺, and Ca²⁺ or a mixture of these being associated with the compound.

DEFINITIONS

In the present description the term “alkyl”, alone or in combination, signifies a straight-chain or branched-chain alkyl group with 1 to 8 carbon atoms, particularly a straight or branched-chain alkyl group with 1 to 6 carbon atoms and more particularly a straight or branched-chain alkyl group with 1 to 4 carbon atoms. Examples of straight-chain and branched-chain C₁-C₈ alkyl groups are methyl, ethyl, propyl, isopropyl, butyl, isobutyl, tert.-butyl, the isomeric pentyls, the isomeric hexyls, the isomeric heptyls and the isomeric octyls, particularly methyl, ethyl, propyl, butyl and pentyl. Particular examples of alkyl are methyl, ethyl and propyl.

The term “cycloalkyl”, alone or in combination, signifies a cycloalkyl ring with 3 to 8 carbon atoms and particularly a cycloalkyl ring with 3 to 6 carbon atoms. Examples of cycloalkyl are

cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, cycloheptyl and cyclooctyl, more particularly cyclopropyl and cyclobutyl. A particular example of "cycloalkyl" is cyclopropyl.

The term "alkoxy", alone or in combination, signifies a group of the formula alkyl-O- in which the term "alkyl" has the previously given significance, such as methoxy, ethoxy, n-propoxy,

5 isopropoxy, n-butoxy, isobutoxy, sec.butoxy and tert.butoxy. Particular "alkoxy" are methoxy and ethoxy. Methoxyethoxy is a particular example of "alkoxyalkoxy".

The term "oxy", alone or in combination, signifies the -O- group.

The term "alkenyl", alone or in combination, signifies a straight-chain or branched hydrocarbon residue comprising an olefinic bond and up to 8, preferably up to 6, particularly preferred up to 4
10 carbon atoms. Examples of alkenyl groups are ethenyl, 1-propenyl, 2-propenyl, isopropenyl, 1-butenyl, 2-butenyl, 3-butenyl and isobutenyl.

The term "alkynyl", alone or in combination, signifies a straight-chain or branched hydrocarbon residue comprising a triple bond and up to 8, preferably up to 6, particularly preferred up to 4 carbon atoms.

15 The terms "halogen" or "halo", alone or in combination, signifies fluorine, chlorine, bromine or iodine and particularly fluorine, chlorine or bromine, more particularly fluorine. The term "halo", in combination with another group, denotes the substitution of said group with at least one halogen, particularly substituted with one to five halogens, particularly one to four halogens, *i.e.* one, two, three or four halogens.

20 The term "haloalkyl", alone or in combination, denotes an alkyl group substituted with at least one halogen, particularly substituted with one to five halogens, particularly one to three halogens. Examples of haloalkyl include monofluoro-, difluoro- or trifluoro-methyl, -ethyl or -propyl, for example 3,3,3-trifluoropropyl, 2-fluoroethyl, 2,2,2-trifluoroethyl, fluoromethyl or trifluoromethyl. Fluoromethyl, difluoromethyl and trifluoromethyl are particular "haloalkyl".

25 The term "halocycloalkyl", alone or in combination, denotes a cycloalkyl group as defined above substituted with at least one halogen, particularly substituted with one to five halogens, particularly one to three halogens. Particular example of "halocycloalkyl" are halocyclopropyl, in particular fluorocyclopropyl, difluorocyclopropyl and trifluorocyclopropyl.

The terms "hydroxyl" and "hydroxy", alone or in combination, signify the -OH group.

30 The terms "thiohydroxyl" and "thiohydroxy", alone or in combination, signify the -SH group.

The term "carbonyl", alone or in combination, signifies the -C(O)- group.

The term "carboxy" or "carboxyl", alone or in combination, signifies the -COOH group.

The term "amino", alone or in combination, signifies the primary amino group (-NH₂), the secondary amino group (-NH-), or the tertiary amino group (-N-).

35 The term "alkylamino", alone or in combination, signifies an amino group as defined above substituted with one or two alkyl groups as defined above.

The term "sulfonyl", alone or in combination, means the -SO₂ group.

The term “sulfinyl”, alone or in combination, signifies the -SO- group.

The term “sulfanyl”, alone or in combination, signifies the -S- group.

The term “cyano”, alone or in combination, signifies the -CN group.

The term “azido”, alone or in combination, signifies the -N₃ group.

5 The term “nitro”, alone or in combination, signifies the NO₂ group.

The term “formyl”, alone or in combination, signifies the -C(O)H group.

The term “carbamoyl”, alone or in combination, signifies the -C(O)NH₂ group.

The term “cabamido”, alone or in combination, signifies the -NH-C(O)-NH₂ group.

The term “aryl”, alone or in combination, denotes a monovalent aromatic carbocyclic mono- or
10 bicyclic ring system comprising 6 to 10 carbon ring atoms, optionally substituted with 1 to 3
substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy,
alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl and formyl. Examples of aryl
include phenyl and naphthyl, in particular phenyl.

The term “heteroaryl”, alone or in combination, denotes a monovalent aromatic heterocyclic
15 mono- or bicyclic ring system of 5 to 12 ring atoms, comprising 1, 2, 3 or 4 heteroatoms
selected from N, O and S, the remaining ring atoms being carbon, optionally substituted with 1
to 3 substituents independently selected from halogen, hydroxyl, alkyl, alkenyl, alkynyl, alkoxy,
alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl and formyl. Examples of
heteroaryl include pyrrolyl, furanyl, thienyl, imidazolyl, oxazolyl, thiazolyl, triazolyl, oxadiazolyl,
20 thiadiazolyl, tetrazolyl, pyridinyl, pyrazinyl, pyrazolyl, pyridazinyl, pyrimidinyl, triazinyl, azepinyl,
diazepinyl, isoxazolyl, benzofuranyl, isothiazolyl, benzothienyl, indolyl, isoindolyl,
isobenzofuranyl, benzimidazolyl, benzoxazolyl, benzoisoxazolyl, benzothiazolyl,
benzoisothiazolyl, benzooxadiazolyl, benzothiadiazolyl, benzotriazolyl, purinyl, quinolinyl,
isoquinolinyl, quinazolinyl, quinoxalyl, carbazolyl or acridinyl.

25 The term “heterocyclyl”, alone or in combination, signifies a monovalent saturated or partly
unsaturated mono- or bicyclic ring system of 4 to 12, in particular 4 – 9, ring atoms, comprising 1,
2, 3 or 4 ring heteroatoms selected from N, O and S, the remaining ring atoms being carbon,
optionally substituted with 1 to 3 substituents independently selected from halogen, hydroxyl,
alkyl, alkenyl, alkynyl, alkoxy, alkoxyalkyl, alkenyloxy, carboxyl, alkoxycarbonyl, alkylcarbonyl
30 and formyl. Examples for monocyclic saturated heterocyclyl are azetidiny, pyrrolidinyl,
tetrahydrofuranyl, tetrahydro-thienyl, pyrazolidinyl, imidazolidinyl, oxazolidinyl, isoxazolidinyl,
thiazolidinyl, piperidinyl, tetrahydropyranyl, tetrahydrothiopyranyl, piperazinyl, morpholinyl,
thiomorpholinyl, 1,1-dioxo-thiomorpholin-4-yl, azepanyl, diazepanyl, homopiperazinyl, or
oxazepanyl. Examples for bicyclic saturated heterocycloalkyl are 8-aza-bicyclo[3.2.1]octyl,
35 quinuclidinyl, 8-oxa-3-aza-bicyclo[3.2.1]octyl, 9-aza-bicyclo[3.3.1]nonyl, 3-oxa-9-aza-
bicyclo[3.3.1]nonyl, or 3-thia-9-aza-bicyclo[3.3.1]nonyl. Examples for partly unsaturated

heterocycloalkyl are dihydrofuryl, imidazoliny, dihydro-oxazolyl, tetrahydro-pyridinyl or dihydropyranyl.

The term "pharmaceutically acceptable salts" refers to those salts which retain the biological effectiveness and properties of the free bases or free acids, which are not biologically or

5 otherwise undesirable. The salts are formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, particularly hydrochloric acid, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, N-acetylcystein. In addition these salts may be prepared from addition of an inorganic
10 base or an organic base to the free acid. Salts derived from an inorganic base include, but are not limited to, the sodium, potassium, lithium, ammonium, calcium, magnesium salts. Salts derived from organic bases include, but are not limited to salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic
15 amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, ethanolamine, lysine, arginine, N-ethylpiperidine, piperidine, polyamine resins. The compound of formula (I) can also be present in the form of zwitterions. Particularly preferred pharmaceutically acceptable salts of compounds of formula (I) are the salts of hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid and methanesulfonic
20 acid.

The term "protecting group", alone or in combination, signifies a group which selectively blocks a reactive site in a multifunctional compound such that a chemical reaction can be carried out selectively at another unprotected reactive site. Protecting groups can be removed. Exemplary
25 protecting groups are amino-protecting groups, carboxy-protecting groups or hydroxy-protecting groups.

If one of the starting materials or compounds of the invention contain one or more functional groups which are not stable or are reactive under the reaction conditions of one or more reaction steps, appropriate protecting groups (as described e.g. in "Protective Groups in Organic Chemistry" by T. W. Greene and P. G. M. Wuts, 3rd Ed., 1999, Wiley, New York) can be
30 introduced before the critical step applying methods well known in the art. Such protecting groups can be removed at a later stage of the synthesis using standard methods described in the literature. Examples of protecting groups are tert-butoxycarbonyl (Boc), 9-fluorenylmethyl carbamate (Fmoc), 2-trimethylsilylethyl carbamate (Teoc), carbobenzyloxy (Cbz) and p-methoxybenzyloxycarbonyl (Moz).

35 The compounds described herein can contain several asymmetric centers and can be present in the form of optically pure enantiomers, mixtures of enantiomers such as, for example,

racemates, mixtures of diastereoisomers, diastereoisomeric racemates or mixtures of diastereoisomeric racemates.

The term “asymmetric carbon atom” means a carbon atom with four different substituents.

According to the Cahn-Ingold-Prelog Convention an asymmetric carbon atom can be of the “R” or “S” configuration.

Nucleic acid molecule

The term “nucleic acid molecule” or “therapeutic nucleic acid molecule” as used herein is defined as it is generally understood by the skilled person as a molecule comprising two or more covalently linked nucleosides (i.e. a nucleotide sequence). The nucleic acid molecule(s) referred to in the invention are generally oligonucleotides of 10 - 50 nucleotides in length, and they are generally composed of one or two oligonucleotides. The nucleic acid molecules may be or comprise an antisense oligonucleotide, or may be another oligomeric nucleic acid molecule, such as a CRISPR RNA, a siRNA, shRNA, an aptamer, or a ribozyme. Therapeutic nucleic acid molecules are commonly made in the laboratory by solid-phase chemical synthesis followed by purification and isolation. shRNA's are however often delivered to cells using lentiviral vectors (see for example Soan and Yang 2010 N Am J Med Sci 2(12): 598) which are then transcribed to produce the single stranded RNA that will form a stem loop (hairpin) RNA structure that is capable of interacting with the RNA interference machinery (including the RNA-induced silencing complex (RISC)). When referring to a sequence of the nucleic acid molecule, reference is made to the sequence or order of nucleobase moieties, or modifications thereof, of the covalently linked nucleotides or nucleosides. The nucleic acid molecule(s) of the invention is man-made, and is chemically synthesized, and is typically purified or isolated. The nucleic acid molecule of the invention may comprise one or more modified nucleosides or nucleotides, such as 2'-sugar modified nucleosides, such as a high affinity modified antisense oligonucleotide.

In some embodiments, the nucleic acid molecule of the invention comprises or consists of 8 to 70 nucleotides in length, 10 to 60 nucleotides in length, 12 to 50 nucleotides in length, such as 8 to 40 nucleotides in length, such as from 9 to 35, such as from 10 to 30, such as from 11 to 22, such as from 12 to 20, such as from 13 to 18 or 14 to 16 contiguous nucleotides in length.

In some embodiments, the nucleic acid molecule or contiguous nucleotide sequence thereof comprises or consists of 24 or less nucleotides, such as 22 or less nucleotides, such as 20 or less nucleotides, such as 18 or less nucleotides, such as 14, 15, 16 or 17 nucleotides. It is to be understood that any range given herein includes the range endpoints. Accordingly, if a nucleic acid molecule is said to include from 10 to 30 nucleotides, both 10 and 30 nucleotides are included.

In some embodiments, the contiguous nucleotide sequence comprises or consists of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 contiguous nucleotides in length.

The nucleic acid molecule(s) is typically for modulating the expression of a target nucleic acid in a mammal. In some embodiments the nucleic acid molecule(s), such as siRNAs, shRNAs or antisense oligonucleotides, is typically for inhibiting the expression of a target nucleic acid.

In one embodiment of the invention the nucleic acid molecule is selected from a RNAi agent, such as a siRNA, shRNA.

In another embodiment the nucleic acid molecule is an antisense oligonucleotide, such as single stranded antisense oligonucleotide, such as a high affinity modified antisense oligonucleotide interacting with RNaseH.

In some embodiments the nucleic acid molecule comprises phosphorothioate internucleoside linkages. In some embodiments nucleic acid molecule comprise phosphorothioate linkages in the 5' end and the 3' end (e.g. independently 1-3 linkages in each end). In some embodiments the all the internucleoside linkages in nucleic acid molecule consists of phosphorothioate.

In some embodiments the nucleic acid molecule(s) may be conjugated to non-nucleosidic moieties (conjugate moieties).

Oligonucleotide

The term "oligonucleotide" or "therapeutic oligonucleotide" as used herein is defined as it is generally understood by the skilled person as a molecule comprising two or more covalently linked nucleosides. Such covalently bound nucleosides may also be referred to as nucleic acid molecules, oligonucleotides or oligomers. Oligonucleotides are commonly made in the laboratory by solid-phase chemical synthesis followed by purification. When referring to a sequence of the oligonucleotide, reference is made to the sequence or order of nucleobase moieties, or modifications thereof, of the covalently linked nucleotides or nucleosides. The oligonucleotide of the invention is man-made, and is chemically synthesized, and is typically purified or isolated. The oligonucleotide of the invention may comprise one or more modified nucleosides or nucleotides such as 2' sugar modified nucleosides.

The oligonucleotide of the invention comprises a contiguous nucleotide sequence which is complementary to the target nucleic acid or target sequence, and may, in some embodiments further comprise one or more additional nucleotides, such as 1 – 30, such as 1 – 20, such as 1 – 10, such as 1, 2, 3, 4 or 5 further nucleotides in addition to the contiguous nucleotide sequence. In some embodiments the additional nucleotides are complementary to the contiguous nucleotide sequence and are capable of forming a stem loop (hairpin) structure by hybridizing to the contiguous nucleotide sequence. In some embodiments the additional

nucleotides are 1 to 5 phosphodiester linked nucleotides. In some embodiments, all the nucleotides of the oligonucleotide form the contiguous nucleotide sequence.

Antisense oligonucleotides

The term "Antisense oligonucleotide" as used herein is defined as oligonucleotides capable of modulating expression of a target gene by hybridizing to a target nucleic acid, in particular to a contiguous sequence on a target nucleic acid. The antisense oligonucleotides are not essentially double stranded and are therefore not siRNAs or shRNAs. Preferably, the antisense oligonucleotides of the present invention are single stranded. It is understood that single stranded oligonucleotides of the present invention can form hairpins or intermolecular duplex structures (duplex between two molecules of the same oligonucleotide), as long as the degree of intra or inter self-complementarity is less than 50% across of the full length of the oligonucleotide.

Advantageously, the single stranded antisense oligonucleotide of the invention does not contain RNA nucleosides, since this will decrease nuclease resistance.

Advantageously, the antisense oligonucleotide of the invention comprises one or more modified nucleosides or nucleotides, such as 2' sugar modified nucleosides. Furthermore, it is advantageous that the nucleosides which are not modified are DNA nucleosides.

RNAi or siRNA

Herein, the term "RNA interference (RNAi) molecule" refers to any molecule inhibiting RNA expression or translation via the RNA reducing silencing complex (RISC) in a cell's cytoplasm, where the RNAi molecule interact with the catalytic RISC component argonaute. A small interfering RNA (siRNA) is typically a double-stranded RNA complex comprising a passenger (sense) and a guide (antisense) oligonucleotide (strand), which when administered to a cell, results in the incorporation of the guide (antisense) strand into the RISC complex (siRISC) resulting in the RISC associated inhibition of translation or degradation of complementary RNA target nucleic acids in the cell. The sense strand is also referred to as the passenger strand, and the antisense strand as the guide strand. A small hairpin RNA (shRNA) is a single nucleic acid molecule which forms a stem loop (hairpin) structure that is able to degrade mRNA via RISC. RNAi nucleic acid molecules may be synthesized chemically (typical for siRNA complexes) or by in vitro transcription, or expressed from a vector.

shRNA molecules are generally between 40 and 70 nucleotides in length, such as between 45 and 65 nucleotides in length, such as 50 and 60 nucleotides in length, and interacts with the endonuclease known as Dicer which is believed to process dsRNA into 19-23 base pair short interfering RNAs with characteristic two base 3' overhangs which are then incorporated into an RNA-induced silencing complex (RISC).

Typically, the guide (antisense) strand of an siRNA (or antisense region of a shRNA) is 17 – 25 nucleotide in length, such as 19 – 23 nucleotides in length and complementary to the target nucleic acid or target sequence. In an siRNA complex, the guide (antisense) strand and passenger (sense) strand form a double stranded duplex, which may comprise 3' terminal overhangs of e.g. 1- 3 nucleotides (resembles the product produced by Dicer), or may be blunt ended (no overhang at one or both ends of the duplex).

It will be recognized that RNAi may be mediated by longer dsRNA substrates which are processed into siRNAs within the cell (a process which is thought to involve the dsRNA endonuclease DICER). Effective extended forms of Dicer substrates have been described in US 8,349,809 and US 8,513,207, hereby incorporated by reference.

RNAi oligonucleotides may be chemically modified using modified internucleotide linkages and high affinity nucleosides such as 2' sugar modified nucleosides, such as 2'-4' bicyclic ribose modified nucleosides, including LNA and cET or 2' substituted modifications like of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA. See for example WO 2002/044321 which discloses 2'O-Methyl modified siRNAs, WO2004083430 which discloses the use of LNA nucleosides in siRNA complexes, known as siLNAs, and WO2007107162 which discloses the use of discontinuous passenger strands in siRNA such as siLNA complexes. WO03006477 discloses siRNA and shRNA (also referred to as stRNA) oligonucleotide mediators of RNAi. Harborth *et al.*, Antisense Nucleic Acid Drug Dev. 2003 Apr;13(2):83-105 refers to the sequence, chemical, and structural variation of small interfering RNAs and short hairpin RNAs and the effect on mammalian gene silencing.

In some embodiments RNAi oligonucleotides comprise one or more phosphorothioate internucleoside linkages. In RNAi molecules phosphorothioate internucleoside linkages may reduce or the nuclease cleavage in RICS it is therefore advantageous that not all internucleoside linkages are modified. Phosphorothioate internucleoside linkages can advantageously be placed in the 3' and/or 5' end of the RNAi nucleic acid molecule, in particular in the part of the molecule that is not complementary to the target nucleic acid (e.g. the sense strand or passenger strand in an siRNA molecule). The region of the RNAi molecule that is complementary to the target nucleic acid (e.g. the antisense or guide strand in a siRNA molecule) may however also be modified in the first 2 to 3 internucleoside linkages in the 3' and/or 5' terminal.

Contiguous Nucleotide Sequence

The term "contiguous nucleotide sequence" refers to the region of the oligonucleotide which is complementary to the target nucleic acid. The term is used interchangeably herein with the term "contiguous nucleobase sequence" and the term "oligonucleotide motif sequence". In

some embodiments all the nucleotides of the oligonucleotide constitute the contiguous nucleotide sequence. In some embodiments the oligonucleotide comprises the contiguous nucleotide sequence, such as the flank (also known as wing) and gap region of a gapmer, such as a F-G-F' gapmer region, and may optionally comprise further nucleotide(s), for example a nucleotide linker region which may be used to attach a functional group to the contiguous nucleotide sequence. The nucleotide linker region may or may not be complementary to the target nucleic acid.

Nucleotides

Nucleotides are the building blocks of oligonucleotides and polynucleotides, and for the purposes of the present invention include both naturally occurring and non-naturally occurring nucleotides. In nature, nucleotides, such as DNA and RNA nucleotides comprise a ribose sugar moiety, a nucleobase moiety and one or more phosphate groups (which is absent in nucleosides). Nucleosides and nucleotides may also interchangeably be referred to as "units" or "monomers".

Modified nucleoside

The term "modified nucleoside" or "nucleoside modification" as used herein refers to nucleosides modified as compared to the equivalent DNA or RNA nucleoside by the introduction of one or more modifications of the sugar moiety or the (nucleo)base moiety. In a preferred embodiment the modified nucleoside comprises a modified sugar moiety. The term modified nucleoside may also be used herein interchangeably with the term "nucleoside analogue" or modified "units" or modified "monomers". Nucleosides with an unmodified DNA or RNA sugar moiety are termed DNA or RNA nucleosides herein. Nucleosides with modifications in the base region of the DNA or RNA nucleoside are still generally termed DNA or RNA if they allow Watson Crick base pairing.

Modified internucleoside linkages

The term "modified internucleoside linkage" is defined as generally understood by the skilled person as linkages other than phosphodiester (PO) linkages, that covalently couples two nucleosides together. The oligonucleotides of the invention may therefore comprise modified internucleoside linkages. In some embodiments, the modified internucleoside linkage increases the nuclease resistance of the oligonucleotide compared to a phosphodiester linkage, this is a particular advantage for therapeutic oligonucleotides. For naturally occurring oligonucleotides, the internucleoside linkage includes phosphate groups creating a phosphodiester bond between adjacent nucleosides. Modified internucleoside linkages are particularly useful in stabilizing oligonucleotides for *in vivo* use, and may serve to protect against nuclease cleavage at regions of DNA or RNA nucleosides in the oligonucleotide of the invention, for example within the gap

region of a gapmer oligonucleotide, as well as in regions of modified nucleosides, such as region F and F'.

In an embodiment, the oligonucleotide, e.g. the therapeutic antisense oligonucleotide, shRNA or siRNA, comprises one or more internucleoside linkages modified from the natural

5 phosphodiester, such one or more modified internucleoside linkages that is for example more resistant to nuclease attack. Nuclease resistance may be determined by incubating the oligonucleotide in blood serum or by using a nuclease resistance assay (e.g. snake venom phosphodiesterase (SVPD)), both are well known in the art. Internucleoside linkages which are capable of enhancing the nuclease resistance of an oligonucleotide are referred to as nuclease
10 resistant internucleoside linkages. In some embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are modified, such as at least 60%, such as at least 70%, such as at least 80 or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages. In some embodiments all of the internucleoside
15 linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are nuclease resistant internucleoside linkages. It will be recognized that, in some embodiments the nucleosides which link the oligonucleotide of the invention to a non-nucleotide functional group, such as a conjugate, may be phosphodiester.

A preferred modified internucleoside linkage is phosphorothioate.

20 Phosphorothioate internucleoside linkages are particularly useful due to nuclease resistance, beneficial pharmacokinetics and ease of manufacture. In some embodiments at least 50% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate, such as at least 60%, such as at least 70%, such as at least 80% or such as at least 90% of the internucleoside linkages in the oligonucleotide, or contiguous nucleotide
25 sequence thereof, are phosphorothioate. In some embodiments all of the internucleoside linkages of the oligonucleotide, or contiguous nucleotide sequence thereof, are phosphorothioate. The use of fully phosphorothioate modified oligonucleotides or contiguous nucleotide sequences is often used in antisense oligonucleotides, although in siRNAs partial phosphorothioate modifications may be preferred as fully phosphorothioate modifications have
30 been reported to limit RNAi activity, particularly when used in the guide (antisense) strand. Phosphorothioate modifications may be incorporated into the 5' and 3' ends of an antisense strand of a siRNA without unduly limiting RNAi activity.

Nuclease resistant linkages, such as phosphorothioate linkages, are particularly useful in oligonucleotide regions capable of recruiting nuclease when forming a duplex with the target
35 nucleic acid, such as region G for gapmers. Phosphorothioate linkages may, however, also be useful in non-nuclease recruiting regions and/or affinity enhancing regions such as regions F

and F' for gapmers. Gapmer oligonucleotides may, in some embodiments comprise one or more phosphodiester linkages in region F or F', or both region F and F', which the internucleoside linkage in region G may be fully phosphorothioate. Advantageously, all the internucleoside linkages in the contiguous nucleotide sequence of the antisense oligonucleotide are phosphorothioate linkages.

It is recognized that, as disclosed in EP2 742 135, antisense oligonucleotide may comprise other internucleoside linkages (other than phosphodiester and phosphorothioate), for example alkyl phosphonate / methyl phosphonate internucleosides, which according to EP2 742 135 may for example be tolerated in an otherwise DNA phosphorothioate the gap region.

Nucleobase

The term nucleobase includes the purine (e.g. adenine and guanine) and pyrimidine (e.g. uracil, thymine and cytosine) moiety present in nucleosides and nucleotides which form hydrogen bonds in nucleic acid hybridization. In the context of the present invention the term nucleobase also encompasses modified nucleobases which may differ from naturally occurring nucleobases, but are functional during nucleic acid hybridization. In this context "nucleobase" refers to both naturally occurring nucleobases such as adenine, guanine, cytosine, thymidine, uracil, xanthine and hypoxanthine, as well as non-naturally occurring variants. Such variants are for example described in Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1.

In some embodiments the nucleobase moiety is modified by changing the purine or pyrimidine into a modified purine or pyrimidine, such as substituted purine or substituted pyrimidine, such as a nucleobase selected from isocytosine, pseudoisocytosine, 5-methyl cytosine, 5-thiozolo-cytosine, 5-propynyl-cytosine, 5-propynyl-uracil, 5-bromouracil 5-thiazolo-uracil, 2-thio-uracil, 2'thio-thymine, inosine, diaminopurine, 6-aminopurine, 2-aminopurine, 2,6-diaminopurine and 2-chloro-6-aminopurine.

The nucleobase moieties may be indicated by the letter code for each corresponding nucleobase, e.g. A, T, G, C or U, wherein each letter may optionally include modified nucleobases of equivalent function. For example, in the exemplified oligonucleotides, the nucleobase moieties are selected from A, T, G, C, and 5-methyl cytosine. Optionally, for LNA gapmers, 5-methyl cytosine LNA nucleosides may be used.

Modified oligonucleotide

The term modified oligonucleotide describes an oligonucleotide comprising one or more sugar-modified nucleosides and/or modified internucleoside linkages. The term chimeric oligonucleotide is a term that has been used in the literature to describe oligonucleotides with modified nucleosides.

Complementarity

The term “complementarity” describes the capacity for Watson-Crick base-pairing of nucleosides/nucleotides. Watson-Crick base pairs are guanine (G)-cytosine (C) and adenine (A) - thymine (T)/uracil (U). It will be understood that oligonucleotides may comprise

5 nucleosides with modified nucleobases, for example 5-methyl cytosine is often used in place of cytosine, and as such the term complementarity encompasses Watson Crick base-pairing between non-modified and modified nucleobases (see for example Hirao et al (2012) Accounts of Chemical Research vol 45 page 2055 and Bergstrom (2009) Current Protocols in Nucleic Acid Chemistry Suppl. 37 1.4.1).

10 The term “% complementary” as used herein, refers to the number of nucleotides in percent of a contiguous nucleotide sequence in an oligonucleotide (e.g. oligonucleotide) which, at a given position, are complementary to (*i.e.* form Watson Crick base pairs with) a contiguous nucleotide sequence, at a given position of a separate oligonucleotide (e.g. the target nucleic acid). The percentage is calculated by counting the number of aligned bases that form pairs between the

15 two sequences (when aligned with the target sequence 5'-3' and the oligonucleotide sequence from 3'-5'), dividing by the total number of nucleotides in the oligonucleotide and multiplying by 100. In such a comparison a nucleobase/nucleotide which does not align (form a base pair) is termed a mismatch. Preferably, insertions and deletions are not allowed in the calculation of % complementarity of a contiguous nucleotide sequence.

20 The term “fully complementary”, refers to 100% complementarity.

The following is an example of an oligonucleotide motif (SEQ ID NO: 86) that is fully complementary to the target nucleic acid (SEQ ID NO: 325).

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5' gaataatatggaaaaacgaaaa 3' (SEQ ID NO: 325)
3' tattataccttttttgc 5' (SEQ ID NO: 86)
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Identity

The term “Identity” as used herein, refers to the proportion of nucleotides (expressed in percent) of a contiguous nucleotide sequence in a oligonucleotide (e.g. oligonucleotide) which across the contiguous nucleotide sequence, are identical to a reference sequence (e.g. a sequence motif).

The percentage of identity is thus calculated by counting the number of aligned bases that are

30 identical (a match) between two sequences (in the contiguous nucleotide sequence of the compound of the invention and in the reference sequence), dividing that number by the total number of nucleotides in the oligonucleotide and multiplying by 100. Therefore, Percentage of Identity = (Matches x 100)/Length of aligned region (e.g. the contiguous nucleotide sequence). Insertions and deletions are not allowed in the calculation the percentage of identity of a

35 contiguous nucleotide sequence. It will be understood that in determining identity, chemical

modifications of the nucleobases are disregarded as long as the functional capacity of the nucleobase to form Watson Crick base pairing is retained (e.g. 5-methyl cytosine is considered identical to a cytosine for the purpose of calculating % identity).

Hybridization

5 The term “hybridizing” or “hybridizes” as used herein is to be understood as two nucleic acid strands (e.g. an oligonucleotide and a target nucleic acid) forming hydrogen bonds between base pairs on opposite strands thereby forming a duplex. The affinity of the binding between two nucleic acid strands is the strength of the hybridization. It is often described in terms of the melting temperature (T_m) defined as the temperature at which half of the oligonucleotides are
10 duplexed with the target nucleic acid. At physiological conditions T_m is not strictly proportional to the affinity (Mergny and Lacroix, 2003, *Oligonucleotides* 13:515–537). The standard state Gibbs free energy ΔG° is a more accurate representation of binding affinity and is related to the dissociation constant (K_d) of the reaction by $\Delta G^\circ = -RT \ln(K_d)$, where R is the gas constant and T is the absolute temperature. Therefore, a very low ΔG° of the reaction between an
15 oligonucleotide and the target nucleic acid reflects a strong hybridization between the oligonucleotide and target nucleic acid. ΔG° is the energy associated with a reaction where aqueous concentrations are 1M, the pH is 7, and the temperature is 37°C. The hybridization of oligonucleotides to a target nucleic acid is a spontaneous reaction and for spontaneous reactions ΔG° is less than zero. ΔG° can be measured experimentally, for example, by use of
20 the isothermal titration calorimetry (ITC) method as described in Hansen et al., 1965, *Chem. Comm.* 36–38 and Holdgate et al., 2005, *Drug Discov Today*. The skilled person will know that commercial equipment is available for ΔG° measurements. ΔG° can also be estimated numerically by using the nearest neighbor model as described by SantaLucia, 1998, *Proc Natl Acad Sci USA*. 95: 1460–1465 using appropriately derived thermodynamic parameters
25 described by Sugimoto et al., 1995, *Biochemistry* 34:11211–11216 and McTigue et al., 2004, *Biochemistry* 43:5388–5405. In order to have the possibility of modulating its intended nucleic acid target by hybridization, oligonucleotides of the present invention hybridize to a target nucleic acid with estimated ΔG° values below -10 kcal for oligonucleotides that are 10-30 nucleotides in length. In some embodiments the degree or strength of hybridization is measured
30 by the standard state Gibbs free energy ΔG° . The oligonucleotides may hybridize to a target nucleic acid with estimated ΔG° values below the range of -10 kcal, such as below -15 kcal, such as below -20 kcal and such as below -25 kcal for oligonucleotides that are 8-30 nucleotides in length. In some embodiments the oligonucleotides hybridize to a target nucleic acid with an estimated ΔG° value of -10 to -60 kcal, such as -12 to -40, such as from -15 to -30
35 kcal or -16 to -27 kcal such as -18 to -25 kcal.

Target nucleic acid

According to the present invention, the target nucleic acid is a nucleic acid which encodes mammalian TMEM106B and may for example be a gene, a RNA, a mRNA, and pre-mRNA, a mature mRNA or a cDNA sequence. The target may therefore be referred to as an TMEM106B target nucleic acid. The oligonucleotide of the invention may for example target exon regions of a mammalian TMEM106B RNA, or may for example target intron region in the TMEM106B pre-mRNA (see Table 1).

Table 1: human TMEM106B Exons and Introns regions which may be targeted by the compounds of the invention:

Exonic regions in the human TMEM106B premRNA (SEQ ID NO 1)			Intronic regions in the human TMEM106B premRNA (SEQ ID NO 1)		
ID	start	end	ID	start	end
e1	1	204	i1	205	2979
e2	2980	3173	i2	3174	3587
e3	3588	3806	i3	3807	7236
e4	7237	7300	i4	7301	13004
e5	13005	13164	i5	13165	18457
e6	18458	18598	i6	18599	19167
e7	19168	19217	i7	19218	19840
e8	19841	19894	i8	19895	20615
e9	20616	32146			

Suitably, the target nucleic acid encodes an TMEM106B protein, in particular mammalian TMEM106B, such as human TMEM106B (See for example Tables 2 and 3, which provides the mRNA and pre-mRNA sequences for human, monkey, and mouse TMEM106B).

In some embodiments, the target nucleic acid is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5 and 6 or naturally occurring variants thereof, including SNP variants. A table of known nucleotide polymorphisms (SNPs) of SEQ ID NO: 1 are shown in Table 4. If employing the oligonucleotide of the invention in research or diagnostics the target nucleic acid may be a cDNA or a synthetic nucleic acid derived from DNA or RNA.

The oligonucleotide of the invention is typically capable of inhibiting the expression of the TMEM106B target nucleic acid in a cell which is expressing the TMEM106B target nucleic acid.

The contiguous sequence of nucleobases of the oligonucleotide of the invention is typically complementary to the TMEM106B target nucleic acid, as measured across the length of the oligonucleotide, optionally with the exception of one or two mismatches, and optionally excluding nucleotide based linker regions which may link the oligonucleotide to an optional functional group such as a conjugate, or other non-complementary terminal nucleotides (e.g.

region D' or D"). The target nucleic acid may, in some embodiments, be a mature mRNA or a pre-mRNA.

In some embodiments the target nucleic acid is a RNA which encodes mammalian TMEM106B protein, such as human TMEM106B, e.g. the human TMEM106B pre-mRNA sequence, such as that disclosed as SEQ ID NO: 1, or the human mature mRNA, such as that disclosed in SEQ ID NO: 2. Further information on exemplary target nucleic acids is provided in Tables 2 and 3.

Table 2: Genome and assembly information for TMEM106B across species.

Species	Chr.	Strand	Genomic coordinates Start End	Assembly/ Ensemble Gene ID	NCBI reference sequence* accession number for mRNA
Human	7	Fwd	12211222 12243367	GRCh38/ ENSG00000106460	NM_018374
Cynomolgus monkey	3	Rv	108661057 108693751	Macaca_ fascicularis_5.0	XM_005550096
Mouse	6	Fwd	13069744 13089269	GRCm38/ ENSMUSG00000002 9571	NM_027992

Fwd = forward strand. Rv = reverse strand. The genome coordinates provide the pre-mRNA sequence (genomic sequence). The NCBI reference provides the mRNA sequence (cDNA sequence).

*The National Center for Biotechnology Information reference sequence database is a comprehensive, integrated, non-redundant, well-annotated set of reference sequences including genomic, transcript, and protein. It is hosted at www.ncbi.nlm.nih.gov/refseq.

Table 3: Sequence details for TMEM106B across species.

Species	RNA type	Length (nt)	SEQ ID NO
Human	premRNA	32146	1
Human	mRNA	6514	2
Monkey	premRNA	32695	3
Monkey	mRNA	2740	4
Mouse	premRNA	19526	5
Mouse	mRNA	6099	6

Target Sequence

The term "target sequence" as used herein refers to a sequence of nucleotides present in the target nucleic acid which comprises the nucleobase sequence which is complementary to the oligonucleotide of the invention. In some embodiments, the target sequence consists of a region on the target nucleic acid with a nucleobase sequence that is complementary to the contiguous nucleotide sequence of the oligonucleotide of the invention. This region of the target nucleic acid may interchangeably be referred to as the target nucleotide sequence, target sequence or target region. In some embodiments the target sequence is longer than the complementary sequence of a single oligonucleotide, and may, for example represent a

preferred region of the target nucleic acid which may be targeted by several oligonucleotides of the invention.

In some embodiments, the target sequence is present in an intronic region of the TMEM106B nucleic acid, such as SEQ ID NO: 1.

- 5 In some embodiments, the target sequence is present in exon 9, such as in the 3'UTR of the TMEM106B nucleic acid.

The inventors have identified that the 3'UTR of the human and mouse TMEM106B is an advantageous target sequence. In some embodiments, the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, is at least 90% complementary, such as is fully
10 complementary, to the 3'UTR of a mammalian TMEM106B mRNA, such as the target nucleic acid referred to herein (e.g. SEQ ID NO: 1, 3 or 5). In one embodiment the 3' UTR is located from position 20755-32146 of SEQ ID NO: 1. As illustrated in the examples, the inventors have further identified advantageous target sequences within the 3'UTR of the human TMEM106B transcript. In some embodiments, the target sequence is from position 20755 to position 26403
15 of SEQ ID NO: 1. In some embodiments, the target sequence is from position 21084 to position 21213 of SEQ ID NO: 1. In some embodiments, the target sequence is from position 23086 to position 24077 of SEQ ID NO: 1.

In some embodiments the target sequence is a sequence selected from the group consisting of a human TMEM106B mRNA exon, such as a TMEM106B human mRNA exon selected from the
20 group consisting of e1, e2, e3, e4, e5, e6, e7, e8, and e9 (see Table 1 above). In some embodiments the target sequence is exon e2.

In some embodiments, the target sequence is a sequence selected from the group consisting of a human TMEM106B mRNA intron, such as a TMEM106B human mRNA intron selected from the group consisting of i1, i2, i3, i4, i5, i6, i7, and i8 (see Table 1 above). In some embodiments,
25 the target sequence is intron i8, or the 3'UTR region.

In some embodiments, the target sequence is selected from a TMEM106B human mRNA intron selected from the group consisting of i1, i2, i3, i4, i5, i6, i7, and i8 and the TMEM106B human mRNA 3'UTR.

In some embodiments the target sequence is a sequence the TMEM106B human mRNA intron
30 i8 or 3'UTR (see Table 1 above).

In some embodiments, the target sequence is or comprises the nucleotide sequence from position 20227 to position 20243 of SEQ ID NO 1.

In some embodiments, the target sequence is or comprises the nucleotide sequence from position 20227 to position 26403 of SEQ ID NO 1.

In some embodiments, the target sequence is or comprises the nucleotide sequence from position 20227 to position 21213 of SEQ ID NO 1.

In some embodiments, the target sequence is or comprises the nucleotide sequence from position 20227 to position 24077 of SEQ ID NO 1.

- 5 The oligonucleotide of the invention comprises a contiguous nucleotide sequence which is complementary to or hybridizes to the target nucleic acid, such as a target sequence described herein.

The target sequence to which the oligonucleotide is complementary or hybridizes to generally comprises a contiguous nucleobases sequence of at least 10 nucleotides. In some
10 embodiments, such as antisense oligonucleotides of the invention, the contiguous nucleotide sequence is between 10 to 50 nucleotides, such as 10 to 30 nucleotides, such as 14 to 20, such as 15 to 18 contiguous nucleotides.

For siRNA oligonucleotides, the target sequence to which the antisense strand oligonucleotide is complementary or hybridizes to, may comprise a contiguous nucleobases sequence of at
15 least 16 or 17 nucleotides. In some embodiments, the contiguous nucleotide sequence is between 17 to 25 nucleotides, such as 19 to 23 contiguous nucleotides.

Target Cell

The term a “target cell” as used herein refers to a cell which is expressing the target nucleic acid. In some embodiments the target cell may be *in vivo* or *in vitro*. In some embodiments the
20 target cell is a mammalian cell such as a rodent cell, such as a mouse cell or a rat cell, or a primate cell such as a monkey cell or a human cell.

In some embodiments the target cell is a neuronal cell. In some embodiments the cell which is expressing TMEM106B may be a neuronal cell.

In some embodiments the target cell expresses TMEM106B mRNA, such as the TMEM106B
25 pre-mRNA or TMEM106B mature mRNA. The poly A tail of TMEM106B mRNA is typically disregarded for antisense oligonucleotide targeting.

In some embodiments, human SK-N-BE(2) neuroblastoma cells acquired from ATCC (CRL-2271) or mouse Neuro-2a neuroblastoma cell acquired from ATCC (CCL-131) may be used to determine whether an oligonucleotide is capable of down regulating the target nucleic acid (see
30 examples).

Naturally occurring variant

The term “naturally occurring variant” refers to variants of TMEM106B gene or transcripts which originate from the same genetic loci as the target nucleic acid, but may differ for example, by virtue of degeneracy of the genetic code causing a multiplicity of codons encoding the same

amino acid, or due to alternative splicing of pre-mRNA, or the presence of polymorphisms, such as single nucleotide polymorphisms (SNPs), and allelic variants. Based on the presence of the sufficient complementary sequence to the oligonucleotide, the oligonucleotide of the invention may therefore target the target nucleic acid and naturally occurring variants thereof.

- 5 In some embodiments, the naturally occurring variants have at least 95% such as at least 98% or at least 99% homology to a mammalian TMEM106B target nucleic acid, such as a target nucleic acid selected from the group consisting of SEQ ID NO 1 - 6. In some embodiments the naturally occurring variants have at least 99% homology to the human TMEM106B target nucleic acid of SEQ ID NO: 1 or SEQ ID NO 2. In some embodiments the naturally occurring
- 10 variants are the polymorphisms listed in Table 4.

Table 4: Examples of single nucleotide polymorphisms which are known in the human TMEM106B gene (human premRNA start/reference sequence is SEQ ID NO 1).

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs111783004	92	G	A,G	A	0,02
rs73299040	338	G	A,G	A	0,17
rs4721056	415	T	G,T	T	0,37
rs13223216	641	T	C,T	C	0,03
rs7781670	713	C	C,G	C	0,45
rs73299043	748	C	C,G	G	0,08
rs73678689	822	T	G,T	G	0,17
rs1019309	824	T	T,A	T	0,45
rs77287807	862	A	A,G	G	0,01
rs1019308	879	G	G,C	G	0,32
rs1019307	943	G	G,C	G	0,45
rs1019306	979	C	T,C	C	0,33
rs57209188	1094	A	A,G	G	0,02
rs73301009	1131	A	A,G	G	0,01
rs56761518	1273	-	-,T,TTTT	-	0,47
rs1468800	1296	A	T,A	T	0,09
rs6460895	1693	C	C,G	C	0,41
rs6460896	1812	G	A,G	G	0,41
rs6460897	1894	T	G,T	T	0,41
rs73678692	1897	G	A,G	A	0,13
rs6460898	2046	A	A,G	A	0,41
rs10644564	2056	-	-,CT	-	0,41
rs201303186	2073	-	-,A	A	0,08
rs6460899	2203	A	A,C	A	0,41
rs6460900	2241	A	A,G	A	0,41

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs6974465	2331	T	C,T	T	0,33
rs74964643	2372	G	A,G	A	0,03
rs12699323	2515	T	C,T	T	0,41
rs12699324	2525	T	C,T	T	0,41
rs76235203	2612	C	C,G	G	0,08
rs10234805	2696	T	C,T	T	0,41
rs10278257	2716	C	C,T	C	0,41
rs138861467	2851	C	C,G	G	0,01
rs2043540	3020	A	C,A	C	0,28
rs2043539	3033	G	G,A	G	0,41
rs2043538	3046	T	T,C	C	0,38
rs73301022	3099	C	A,C	A	0,02
rs62435714	3165	A	A,G	G	0,14
rs6959892	3421	C	C,T	T	0,04
rs17149894	4092	C	C,T	T	0,30
rs78492048	4107	A	A,G	G	0,03
rs6460901	4587	C	C,T	C	0,41
rs6460902	4664	G	A,G	G	0,39
rs1020006	4817	G	G,A	G	0,41
rs1020005	4821	C	C,A	C	0,33
rs1020004	4931	T	T,C	C	0,30
rs5882345	5160	A	-,A	A	0,32
rs76689854	5275	T	G,T	G	0,02
rs11974384	5693	A	A,G	G	0,38
rs11971133	5701	T	C,T	T	0,41
rs111886724	5802	G	C,G	C	0,02
rs577850861	5806	TT	-,TT	-	0,35
rs574034412	5807	T	-,T	-	0,49
rs12699325	5827	T	C,T	C	0,03
rs73677511	5863	T	C,T	C	0,13
rs73301032	5952	C	C,G	G	0,08
rs6947327	6322	C	C,G	C	0,32
rs10464275	6381	A	A,C	C	0,08
rs73301035	6512	G	A,G	A	0,14
rs7785189	6680	C	C,T	C	0,41
rs7785087	6702	A	A,G	A	0,41
rs6460903	6881	T	C,T	T	0,33
rs11342660	7019	T	-,T	T	0,45
rs73301040	7079	A	A,G	G	0,02
rs6415232	7091	A	A,G	A	0,33

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs3887296	7119	A	A,G	G	0,08
rs139417104	7220	-	-,A	A	0,02
rs116705963	7413	G	A,G	A	0,01
rs17165735	7587	A	A,G	G	0,08
rs17165736	7675	G	A,G	A	0,14
rs35982495	7819	-	-,A	-	0,40
rs3823612	7908	G	G,C	G	0,40
rs202184519	8740	-	-,A	A	0,01
rs17165737	8788	C	A,C	A	0,13
rs78663549	9001	G	G,T	T	0,09
rs28459566	9243	T	C,T	C	0,11
rs12666249	9699	C	C,T	T	0,38
rs12666279	9705	G	A,G	A	0,14
rs12699326	9719	A	A,G	G	0,03
rs139345875	9974	A	A,T	T	0,01
rs147697289	10156	G	G,T	T	0,01
rs73301046	10400	G	A,G	A	0,05
rs80041000	10520	A	A,G	G	0,08
rs10950391	10982	A	A,G	A	0,40
rs11509880	11064	G	A,G	G	0,42
rs141482004	11096	A	A,T	T	0,01
rs76188878	11318	G	A,G	A	0,02
rs3800847	11395	G	G,A	G	0,40
rs1435527	11724	C	T,C	C	0,41
rs6978684	11740	C	C,G	G	0,14
rs13311466	11755	T	C,T	C	0,03
rs1435526	11807	A	G,A	A	0,33
rs1435525	11870	T	T,C	T	0,41
rs1435524	11954	G	G,A	G	0,41
rs11368032	12122	T	-,T	T	0,41
rs55635711	12156	A	-,A	-	0,12
rs73677523	12199	A	A,G	G	0,09
rs73301054	12213	C	A,C	A	0,04
rs115923636	12244	A	A,G	G	0,01
rs5882346	12337	A	-,A	A	0,41
rs1435543	12387	C	T,C	C	0,32
rs17165744	12442	A	A,G	G	0,13
rs76130803	12457	T	C,T	C	0,02
rs11981005	12523	A	A,G	A	0,32
rs11974335	12531	G	G,T	G	0,40

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs11974304	12590	C	C,T	C	0,40
rs10950392	12691	T	C,T	T	0,40
rs10950393	12699	T	C,T	T	0,40
rs10950394	12740	C	C,T	C	0,40
rs144830416	12745	G	C,G	C	0,08
rs113404588	12766	G	A,G	A	0,05
rs141956872	12776	G	C,G	C	0,01
rs116565082	12794	C	C,T	T	0,03
rs113047067	12829	C	C,G	G	0,03
rs17165746	12878	T	A,T	A	0,14
rs11509137	12952	T	C,T	T	0,40
rs11509153	12953	G	A,G	G	0,41
rs147889591	13124	G	A,G	A	0,01
rs3800845	13304	G	G,C	G	0,33
rs3800844	13373	G	G,C	G	0,33
rs3839693	13415	-	-,A	-	0,40
rs3800843	13450	G	G,A	G	0,40
rs75163637	13487	A	A,G	G	0,01
rs77799203	13585	C	C,G	G	0,06
rs10950395	13620	T	C,T	T	0,40
rs149105187	13795	C	C,T	T	0,02
rs10950396	13819	T	C,T	T	0,40
rs11983898	13862	G	A,G	A	0,27
rs10950397	13890	C	C,T	C	0,41
rs137900300	13937	G	A,G	A	0,03
rs10950398	14024	G	A,G	G	0,39
rs76854159	14212	A	A,G	A	0,39
rs138328979	14275	G	C,G	C	0,01
rs79222644	14302	A	A,T	T	0,06
rs150465020	14345	T	C,T	T	0,40
rs147309966	14427	G	G,T	T	0,27
rs140918518	14440	A	A,G	G	0,01
rs143141037	14462	C	C,T	T	0,04
rs13246340	14476	G	A,G	A	0,03
rs142820543	14492	G	A,G	A	0,04
rs75738247	14583	G	G,T	T	0,27
rs139628525	14595	C	C,G	G	0,01
rs143477885	14618	A	A,G	G	0,14
rs201845319	14754	T	-,T	-	0,02
rs112430481	14891	C	C,G	G	0,08

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs6966602	14892	C	C,G	G	0,30
rs145413472	14911	C	C,T	T	0,11
rs11438918	14921	-	-,T	-	0,33
rs6948844	15001	T	C,T	T	0,40
rs6967026	15058	G	G,T	T	0,27
rs73284389	15080	C	C,G	G	0,14
rs6966757	15105	A	A,T	A	0,40
rs6966915	15141	C	C,T	C	0,41
rs77145882	15152	G	A,G	A	0,09
rs115474060	15154	C	C,G	G	0,02
rs143032237	15190	G	C,G	C	0,01
rs17165750	15272	T	C,T	C	0,14
rs117574031	15285	C	C,G	G	0,01
rs571665718	15455	T	A,T	A	0,01
rs539782765	15456	C	C,T	T	0,01
rs3839692	15474	-	-,A	A	0,30
rs35642626	15705	A	-,A	A	0,40
rs75275529	15780	A	A,G	G	0,08
rs7804433	15859	G	A,G	G	0,39
rs61225336	15864	T	C,T	C	0,19
rs7804234	15967	A	A,G	A	0,40
rs7804736	16020	G	G,T	G	0,41
rs78536513	16336	A	A,C	C	0,02
rs4721057	16374	A	A,G	A	0,40
rs4721058	16409	C	C,T	C	0,40
rs73286304	16568	C	A,C	A	0,03
rs4721059	16648	G	C,G	G	0,40
rs4721060	16705	G	A,G	G	0,40
rs4721061	16712	G	C,G	G	0,40
rs7792410	16767	T	C,T	T	0,40
rs536653563	16768	C	C,T	T	0,04
rs35390376	16806	T	C,T	C	0,03
rs7809700	16887	G	A,G	G	0,40
rs115298566	16902	G	G,T	T	0,01
rs13229988	16990	A	A,G	A	0,40
rs149578700	17020	C	C,T	T	0,02
rs201723928	17022	T	-,T	-	0,01
rs34046032	17236	TTAA	-,TTAA	TTAA	0,40
rs28549831	17270	C	C,T	C	0,40
rs13230513	17396	C	A,C	C	0,40

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs12667950	17621	G	G,T	G	0,41
rs5011431	17704	G	A,G	G	0,40
rs5011432	17821	A	A,C	A	0,48
rs5011433	17848	T	A,T	T	0,32
rs5011434	17870	C	C,T	C	0,40
rs5011435	17879	T	C,T	C	0,13
rs5011436	17911	A	A,C	A	0,40
rs5011437	17945	A	A,T	A	0,40
rs5011438	17951	C	C,T	C	0,40
rs5011439	17964	G	C,G	G	0,40
rs13233991	18067	C	C,T	T	0,03
rs60699002	18199	C	A,C	A	0,09
rs13234238	18366	A	A,C	C	0,03
rs3839691	18414	-	-,TTGT	TTGT	0,49
rs3173615	18570	C	C,G	G	0,50
rs13237715	18728	G	C,G	G	0,41
rs13237518	18746	C	A,C	C	0,39
rs59265139	18794	G	A,G	A	0,04
rs143516511	18796	G	A,G	A	0,01
rs35562417	18833	-	-,A,AA	-	0,41
rs114069088	18885	T	A,T	A	0,01
rs12699332	18915	G	G,T	G	0,41
rs12699333	18957	C	C,T	C	0,40
rs12668625	18970	G	A,G	G	0,40
rs3815535	19672	G	G,A	G	0,40
rs3214372	19719	-	-,T	-	0,41
rs3217132	19737	TTA	-,ATT	-	0,14
rs2302635	19778	G	G,A	G	0,41
rs2302634	19923	T	T,A	A	0,50
rs73677558	19944	T	C,T	C	0,10
rs2302633	19968	C	T,C	C	0,41
rs73677559	19972	A	A,C	C	0,08
rs16877361	20053	C	C,T	T	0,17
rs2302632	20120	A	G,A	G	0,36
rs7808568	20405	T	C,T	T	0,39
rs12699334	20406	G	A,G	A	0,03
rs3800842	20605	A	G,C,A	A	0,40
rs1042946	20819	G	G,T	T	0,03
rs12669919	21150	G	A,G	G	0,41
rs16877363	21179	A	A,G	G	0,14

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs1042949	21269	C	C,G	C	0,41
rs3800841	21721	A	T,A	A	0,40
rs17165789	21903	A	A,C	C	0,03
rs34252347	22017	-	-,TG	TG	0,44
rs14978	22305	A	G,A	G	0,43
rs1054168	22566	C	C,T	C	0,40
rs1054169	22649	G	A,G	G	0,40
rs79340241	22780	-	-,A	A	0,08
rs12539421	22924	T	G,T	G	0,08
rs13309255	23361	G	G,T	T	0,03
rs10488193	23373	A	G,A	G	0,09
rs35337387	23567	-	-,T	-	0,40
rs17165790	24003	A	A,G	G	0,01
rs71529336	24086	A	A,G	G	0,03
rs1468804	24661	T	T,C	T	0,39
rs5882347	24778	-	-,TTTTTC	-	0,40
rs1468803	24828	A	C,A	A	0,39
rs1060700	24971	A	G,A	A	0,39
rs73288318	25015	G	A,G	A	0,03
rs1468802	25164	G	G,A	G	0,39
rs2160268	25178	A	T,A	T	0,13
rs2160267	25187	T	T,A	A	0,33
rs1468801	25198	G	G,C	G	0,39
rs1047601	25674	C	C,T	T	0,08
rs929637	25675	G	T,G	T	0,33
rs57824581	25834	-	-,A	A	0,05
rs112281135	25903	-	-,ATG	-	0,01
rs117623176	25985	C	C,T	T	0,01
rs2356065	26038	T	C,T	T	0,39
rs140537895	26149	TACTT	-,TACTT	-	0,09
rs12699335	26173	T	C,T	C	0,36
rs10488192	26234	G	G,A	A	0,14
rs199711002	26589	T	C,T	C	0,13
rs13234969	26591	T	C,T	T	0,43
rs13234970	26595	T	C,T	T	0,43
rs7797705	26926	G	A,G	G	0,40
rs6460904	27302	G	A,G	A	0,17
rs34391411	27560	CAA	-,CAA	-	0,03
rs6969722	27590	G	A,G	A	0,35
rs4330594	27768	G	A,G	A	0,07

Variant name	Position in SEQ ID NO 1	Ancestral allele (in reference genome)	Variant alleles	Which allele is minor allele	Minor allele frequency
rs62448695	27946	T	C,T	C	0,05
rs73288387	27958	T	C,T	C	0,05
rs10257722	28065	G	A,G	A	0,01
rs548644997	28119	T	G,T	G	0,21
rs7802952	28280	A	A,G	G	0,13
rs2098363	28351	G	G,A	G	0,33
rs57685335	28672	G	A,G	A	0,04
rs1548885	28712	G	G,C	C	0,35
rs75956572	28891	A	A,G	G	0,03
rs1548884	28914	A	C,A	A	0,39
rs1548883	28946	G	G,A	A	0,13
rs2356066	28986	G	A,G	A	0,35
rs73288393	29090	T	G,T	G	0,04
rs77273680	29280	A	A,G	G	0,08
rs73677570	29482	T	C,T	C	0,07
rs149200435	29591	AGA	-,AGA	-	0,08
rs79100376	29598	C	C,G	G	0,09
rs75911624	29661	A	A,G	G	0,02
rs10281425	29883	T	A,T	T	0,39
rs150586332	29900	C	C,G	G	0,01
rs10236369	29991	A	A,G	G	0,37
rs116132326	30039	T	A,T	A	0,02
rs570235340	30253	-	-,TCCCACTTATGA GTGGCAACT	TCCCACTTAT GAGTGGCAAC T	0,04
rs139600599	30445	G	G,T	T	0,07
rs115077070	30833	T	G,T	G	0,02
rs139393760	30857	A	-,A	A	0,39
rs6948681	31146	G	A,G	A	0,10
rs146083730	31293	-	-,T	T	0,01
rs7805419	31604	T	C,T	T	0,46
rs149298119	31821	A	A,T	T	0,01
rs59410610	32000	A	A,G	G	0,07

Modulation of expression

The term “modulation of expression” as used herein is to be understood as an overall term for an oligonucleotide’s ability to alter the amount of TMEM106B when compared to the amount of TMEM106B before administration of the oligonucleotide. Alternatively modulation of expression may be determined by reference to a control experiment. It is generally understood that the

control is an individual or target cell treated with a saline composition or an individual or target cell treated with a non-targeting oligonucleotide (mock).

One type of modulation is an oligonucleotide's ability to inhibit, down-regulate, reduce, suppress, remove, stop, block, prevent, lessen, lower, avoid or terminate expression of TMEM106B, e.g. by degradation of mRNA or blockage of transcription. Another type of modulation is an oligonucleotide's ability to restore, increase or enhance expression of TMEM106B, e.g. by repair of splice sites or prevention of splicing or removal or blockage of inhibitory mechanisms such as microRNA repression.

High affinity modified nucleosides

A high affinity modified nucleoside is a modified nucleotide which, when incorporated into the oligonucleotide enhances the affinity of the oligonucleotide for its complementary target, for example as measured by the melting temperature (T^m). A high affinity modified nucleoside of the present invention preferably result in an increase in melting temperature between +0.5 to +12°C, more preferably between +1.5 to +10°C and most preferably between +3 to +8°C per modified nucleoside. Numerous high affinity modified nucleosides are known in the art and include for example, many 2' substituted nucleosides as well as locked nucleic acids (LNA) (see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213).

Sugar modifications

The oligomer of the invention may comprise one or more nucleosides which have a modified sugar moiety, *i.e.* a modification of the sugar moiety when compared to the ribose sugar moiety found in DNA and RNA.

Numerous nucleosides with modification of the ribose sugar moiety have been made, primarily with the aim of improving certain properties of oligonucleotides, such as affinity and/or nuclease resistance.

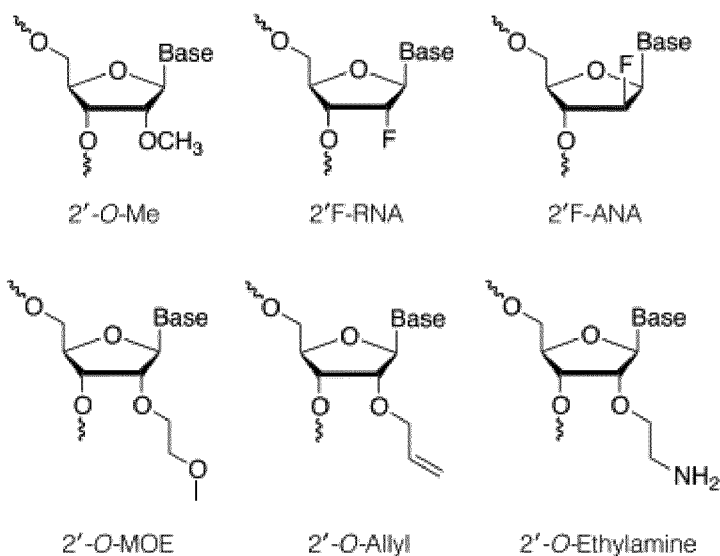
Such modifications include those where the ribose ring structure is modified, e.g. by replacement with a hexose ring (HNA), or a bicyclic ring, which typically have a biradicle bridge between the C2 and C4 carbons on the ribose ring (LNA), or an unlinked ribose ring which typically lacks a bond between the C2 and C3 carbons (e.g. UNA). Other sugar modified nucleosides include, for example, bicyclohexose nucleic acids (WO2011/017521) or tricyclic nucleic acids (WO2013/154798). Modified nucleosides also include nucleosides where the sugar moiety is replaced with a non-sugar moiety, for example in the case of peptide nucleic acids (PNA), or morpholino nucleic acids.

Sugar modifications also include modifications made via altering the substituent groups on the ribose ring to groups other than hydrogen, or the 2'-OH group naturally found in DNA and RNA nucleosides. Substituents may, for example be introduced at the 2', 3', 4' or 5' positions.

2' sugar modified nucleosides

- 5 A 2' sugar modified nucleoside is a nucleoside which has a substituent other than H or -OH at the 2' position (2' substituted nucleoside) or comprises a 2' linked biradicle capable of forming a bridge between the 2' carbon and a second carbon in the ribose ring, such as LNA (2' - 4' biradicle bridged) nucleosides.

Indeed, much focus has been spent on developing 2' substituted nucleosides, and numerous 2' substituted nucleosides have been found to have beneficial properties when incorporated into oligonucleotides. For example, the 2' modified sugar may provide enhanced binding affinity and/or increased nuclease resistance to the oligonucleotide. Examples of 2' substituted modified nucleosides are 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA (MOE), 2'-amino-DNA, 2'-Fluoro-RNA, and 2'-F-ANA nucleoside. For further examples, please see e.g. Freier & Altmann; Nucl. Acid Res., 1997, 25, 4429-4443 and Uhlmann; Curr. Opinion in Drug Development, 2000, 3(2), 293-213, and Deleavey and Damha, Chemistry and Biology 2012, 19, 937. Below are illustrations of some 2' substituted modified nucleosides.



- 20 In relation to the present invention 2' substituted does not include 2' bridged molecules like LNA.

Locked Nucleic Acids (LNA)

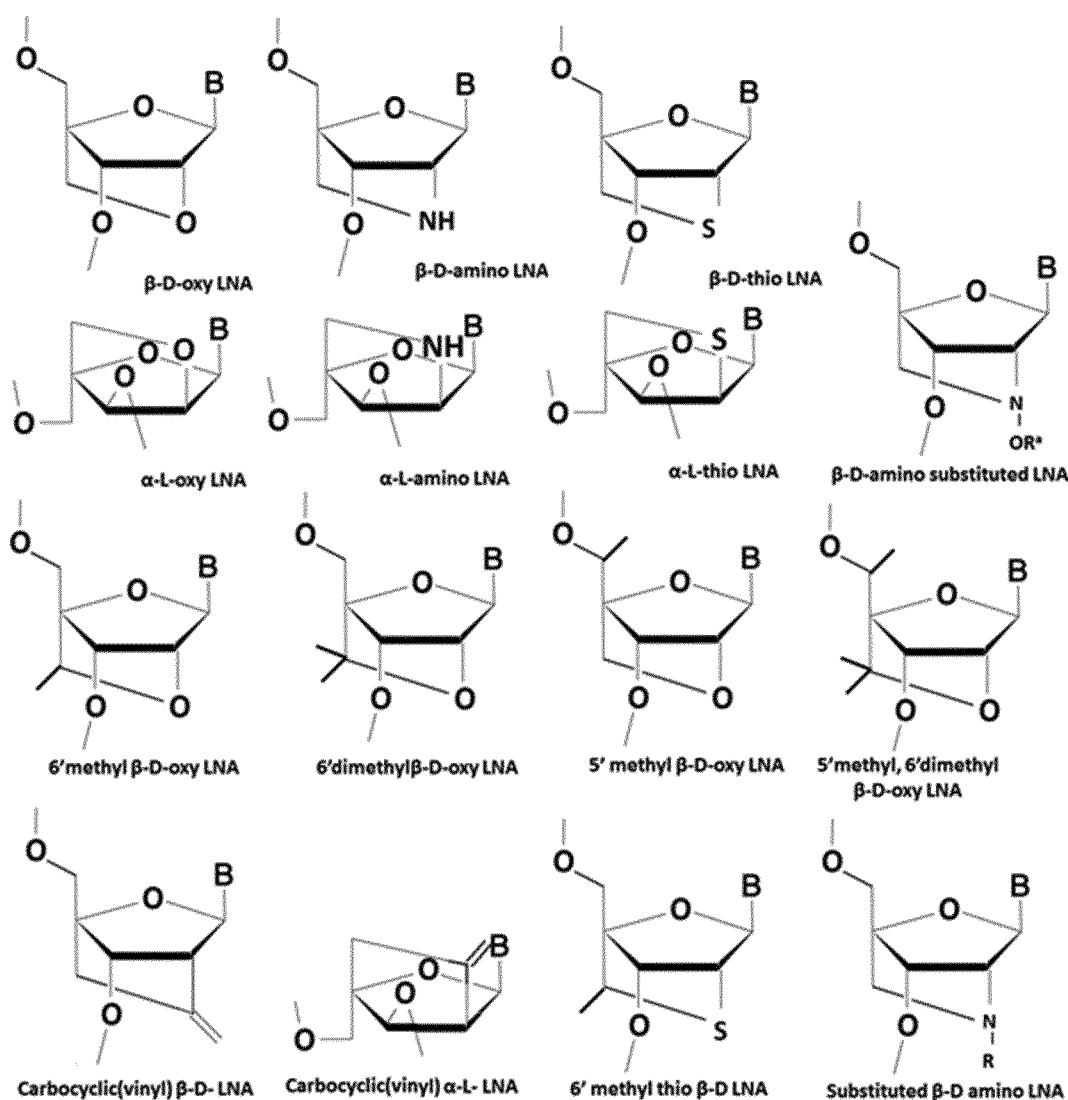
- A "LNA nucleoside" is a 2'- modified nucleoside which comprises a biradical linking the C2' and C4' of the ribose sugar ring of said nucleoside (also referred to as a "2'- 4' bridge"), which restricts or locks the conformation of the ribose ring. These nucleosides are also termed bridged nucleic acid or bicyclic nucleic acid (BNA) in the literature. The locking of the conformation of

the ribose is associated with an enhanced affinity of hybridization (duplex stabilization) when the LNA is incorporated into an oligonucleotide for a complementary RNA or DNA molecule. This can be routinely determined by measuring the melting temperature of the oligonucleotide/complement duplex.

- 5 Non limiting, exemplary LNA nucleosides are disclosed in WO 99/014226, WO 00/66604, WO 98/039352, WO 2004/046160, WO 00/047599, WO 2007/134181, WO 2010/077578, WO 2010/036698, WO 2007/090071, WO 2009/006478, WO 2011/156202, WO 2008/154401, WO 2009/067647, WO 2008/150729, Morita et al., Bioorganic & Med.Chem. Lett. 12, 73-76, Seth et al. J. Org. Chem. 2010, Vol 75(5) pp. 1569-81, and Mitsuoka et al., Nucleic Acids Research
10 2009, 37(4), 1225-1238, and Wan and Seth, J. Medical Chemistry 2016, 59, 9645-9667.

Further non limiting, exemplary LNA nucleosides are disclosed in Scheme 1.

Scheme 1:



- Particular LNA nucleosides are beta-D-oxy-LNA, 6'-methyl-beta-D-oxy LNA such as (S)-6'-
15 methyl-beta-D-oxy-LNA (ScET) and ENA.

A particularly advantageous LNA is beta-D-oxy-LNA. In some embodiments the oligonucleotide of the invention comprises at least one beta-D-oxy-LNA or 6'-methyl-beta-D-oxy-LNA nucleoside.

Nuclease mediated degradation

- 5 Nuclease mediated degradation refers to an oligonucleotide capable of mediating degradation of a complementary nucleotide sequence when forming a duplex with such a sequence.

In some embodiments, the oligonucleotide may function via nuclease mediated degradation of the target nucleic acid, where the oligonucleotides of the invention are capable of recruiting a nuclease, particularly an endonuclease, preferably an endoribonuclease (RNase), such as RNase
10 H. Examples of oligonucleotide designs which operate via nuclease mediated mechanisms are oligonucleotides which typically comprise a region of at least 5 or 6 consecutive DNA nucleosides and are flanked on one side or both sides by affinity enhancing nucleosides, for example gapmers, headmers and tailmers.

RNase H Activity and Recruitment

- 15 The RNase H activity of an antisense oligonucleotide refers to its ability to recruit RNase H when in a duplex with a complementary RNA molecule. WO01/23613 provides *in vitro* methods for determining RNaseH activity, which may be used to determine the ability to recruit RNaseH. Typically an oligonucleotide is deemed capable of recruiting RNase H if it, when provided with a complementary target nucleic acid sequence, has an initial rate, as measured in pmol/l/min, of
20 at least 5%, such as at least 10% or more than 20% of the initial rate determined when using an oligonucleotide having the same base sequence as the modified oligonucleotide being tested, but containing only DNA monomers with phosphorothioate linkages between all monomers in the oligonucleotide, and using the methodology provided by Example 91 - 95 of WO01/23613 (hereby incorporated by reference). For use in determining RNase H activity,
25 recombinant human RNase H1 is available from Lubio Science GmbH, Lucerne, Switzerland.

Gapmer

- The antisense oligonucleotide of the invention, or contiguous nucleotide sequence thereof may be a gapmer. The antisense gapmers are commonly used to inhibit a target nucleic acid via RNase H mediated degradation. A gapmer oligonucleotide comprises at least three distinct
30 structural regions: a 5'-flank, a gap and a 3'-flank, F-G-F' in the '5 -> 3' orientation. The "gap" region (G) comprises a stretch of contiguous DNA nucleotides which enable the oligonucleotide to recruit RNase H. The gap region is flanked by a 5' flanking region (F) comprising one or more sugar modified nucleosides, advantageously high affinity sugar modified nucleosides, and by a 3' flanking region (F') comprising one or more sugar modified nucleosides, advantageously high
35 affinity sugar modified nucleosides. The one or more sugar modified nucleosides in region F and F' enhance the affinity of the oligonucleotide for the target nucleic acid (*i.e.* are affinity

enhancing sugar modified nucleosides). In some embodiments, the one or more sugar modified nucleosides in region F and F' are 2' sugar modified nucleosides, such as high affinity 2' sugar modifications, such as independently selected from LNA and 2'-MOE.

In a gapmer design, the 5' and 3' most nucleosides of the gap region are DNA nucleosides, and are positioned adjacent to a sugar modified nucleoside of the 5' (F) or 3' (F') region respectively. The flanks may further be defined by having at least one sugar modified nucleoside at the end most distant from the gap region, i.e. at the 5' end of the 5' flank and at the 3' end of the 3' flank. Regions F-G-F' form a contiguous nucleotide sequence. Antisense oligonucleotides of the invention, or the contiguous nucleotide sequence thereof, may comprise a gapmer region of formula F-G-F'.

The overall length of the gapmer design F-G-F' may be, for example 12 to 32 nucleosides, such as 13 to 24, such as 14 to 22 nucleosides, Such as from 14 to 17, such as 16 to 18 nucleosides. By way of example, the gapmer oligonucleotide of the present invention can be represented by the following formulae:

$F_{1-8}-G_{5-16}-F'_{1-8}$, such as

$F_{1-8}-G_{7-16}-F'_{2-8}$

with the proviso that the overall length of the gapmer regions F-G-F' is at least 12, such as at least 14 nucleotides in length.

Regions F, G and F' are further defined below and can be incorporated into the F-G-F' formula.

Gapmer - Region G

Region G (gap region) of the gapmer is a region of nucleosides which enables the oligonucleotide to recruit RNaseH, such as human RNase H1, typically DNA nucleosides.

RNaseH is a cellular enzyme which recognizes the duplex between DNA and RNA, and enzymatically cleaves the RNA molecule. Suitably gapmers may have a gap region (G) of at

least 5 or 6 contiguous DNA nucleosides, such as 5 – 16 contiguous DNA nucleosides, such as 6 – 15 contiguous DNA nucleosides, such as 7-14 contiguous DNA nucleosides, such as 8 – 12 contiguous DNA nucleotides, such as 8 – 12 contiguous DNA nucleotides in length. The gap region G may, in some embodiments consist of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16

contiguous DNA nucleosides. One or more cytosine (C) DNA in the gap region may in some instances be methylated (e.g. when a DNA c is followed by a DNA g) such residues are either annotated as 5-methyl-cytosine (^{me}C). In some embodiments the gap region G may consist of 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 contiguous phosphorothioate linked DNA nucleosides. In some embodiments, all internucleoside linkages in the gap are phosphorothioate linkages.

Whilst traditional gapmers have a DNA gap region, there are numerous examples of modified nucleosides which allow for RNaseH recruitment when they are used within the gap region.

Modified nucleosides which have been reported as being capable of recruiting RNaseH when included within a gap region include, for example, alpha-L-LNA, C4' alkylated DNA (as

described in PCT/EP2009/050349 and Vester *et al.*, Bioorg. Med. Chem. Lett. 18 (2008) 2296 – 2300, both incorporated herein by reference), arabinose derived nucleosides like ANA and 2'F-ANA (Mangos *et al.* 2003 J. AM. CHEM. SOC. 125, 654-661), UNA (unlocked nucleic acid) (as described in Fluiter *et al.*, Mol. Biosyst., 2009, 10, 1039 incorporated herein by reference). UNA is unlocked nucleic acid, typically where the bond between C2 and C3 of the ribose has been removed, forming an unlocked “sugar” residue. The modified nucleosides used in such gapmers may be nucleosides which adopt a 2' endo (DNA like) structure when introduced into the gap region, *i.e.* modifications which allow for RNaseH recruitment). In some embodiments the DNA Gap region (G) described herein may optionally contain 1 to 3 sugar modified nucleosides which adopt a 2' endo (DNA like) structure when introduced into the gap region.

Region G - “Gap-breaker”

Alternatively, there are numerous reports of the insertion of a modified nucleoside which confers a 3' endo conformation into the gap region of gapmers, whilst retaining some RNaseH activity. Such gapmers with a gap region comprising one or more 3' endo modified nucleosides are referred to as “gap-breaker” or “gap-disrupted” gapmers, see for example WO2013/022984. Gap-breaker oligonucleotides retain sufficient region of DNA nucleosides within the gap region to allow for RNaseH recruitment. The ability of gapbreaker oligonucleotide design to recruit RNaseH is typically sequence or even compound specific – see Rukov *et al.* 2015 Nucl. Acids Res. Vol. 43 pp. 8476-8487, which discloses “gapbreaker” oligonucleotides which recruit RNaseH which in some instances provide a more specific cleavage of the target RNA. Modified nucleosides used within the gap region of gap-breaker oligonucleotides may for example be modified nucleosides which confer a 3' endo confirmation, such as 2' -O-methyl (OMe) or 2'-O-MOE (MOE) nucleosides, or beta-D LNA nucleosides (the bridge between C2' and C4' of the ribose sugar ring of a nucleoside is in the beta conformation), such as beta-D-oxy LNA or ScET nucleosides.

As with gapmers containing region G described above, the gap region of gap-breaker or gap-disrupted gapmers, have a DNA nucleoside at the 5' end of the gap (adjacent to the 3' nucleoside of region F), and a DNA nucleoside at the 3' end of the gap (adjacent to the 5' nucleoside of region F'). Gapmers which comprise a disrupted gap typically retain a region of at least 3 or 4 contiguous DNA nucleosides at either the 5' end or 3' end of the gap region. Exemplary designs for gap-breaker oligonucleotides include

$$F_{1-8}-[D_{3-4}-E_{1-} D_{3-4}]-F'_{1-8}$$

$$F_{1-8}-[D_{1-4}-E_{1-} D_{3-4}]-F'_{1-8}$$

$$F_{1-8}-[D_{3-4}-E_{1-} D_{1-4}]-F'_{1-8}$$

wherein region G is within the brackets $[D_n-E_r-D_m]$, D is a contiguous sequence of DNA nucleosides, E is a modified nucleoside (the gap-breaker or gap-disrupting nucleoside), and F

and F' are the flanking regions as defined herein, and with the proviso that the overall length of the gapmer regions F-G-F' is at least 12, such as at least 14 nucleotides in length.

In some embodiments, region G of a gap disrupted gapmer comprises at least 6 DNA nucleosides, such as 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or 16 DNA nucleosides. As described above, the DNA nucleosides may be contiguous or may optionally be interspersed with one or more modified nucleosides, with the proviso that the gap region G is capable of mediating RNaseH recruitment.

Gapmer - flanking regions, F and F'

Region F is positioned immediately adjacent to the 5' DNA nucleoside of region G. The 3' most nucleoside of region F is a sugar modified nucleoside, such as a high affinity sugar modified nucleoside, for example a 2' substituted nucleoside, such as a MOE nucleoside, or an LNA nucleoside.

Region F' is positioned immediately adjacent to the 3' DNA nucleoside of region G. The 5' most nucleoside of region F' is a sugar modified nucleoside, such as a high affinity sugar modified nucleoside, for example a 2' substituted nucleoside, such as a MOE nucleoside, or an LNA nucleoside.

Region F is 1 – 8 contiguous nucleotides in length, such as 2-6, such as 3-4 contiguous nucleotides in length. Advantageously the 5' most nucleoside of region F is a sugar modified nucleoside. In some embodiments the two 5' most nucleoside of region F are sugar modified nucleoside. In some embodiments the 5' most nucleoside of region F is an LNA nucleoside. In some embodiments the two 5' most nucleoside of region F are LNA nucleosides. In some embodiments the two 5' most nucleoside of region F are 2' substituted nucleoside nucleosides, such as two 3' MOE nucleosides. In some embodiments the 5' most nucleoside of region F is a 2' substituted nucleoside, such as a MOE nucleoside.

Region F' is 2 – 8 contiguous nucleotides in length, such as 3-6, such as 4-5 contiguous nucleotides in length. Advantageously, embodiments the 3' most nucleoside of region F' is a sugar modified nucleoside. In some embodiments the two 3' most nucleoside of region F' are sugar modified nucleoside. In some embodiments the two 3' most nucleoside of region F' are LNA nucleosides. In some embodiments the 3' most nucleoside of region F' is an LNA nucleoside. In some embodiments the two 3' most nucleoside of region F' are 2' substituted nucleoside nucleosides, such as two 3' MOE nucleosides. In some embodiments the 3' most nucleoside of region F' is a 2' substituted nucleoside, such as a MOE nucleoside.

It should be noted that when the length of region F or F' is one, it is advantageously an LNA nucleoside.

In some embodiments, region F and F' independently consists of or comprises a contiguous sequence of sugar modified nucleosides. In some embodiments, the sugar modified nucleosides of region F may be independently selected from 2'-O-alkyl-RNA units, 2'-O-methyl-

RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, LNA units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units.

In some embodiments, region F and F' independently comprises both LNA and a 2' substituted modified nucleosides (mixed wing design).

- 5 In some embodiments, region F and F' consists of only one type of sugar modified nucleosides, such as only MOE or only beta-D-oxy LNA or only ScET. Such designs are also termed uniform flanks or uniform gapmer design.

In some embodiments, all the nucleosides of region F or F', or F and F' are LNA nucleosides, such as independently selected from beta-D-oxy LNA, ENA or ScET nucleosides. In some

- 10 embodiments region F consists of 1-5, such as 2-4, such as 3-4 such as 1, 2, 3, 4 or 5 contiguous LNA nucleosides. In some embodiments, all the nucleosides of region F and F' are beta-D-oxy LNA nucleosides.

In some embodiments, all the nucleosides of region F or F', or F and F' are 2' substituted nucleosides, such as OMe or MOE nucleosides. In some embodiments region F consists of 1,

- 15 2, 3, 4, 5, 6, 7, or 8 contiguous OMe or MOE nucleosides. In some embodiments only one of the flanking regions can consist of 2' substituted nucleosides, such as OMe or MOE nucleosides. In some embodiments it is the 5' (F) flanking region that consists 2' substituted nucleosides, such as OMe or MOE nucleosides whereas the 3' (F') flanking region comprises at least one LNA nucleoside, such as beta-D-oxy LNA nucleosides or cET nucleosides. In some embodiments it is the 3' (F') flanking region that consists 2' substituted nucleosides, such as OMe or MOE
- 20 nucleosides whereas the 5' (F) flanking region comprises at least one LNA nucleoside, such as beta-D-oxy LNA nucleosides or cET nucleosides.

In some embodiments, all the modified nucleosides of region F and F' are LNA nucleosides, such as independently selected from beta-D-oxy LNA, ENA or ScET nucleosides, wherein

- 25 region F or F', or F and F' may optionally comprise DNA nucleosides (an alternating flank, see definition of these for more details). In some embodiments, all the modified nucleosides of region F and F' are beta-D-oxy LNA nucleosides, wherein region F or F', or F and F' may optionally comprise DNA nucleosides (an alternating flank, see definition of these for more details).

- 30 In some embodiments the 5' most and the 3' most nucleosides of region F and F' are LNA nucleosides, such as beta-D-oxy LNA nucleosides or ScET nucleosides.

In some embodiments, the internucleoside linkage between region F and region G is a phosphorothioate internucleoside linkage. In some embodiments, the internucleoside linkage between region F' and region G is a phosphorothioate internucleoside linkage. In some

- 35 embodiments, the internucleoside linkages between the nucleosides of region F or F', F and F' are phosphorothioate internucleoside linkages.

LNA Gapmer

An LNA gapmer is a gapmer wherein either one or both of region F and F' comprises or consists of LNA nucleosides. A beta-D-oxy gapmer is a gapmer wherein either one or both of region F and F' comprises or consists of beta-D-oxy LNA nucleosides.

- 5 In some embodiments the LNA gapmer is of formula: [LNA]₁₋₅-[region G]-[LNA]₁₋₅, wherein region G is as defined in the Gapmer region G definition.

MOE Gapmers

A MOE gapmer is a gapmer wherein regions F and F' consist of MOE nucleosides. In some embodiments the MOE gapmer is of design [MOE]₁₋₈-[Region G]-[MOE]₁₋₈, such as [MOE]₂₋₇-
 10 [Region G]₅₋₁₆-[MOE]₂₋₇, such as [MOE]₃₋₆-[Region G]-[MOE]₃₋₆, wherein region G is as defined in the Gapmer definition. MOE gapmers with a 5-10-5 design (MOE-DNA-MOE) have been widely used in the art.

Mixed Wing Gapmer

- A mixed wing gapmer is an LNA gapmer wherein one or both of region F and F' comprise a 2'
 15 substituted nucleoside, such as a 2' substituted nucleoside independently selected from the group consisting of 2'-O-alkyl-RNA units, 2'-O-methyl-RNA, 2'-amino-DNA units, 2'-fluoro-DNA units, 2'-alkoxy-RNA, MOE units, arabino nucleic acid (ANA) units and 2'-fluoro-ANA units, such as a MOE nucleoside. In some embodiments wherein at least one of region F and F', or both region F and F' comprise at least one LNA nucleoside, the remaining nucleosides of region F
 20 and F' are independently selected from the group consisting of MOE and LNA. In some embodiments wherein at least one of region F and F', or both region F and F' comprise at least two LNA nucleosides, the remaining nucleosides of region F and F' are independently selected from the group consisting of MOE and LNA. In some mixed wing embodiments, one or both of region F and F' may further comprise one or more DNA nucleosides.
 25 Mixed wing gapmer designs are disclosed in WO2008/049085 and WO2012/109395, both of which are hereby incorporated by reference.

Alternating Flank Gapmers

- Oligonucleotides with alternating flanks are LNA gapmer oligonucleotides where at least one of the flanks (F or F') comprises DNA in addition to the LNA nucleoside(s). In some embodiments
 30 at least one of region F or F', or both region F and F', comprise both LNA nucleosides and DNA nucleosides. In such embodiments, the flanking region F or F', or both F and F' comprise at least three nucleosides, wherein the 5' and 3' most nucleosides of the F and/or F' region are LNA nucleosides.

- In some embodiments at least one of region F or F', or both region F and F', comprise both LNA
 35 nucleosides and DNA nucleosides. In such embodiments, the flanking region F or F', or both F and F' comprise at least three nucleosides, wherein the 5' and 3' most nucleosides of the F or F'

region are LNA nucleosides, and there is at least one DNA nucleoside positioned between the 5' and 3' most LNA nucleosides of region F or F' (or both region F and F').

Region D' or D'' in an oligonucleotide

The oligonucleotide of the invention may in some embodiments comprise or consist of the contiguous nucleotide sequence of the oligonucleotide which is complementary to the target nucleic acid, such as the gapmer F-G-F', and further 5' and/or 3' nucleosides. The further 5' and/or 3' nucleosides may or may not be fully complementary to the target nucleic acid. Such further 5' and/or 3' nucleosides may be referred to as region D' and D'' herein.

The addition of region D' or D'' may be used for the purpose of joining the contiguous nucleotide sequence, such as the gapmer, to a conjugate moiety or another functional group. When used for joining the contiguous nucleotide sequence with a conjugate moiety it can serve as a biocleavable linker. Alternatively, it may be used to provide exonuclease protection or for ease of synthesis or manufacture.

Region D' and D'' can be attached to the 5' end of region F or the 3' end of region F', respectively to generate designs of the following formulas D'-F-G-F', F-G-F'-D'' or D'-F-G-F'-D''. In this instance the F-G-F' is the gapmer portion of the oligonucleotide and region D' or D'' constitute a separate part of the oligonucleotide.

Region D' or D'' may independently comprise or consist of 1, 2, 3, 4 or 5 additional nucleotides, which may be complementary or non-complementary to the target nucleic acid. The nucleotide adjacent to the F or F' region is not a sugar-modified nucleotide, such as a DNA or RNA or base modified versions of these. The D' or D'' region may serve as a nuclease susceptible biocleavable linker (see definition of linkers). In some embodiments the additional 5' and/or 3' end nucleotides are linked with phosphodiester linkages, and are DNA or RNA. Nucleotide based biocleavable linkers suitable for use as region D' or D'' are disclosed in WO2014/076195, which include by way of example a phosphodiester linked DNA dinucleotide. The use of biocleavable linkers in poly-oligonucleotide constructs is disclosed in WO2015/113922, where they are used to link multiple antisense constructs (e.g. gapmer regions) within a single oligonucleotide.

In one embodiment the oligonucleotide of the invention comprises a region D' and/or D'' in addition to the contiguous nucleotide sequence which constitutes the gapmer.

In some embodiments, the oligonucleotide of the present invention can be represented by the following formulae:

F-G-F'; in particular F₁₋₈-G₅₋₁₆-F'₂₋₈

D'-F-G-F', in particular D'₁₋₃-F₁₋₈-G₅₋₁₆-F'₂₋₈

F-G-F'-D'', in particular F₁₋₈-G₅₋₁₆-F'₂₋₈-D''₁₋₃

D'-F-G-F'-D'', in particular D'₁₋₃-F₁₋₈-G₅₋₁₆-F'₂₋₈-D''₁₋₃

In some embodiments the internucleoside linkage positioned between region D' and region F is a phosphodiester linkage. In some embodiments the internucleoside linkage positioned between region F' and region D'' is a phosphodiester linkage.

Conjugate

5 The term conjugate as used herein refers to an oligonucleotide which is covalently linked to a non-nucleotide moiety (conjugate moiety or region C or third region).

Conjugation of the oligonucleotide of the invention to one or more non-nucleotide moieties may improve the pharmacology of the oligonucleotide, e.g. by affecting the activity, cellular distribution, cellular uptake or stability of the oligonucleotide. In some embodiments the

10 conjugate moiety modifies or enhances the pharmacokinetic properties of the oligonucleotide by improving cellular distribution, bioavailability, metabolism, excretion, permeability, and/or cellular uptake of the oligonucleotide. In particular the conjugate may target the oligonucleotide to a specific organ, tissue or cell type and thereby enhance the effectiveness of the oligonucleotide in that organ, tissue or cell type. At the same time the conjugate may serve to reduce activity of
15 the oligonucleotide in non-target cell types, tissues or organs, e.g. off target activity or activity in non-target cell types, tissues or organs.

In an embodiment, the non-nucleotide moiety (conjugate moiety) is selected from the group consisting of carbohydrates, cell surface receptor ligands, drug substances, hormones, lipophilic substances, polymers, proteins, peptides, toxins (e.g. bacterial toxins), vitamins, viral proteins
20 (e.g. capsids) or combinations thereof.

In some embodiments, the conjugate is an antibody or an antibody fragment which has a specific affinity for a transferrin receptor, for example as disclosed in WO 2012/143379 hereby incorporated by reference. In some embodiments the non-nucleotide moiety is an antibody or antibody fragment, such as an antibody or antibody fragment that facilitates delivery across the
25 blood-brain-barrier, in particular an antibody or antibody fragment targeting the transferrin receptor.

Linkers

A linkage or linker is a connection between two atoms that links one chemical group or segment of interest to another chemical group or segment of interest via one or more covalent bonds.

30 Conjugate moieties can be attached to the oligonucleotide directly or through a linking moiety (e.g. linker or tether). Linkers serve to covalently connect a third region, e.g. a conjugate moiety (Region C), to a first region, e.g. an oligonucleotide or contiguous nucleotide sequence or gapmer region F-G-F' (region A).

In some embodiments of the invention the conjugate or oligonucleotide conjugate of the
35 invention may optionally, comprise a linker region (second region or region B and/or region Y) which is positioned between the oligonucleotide or contiguous nucleotide sequence

complementary to the target nucleic acid (region A or first region) and the conjugate moiety (region C or third region).

Region B refers to biocleavable linkers comprising or consisting of a physiologically labile bond that is cleavable under conditions normally encountered or analogous to those encountered

5 within a mammalian body. Conditions under which physiologically labile linkers undergo chemical transformation (e.g., cleavage) include chemical conditions such as pH, temperature, oxidative or reductive conditions or agents, and salt concentration found in or analogous to those encountered in mammalian cells. Mammalian intracellular conditions also include the presence of enzymatic activity normally present in a mammalian cell such as from proteolytic
10 enzymes or hydrolytic enzymes or nucleases. In one embodiment the biocleavable linker is susceptible to S1 nuclease cleavage. DNA phosphodiester containing biocleavable linkers are described in more detail in WO 2014/076195 (hereby incorporated by reference) – see also region D' or D'' herein.

Region Y refers to linkers that are not necessarily biocleavable but primarily serve to covalently
15 connect a conjugate moiety (region C or third region), to an oligonucleotide (region A or first region). The region Y linkers may comprise a chain structure or an oligomer of repeating units such as ethylene glycol, amino acid units or amino alkyl groups. The oligonucleotide conjugates of the present invention can be constructed of the following regional elements A-C, A-B-C, A-B-Y-C, A-Y-B-C or A-Y-C. In some embodiments the linker (region Y) is an amino
20 alkyl, such as a C2 – C36 amino alkyl group, including, for example C6 to C12 amino alkyl groups. In a preferred embodiment the linker (region Y) is a C6 amino alkyl group.

Treatment

The term 'treatment' as used herein refers to both treatment of an existing disease (e.g. a disease or disorder as herein referred to), or prevention of a disease, *i.e.* prophylaxis. It will
25 therefore be recognized that treatment as referred to herein may, in some embodiments, be prophylactic. In some embodiments treatment is performed on a patient who has been diagnosed with a neurological disorder, such as a neurological disorder selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and
30 multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

In some embodiments the compounds of the invention are for use in the treatment of frontotemporal lobar degeneration (FTLD).

A desired effect of the treatment is to reduce the *TMEM106B* mRNA in the frontal cortex of the
35 subject to be treated to normal levels which corresponds to the average *TMEM106B* mRNA levels in non-demented individuals. It is advantageous the the reduction of *TMEM106B* mRNA

is not reduced below 40% of normal levels, such as less than 30% below normal levels, such as less than 20% below of normal levels, such as within the range of 40% below normal levels and 20% above normal levels, such as 30% below normal levels and 15% above normal levels, such as 20% below normal levels and 10% above normal levels.

5 ***Pharmaceutically acceptable salts***

The term “pharmaceutically acceptable salts” refers to those salts which retain the biological effectiveness and properties of the free bases or free acids, which are not biologically or otherwise undesirable. The salts are formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, particularly hydrochloric acid, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, N-acetylcystein. In addition these salts may be prepared from addition of an inorganic base or an organic base to the free acid. Salts derived from an inorganic base include, but are not limited to, the sodium, potassium, lithium, ammonium, calcium, magnesium salts. Salts derived from organic bases include, but are not limited to salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, ethanolamine, lysine, arginine, N-ethylpiperidine, piperidine, polyamine resins. The compound of formula (I) can also be present in the form of zwitterions. Particularly preferred pharmaceutically acceptable salts of compounds of formula (I) are the salts of hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid and methanesulfonic acid.

Protecting group

The term “protecting group”, alone or in combination, signifies a group which selectively blocks a reactive site in a multifunctional compound such that a chemical reaction can be carried out selectively at another unprotected reactive site. Protecting groups can be removed. Exemplary protecting groups are amino-protecting groups, carboxy-protecting groups or hydroxy-protecting groups.

30 **DETAILED DESCRIPTION OF THE INVENTION**

The Oligonucleotides of the Invention

The invention relates to an oligonucleotide capable of modulating expression of TMEM106B, such as inhibiting (down-regulating) TMEM106B. The modulation is achieved by hybridizing to a target nucleic acid encoding TMEM106B or which is involved in the regulation of TMEM106B.

The target nucleic acid may be a mammalian TMEM106B sequence, such as a sequence selected from the group consisting of SEQ ID NO: 1 – 6.

Advantageously, the oligonucleotide of the invention may be selected from an antisense oligonucleotide, an siRNA or shRNA which targets TMEM106B.

- 5 In some embodiments the oligonucleotide of the invention is capable of modulating the expression of the target by inhibiting or down-regulating it. Preferably, such modulation produces an inhibition of expression of at least 20% compared to the normal expression level of the target, more preferably at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% inhibition compared to the normal expression level of the target. In
- 10 some embodiments oligonucleotides of the invention may be capable of inhibiting expression levels of TMEM106B mRNA by at least 60% or 70% *in vitro* using human SK-N-BE(2) neuroblastoma cells, which may be acquired from ATCC (CRL-2271). In some embodiments compounds of the invention may be capable of inhibiting expression levels of TMEM106B protein by at least 50% *in vitro* using human SK-N-BE(2) neuroblastoma cells. Suitably, the
- 15 examples provide assays which may be used to measure TMEM106B RNA or protein inhibition. The target modulation is triggered by the hybridization between a contiguous nucleotide sequence of the oligonucleotide and the target nucleic acid. In some embodiments the oligonucleotide of the invention comprises mismatches between the oligonucleotide and the target nucleic acid. Despite mismatches hybridization to the target nucleic acid may still be
- 20 sufficient to show a desired modulation of TMEM106B expression. Reduced binding affinity resulting from mismatches may advantageously be compensated by increased number of nucleotides in the oligonucleotide and/or an increased number of modified nucleosides capable of increasing the binding affinity to the target, such as 2' sugar modified nucleosides, including LNA, present within the oligonucleotide sequence.
- 25 An aspect of the present invention relates to an antisense oligonucleotide which comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementarity to a mammalian TMEM106B nucleic acid, for example SEQ ID NO: 1 – 6, such as SEQ ID NO: 1, 2, 3, 4, 5 or 6.

In some embodiments, the oligonucleotide comprises a contiguous sequence of 10 to 30

30 nucleotides in length, which is at least 90% complementary, such as at least 91%, such as at least 92%, such as at least 93%, such as at least 94%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, or 100% complementary with a region of the target nucleic acid or a target sequence.

In a preferred embodiment the oligonucleotide of the invention, or contiguous nucleotide

35 sequence thereof is fully complementary (100% complementary) to a region of the target

nucleic acid, or in some embodiments may comprise one or two mismatches between the oligonucleotide and the target nucleic acid.

In some embodiments the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as fully (or 100%)

- 5 complementary, to a region target nucleic acid region present in SEQ ID NO: 1 and/or 2. In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present in SEQ ID NO: 1 and either SEQ ID NO: 3 or SEQ ID NO 5 (or both SEQ ID NO: 3 & 5). In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present SEQ ID NO: 1, 3 and 5.
- 10 In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present in SEQ ID NO: 2 and either SEQ ID NO: 4 or SEQ ID NO: 6 (or both SEQ ID NO: 4 & 6). In some embodiments the oligonucleotide sequence is 100% complementary to a corresponding target nucleic acid region present SEQ ID NO: 2, 4 and 6.
- 15 In some embodiments, the oligonucleotide of the invention is at least 90% complementary, such as 100 % complementary to exon 9 of SEQ ID NO 1.

In some embodiments, the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as 100% complementarity, to a corresponding target nucleic acid region present in SEQ ID NO: 1, wherein the target nucleic acid region is selected from the group consisting of Reg. A1 to A80 in Table 5.

Table 5: Selected regions of SEQ ID NO: 1 which may be targeted using oligonucleotide of the invention

Reg. A	Position in SEQ ID NO 1		Reg. A	Position in SEQ ID NO 1		Reg. A	Position in SEQ ID NO 1	
	from	to		from	to		from	to
1	546	563	31	6837	6853	61	21425	21442
2	2122	2140	32	8453	8472	62	22110	22128
3	2143	2160	33	8983	9001	63	23374	23393
4	2165	2183	34	9533	9549	64	23435	23452
5	2300	2317	35	9628	9644	65	23806	23822
6	2392	2410	36	11065	11083	66	23874	23890
7	2548	2565	37	11117	11134	67	24045	24063
8	3507	3524	38	11264	11281	68	24060	24077
9	3678	3694	39	12310	12325	69	24060	24076
10	3736	3753	40	12870	12887	70	24064	24083
11	3752	3767	41	13050	13065	71	24081	24098
12	3802	3819	42	13397	13414	72	24801	24819

Reg. A	Position in SEQ ID NO 1		Reg. A	Position in SEQ ID NO 1		Reg. A	Position in SEQ ID NO 1	
	from	to		from	to		from	to
13	3908	3925	43	15061	15079	73	24812	24828
14	4321	4337	44	15249	15266	74	25050	25067
15	4701	4720	45	15318	15336	75	25372	25387
16	4948	4965	46	15368	15385	76	25392	25406
17	5063	5080	47	15440	15457	77	25773	25790
18	5069	5086	48	15632	15649	78	25796	25814
19	5172	5190	49	15823	15842	79	25969	25985
20	5512	5530	50	16496	16513	80	29351	29367
21	5583	5599	51	19090	19109	81		
22	6015	6032	52	19198	19217	82		
23	6032	6047	53	19211	19228	83		
24	6125	6140	54	19699	19718	84		
25	6136	6154	55	20217	20236	85		
26	6172	6189	56	20227	20243	86		
27	6200	6216	57	20767	20786	87		
28	6214	6231	58	20880	20896	88		
29	6401	6417	59	21084	21101	89		
30	6458	6476	60	21214	21231	90		

In some embodiments, the oligonucleotide comprises a contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90% complementary, such as 100% complementarity, to a corresponding target nucleic acid region present in SEQ ID NO: 1, wherein the target nucleic acid region is selected from the group consisting of Reg B1 to B29 in Table 6.

- 5 Table 6: Selected regions of SEQ ID NO: 2 which may be targeted using oligonucleotide of the invention

Reg. B	Position in SEQ ID NO 2		Reg.	Position in SEQ ID NO 2		Reg.	Position in SEQ ID NO 2	
	To	From		To	From		To	From
1	489	505	13	3906	3923	25	5863	5877
2	547	564	14	4277	4293	26	6244	6261
3	563	578	15	4345	4361	27	6267	6285
4	727	742	16	4516	4534	28	6440	6456
5	1013	1032	17	4531	4548	29	574	578
6	1238	1257	18	4531	4547			
7	1351	1367	19	4535	4554			
8	1555	1572	20	4552	4569			
9	1685	1702	21	5272	5290			
10	1896	1913	22	5283	5299			
11	2581	2599	23	5521	5538			

Reg. B	Position in SEQ ID NO 2		Reg.	Position in SEQ ID NO 2		Reg.	Position in SEQ ID NO 2	
	To	From		To	From		To	From
12	3845	3864	24	5843	5858			

In some embodiments, the oligonucleotide of the invention comprises or consists of 8 to 70 nucleotides in length, such as 10 to 60 nucleotides in length, such as 10 to 50 nucleotides in length, such as 12 to 50 nucleotides in length, such as 8 to 40 nucleotides in length, such as from 9 to 35, such as from 10 to 30, such as from 11 to 22, such as from 12 to 20, such as from 13 to 18 or 14 to 16 nucleotides in length.

In some embodiments, the antisense oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises or consists of 10 to 35 nucleotides in length, such as from 10 to 30, such as 11 to 22, such as from 12 to 20, such as from 14 to 18 or 14 to 16 contiguous nucleotides in length. Advantageously, the antisense oligonucleotide, or contiguous nucleotide sequence thereof, comprises or consists of 14, 15, 16, 17 or 18 nucleotides in length.

In some embodiments, the antisense oligonucleotide or contiguous nucleotide sequence thereof comprises or consists of 22 or less nucleotides, such as 20 or less nucleotides, such as 18 or less nucleotides, such as 14, 15, 16 or 17 nucleotides. It is to be understood that any range given herein includes the range endpoints. Accordingly, if an oligonucleotide is said to include from 10 to 30 nucleotides, both 10 and 30 nucleotides are included.

In some embodiments, the contiguous nucleotide sequence thereof, comprises or consists of 10 to 35 nucleotides in length, such as from 10 to 30, such as 11 to 22, such as from 12 to 20, such as from 14 to 18 or 14 to 16 contiguous nucleotides in length.

In some embodiments, the contiguous nucleotide sequence comprises or consists of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 contiguous nucleotides in length. It is generally understood that the oligonucleotide cannot be shorter than the contiguous nucleotide sequence.

In some embodiments, the oligonucleotide or contiguous nucleotide sequence comprises or consists of a sequence which is fully complementary to a target sequence RegA1 – A80 or RegB1 to B29 as provided in tables 5 and 6 respectively.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence thereof comprises at least 10 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86 (see motif

sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 12 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86 (see motif sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 13 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86 (see motif sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 14 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86 (see motif

sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 15 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86. It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: : 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 16 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7 to 164, such as SEQ ID NOs 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86 (see motif sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

In some embodiments, the oligonucleotide of the invention or the contiguous nucleotide sequence there comprises at least 17 contiguous nucleotides which are at least 90% identical, such as 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 65, 66, 71, 74 and 75 (see motif sequences listed in Table 7 & 8). It is advantageous if the sequence is complementary to both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 65, 66, and 71.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 10 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 10 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 12 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 12 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253,
5 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous
10 nucleotide sequence thereof, comprises at least 13 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211,
15 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192,
20 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 13 contiguous nucleotides which are is at least
25 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310,
30 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 14 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173,
35 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211,

212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 14 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 15 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 15 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291,

292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 16 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, comprises at least 16 contiguous nucleotides which are is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, is at least 90% complementary to, such as fully complementary to a sequence selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206,

208, 209, 210, 211, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the oligonucleotide of the invention, or contiguous nucleotide sequence thereof, is at least 90% complementary to, such as fully complementary to

5 a sequence selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

10 In some embodiments of the invention the target sequence is selected from the group consisting of SEQ ID Nos 167-246, such as SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230,
15 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246. It is advantageous to target sequences which are present in both human and cyno, such as a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214,
20 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240, 241, 243, 244 and 245.

In some embodiments of the invention the target sequence is selected from the group consisting of SEQ ID Nos 247-326, such as SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272,
25 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.

In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 10 contiguous nucleotides which are fully complementary to a region of the target nucleic acid,
30 such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226, 231, 234 and 235.

In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 12 contiguous nucleotides which are fully complementary to a region of the target nucleic acid, such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226,
35 231, 234 and 235.

In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 13 contiguous nucleotides which are fully complementary to a region of the target nucleic acid, such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226, 231, 234 and 235.

- 5 In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 14 contiguous nucleotides which are fully complementary to a region of the target nucleic acid, such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226, 231, 234 and 235.

- 10 In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 15 contiguous nucleotides which are fully complementary to a region of the target nucleic acid, such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226, 231, 234 and 235.

- 15 In some embodiment the oligonucleotide or contiguous nucleotide sequence comprises at least 16, such as at least 17, contiguous nucleotides which are fully complementary to a region of the target nucleic acid, such as a target sequence selected from the group consisting of SEQ ID NO 222, 225, 226, 231, 234 and 235.

- In some embodiments the oligonucleotide or contiguous nucleotide sequence comprises at least 16, such as at least 17, contiguous nucleotides which are fully complementary to a region of the target nucleic acid from position 21084 to 21101 (Region A59, Table 5), position 21214-21231 (Region A60 Table 5), position 23806 to 23822 (Region A70 Table 5), position 24060 to 24077 (Region A68 Table 5) or position 24045 to 24098 (Region A67-A70 Table 5) of SEQ ID NO: 1. In some embodiments, the oligonucleotide comprises or consists of a contiguous nucleotide sequence which is 100% identical to a sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides thereof.

- 30 In some embodiments, the oligonucleotide comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides thereof.

In some embodiments, the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence which is 100% identical to a sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides thereof.

In some embodiments, the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides thereof.

In some embodiments, the antisense oligonucleotide comprises or consists of a contiguous nucleotide sequence which is 100% identical to a sequence selected from the group consisting of SEQ ID NO 65, 66, 71, 74 and 75, or at least 16 contiguous nucleotides thereof.

It is understood that the contiguous nucleobase sequences (motif sequence) can be modified to for example increase nuclease resistance and/or binding affinity to the target nucleic acid.

The pattern in which the modified nucleosides (such as high affinity modified nucleosides) are incorporated into the oligonucleotide sequence is generally termed oligonucleotide design.

The oligonucleotides of the invention are designed with modified nucleosides and DNA nucleosides. Advantageously, high affinity modified nucleosides are used.

In an embodiment, the oligonucleotide comprises at least 1 modified nucleoside, such as at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, 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 modified nucleosides. In an embodiment the oligonucleotide comprises from 1 to 10 modified nucleosides, such as from 2 to 9 modified nucleosides, such as from 3 to 8 modified nucleosides, such as from 4 to 7 modified nucleosides, such as 6 or 7 modified nucleosides. Suitable modifications are described in the “Definitions” section under “modified nucleoside”, “high affinity modified nucleosides”, “sugar modifications”, “2’ sugar modifications” and Locked nucleic acids (LNA).²

In an embodiment, the oligonucleotide comprises one or more sugar modified nucleosides, such as 2’ sugar modified nucleosides. Preferably the oligonucleotide of the invention comprises one or more 2’ sugar modified nucleoside independently selected from the group consisting of 2’-O-alkyl-RNA, 2’-O-methyl-RNA, 2’-alkoxy-RNA, 2’-O-methoxyethyl-RNA, 2’-amino-DNA, 2’-fluoro-

DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides. It is advantageous if one or more of the modified nucleoside(s) is a locked nucleic acid (LNA).

In a further embodiment the oligonucleotide comprises at least one modified internucleoside linkage. Suitable internucleoside modifications are described in the "Definitions" section under

5 "Modified internucleoside linkage". It is advantageous if at least 75%, such as all, the internucleoside linkages within the contiguous nucleotide sequence are phosphorothioate or boranophosphate internucleoside linkages. In some embodiments all the internucleotide linkages in the contiguous sequence of the oligonucleotide are phosphorothioate linkages.

In some embodiments, the oligonucleotide of the invention comprises at least one LNA
10 nucleoside, such as 1, 2, 3, 4, 5, 6, 7, or 8 LNA nucleosides, such as from 2 to 6 LNA nucleosides, such as from 3 to 7 LNA nucleosides, 4 to 8 LNA nucleosides or 3, 4, 5, 6, 7 or 8 LNA nucleosides. In some embodiments, at least 75% of the modified nucleosides in the oligonucleotide are LNA nucleosides, such as 80%, such as 85%, such as 90% of the modified nucleosides are LNA nucleosides. In a still further embodiment all the modified nucleosides in
15 the oligonucleotide are LNA nucleosides. In a further embodiment, the oligonucleotide may comprise both beta-D-oxy-LNA, and one or more of the following LNA nucleosides: thio-LNA, amino-LNA, oxy-LNA, ScET and/or ENA in either the beta-D or alpha-L configurations or combinations thereof. In a further embodiment, all LNA cytosine units are 5-methyl-cytosine. It is advantageous for the nuclease stability of the oligonucleotide or contiguous nucleotide
20 sequence to have at least 1 LNA nucleoside at the 5' end and at least 2 LNA nucleosides at the 3' end of the nucleotide sequence.

In an embodiment of the invention the oligonucleotide of the invention is capable of recruiting RNase H.

In the current invention an advantageous structural design is a gapmer design as described in
25 the "Definitions" section under for example "Gapmer", "LNA Gapmer", "MOE gapmer" and "Mixed Wing Gapmer" "Alternating Flank Gapmer". The gapmer design includes gapmers with uniform flanks, mixed wing flanks, alternating flanks, and gapbreaker designs. In the present invention it is advantageous if the oligonucleotide of the invention is a gapmer with an F-G-F' design. In some embodiments the gapmer is an LNA gapmer wherein at least one or both of
30 regions F and F' comprise at least one LNA unit.

In some embodiments the oligonucleotide of the invention does not comprise 6'-methyl-beta-D-oxy-LNA nucleosides. In some embodiments the oligonucleotide of the invention does not comprise 2'-O-methoxyethyl nucleosides.

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide
35 sequence which is 100% identical to a sequence selected from the group consisting of SEQ ID

NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides

5 thereof.

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 12 contiguous nucleotides thereof.

10

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 13 contiguous nucleotides thereof.

15

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 14 contiguous nucleotides thereof.

20

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 15 contiguous nucleotides thereof.

25

In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, or at least 16 contiguous nucleotides thereof.

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In some embodiments, the LNA gapmer comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO 65, 66, 71, 74, and 75, or at least 16 contiguous nucleotides thereof

In some embodiments, the compound of the invention comprises or consists of a contiguous nucleotide sequence selected from the group consisting of SEQ ID NO: 7 – 86, such as SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86, wherein the designs of the sequence correspond to that listed in Table 7.

In particular the flanks (F and F') are selected from 2'-sugar modified nucleosides (M), such as LNA, cET, or MOE, and the gap constitutes a stretch of DNA (D). In gapmers with alternating flank designs the flanks of oligonucleotide is annotated as a series of integers, representing a number of 2' sugar modified nucleosides (M) followed by a number of DNA nucleosides (D). For example a flank with a 2-2-1 motif represents 5' [M]₂[D]₂[M] 3' and a 1-1-1-1-1 motif represents 5' [M]-[D]-[M]-[D]-[M] 3'. Both flanks have a 2' sugar modified nucleoside at the 5' and 3' terminal. The gap region (G), is constituted of a number of DNA nucleosides (typically between 5 and 16), located between the flanks.

In some embodiments, the compound of the invention comprises or consists of a contiguous nucleotide sequence selected from the group consisting of CMP ID NO: 7_1 – 86_1, such as 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, and 86_1, wherein a capital letter is a LNA nucleoside, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA, DNA cytosine are optionally 5-methyl cytosine DNA.

In some embodiments, the compound of the invention comprises or consists of a contiguous nucleotide sequence selected from the group consisting of CMP-ID-NO: 7_1 – 86_1, such as 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, and 86_1, wherein a capital letter is a LNA nucleoside, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA,

DNA cytosine are optionally 5-methyl cytosine DNA, and the internucleoside linkages between all nucleosides within the contiguous nucleotide sequence are phosphorothioate internucleoside linkages.

In some embodiments, the compound of the invention comprises or consists of a contiguous nucleotide sequence selected from the group consisting of CMP-ID-NO: 7_1 – 86_1, such as 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, and 86_1, wherein a capital letter is a beta-D-oxy LNA nucleoside, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are 5 methyl cytosine LNA, and the internucleoside linkages between all nucleosides within the contiguous nucleotide sequence are phosphorothioate internucleoside linkages, as indicated in Table 7.

In some embodiments, the compound of the invention is selected from the group of compounds of CMP-ID-NO: 7_1 – 86_1, 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, and 86_1, wherein a capital letter is a LNA nucleoside, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA, DNA cytosine are optionally 5-methyl cytosine DNA, and the internucleoside linkages between DNA nucleosides are phosphorothioate internucleoside linkages.

In some embodiments, the compound of the invention is selected from the group of compounds, ATGTttatcaccaaAATT (SEQ ID NO: 65, CMP ID NO: 65_1)

CTGAaatactaccaTATA (SEQ ID NO: 66, CMP ID NO: 66_1)

TTTAatcataccaATCT (SEQ ID NO: 71, CMP ID NO: 71_1)

TTCTtatttcaaCTCA (SEQ ID NO: 74, CMP ID NO: 74_1)

TCTTatttcaaCTCA (SEQ ID NO: 75, CMP ID NO: 75_1)

wherein a capital letter is a LNA nucleoside, such as a beta-D-oxy-LNA, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA, DNA cytosine nucleosides are optionally 5-methyl cytosine DNA, the internucleoside linkages between DNA nucleosides are phosphorothioate internucleoside linkages.

In some embodiments, the compound of the invention is selected from the group of compounds of CMP-ID-NO: 7_1 – 86_1, wherein a capital letter is a LNA nucleoside, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA, DNA cytosine are optionally 5-methyl cytosine DNA, and all the internucleoside linkages the nucleosides are phosphorothioate internucleoside linkages.

Advantageously, the compound of the invention is in the form of a pharmaceutically acceptable salt.

In a further embodiment of the invention the oligonucleotide may comprise at least one stereodefined internucleoside linkages, such as a stereodefined phosphorothioate internucleoside linkage. An advantage of generating stereodefined oligonucleotide variants is the ability to increase the diversity across a sequence motif, and select stereodefined oligonucleotides including sub-libraries of stereodefined oligonucleotides, which have improved medicinal chemical properties as compared to a non stereodefined oligonucleotide.

The invention provides a conjugate comprising the oligonucleotide or antisense oligonucleotide according to the invention, and at least one conjugate moiety covalently attached to said oligonucleotide. In some embodiments the conjugate moiety is a conjugate that facilitates delivery across the blood brain barrier, such as an antibody or antibody fragment targeting the transferrin receptor.

The invention provides a pharmaceutically acceptable salt of the oligonucleotide or antisense oligonucleotide, or the conjugate, of the invention.

In some embodiments the contiguous nucleotide sequence of the invention does not comprise 10 or more contiguous nucleotides present in the sequence GATCAGAGATTAAGGCCAA (SEQ ID NO 322). In some embodiments the contiguous nucleotide sequence of the invention does not comprise 10 or more contiguous nucleotides present in the sequence GCAGATTGATTATACGGTA (SEQ ID NO 323) or GTGGAAGGAACACGACTTA (SEQ ID NO 324).

Method of manufacture

In a further aspect, the invention provides methods for manufacturing the oligonucleotides of the invention comprising reacting nucleotide units and thereby forming covalently linked contiguous nucleotide units comprised in the oligonucleotide. Preferably, the method uses phosphoramidite chemistry (see for example Caruthers et al, 1987, Methods in Enzymology vol. 154, pages 287-313). In a further embodiment the method further comprises reacting the contiguous nucleotide sequence with a conjugating moiety (ligand) to covalently attach the conjugate moiety to the oligonucleotide. In a further aspect a method is provided for manufacturing the composition of

the invention, comprising mixing the oligonucleotide or conjugated oligonucleotide of the invention with a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

Pharmaceutical salt

The compounds according to the present invention may exist in the form of their
5 pharmaceutically acceptable salts. The term "pharmaceutically acceptable salt" refers to conventional acid-addition salts or base-addition salts that retain the biological effectiveness and properties of the compounds of the present invention and are formed from suitable non-toxic organic or inorganic acids or organic or inorganic bases. Acid-addition salts include for example those derived from inorganic acids such as hydrochloric acid, hydrobromic acid,
10 hydroiodic acid, sulfuric acid, sulfamic acid, phosphoric acid and nitric acid, and those derived from organic acids such as *p*-toluenesulfonic acid, salicylic acid, methanesulfonic acid, oxalic acid, succinic acid, citric acid, malic acid, lactic acid, fumaric acid, and the like. Base-addition salts include those derived from ammonium, potassium, sodium and, quaternary ammonium hydroxides, such as for example, tetramethyl ammonium hydroxide. The chemical modification
15 of a pharmaceutical compound into a salt is a technique well known to pharmaceutical chemists in order to obtain improved physical and chemical stability, hygroscopicity, flowability and solubility of compounds. It is for example described in Bastin, Organic Process Research & Development 2000, 4, 427-435 or in Ansel, In: Pharmaceutical Dosage Forms and Drug Delivery Systems, 6th ed. (1995), pp. 196 and 1456-1457. For example, the pharmaceutically
20 acceptable salt of the compounds provided herein may be a sodium salt.

In a further aspect the invention provides a pharmaceutically acceptable salt of the antisense oligonucleotide or a conjugate thereof. In a preferred embodiment, the pharmaceutically acceptable salt is a sodium or a potassium salt.

Pharmaceutical Composition

25 In a further aspect, the invention provides pharmaceutical compositions comprising any of the aforementioned oligonucleotides and/or oligonucleotide conjugates or salts thereof and a pharmaceutically acceptable diluent, carrier, salt and/or adjuvant. A pharmaceutically acceptable diluent includes phosphate-buffered saline (PBS) and pharmaceutically acceptable salts include, but are not limited to, sodium and potassium salts. In some embodiments the
30 pharmaceutically acceptable diluent is sterile phosphate buffered saline. In some embodiments the oligonucleotide is used in the pharmaceutically acceptable diluent at a concentration of 50 - 300µM solution.

Suitable formulations for use in the present invention are found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of
35 methods for drug delivery, see, e.g., Langer (Science 249:1527-1533, 1990). WO 2007/031091

provides further suitable and preferred examples of pharmaceutically acceptable diluents, carriers and adjuvants (hereby incorporated by reference). Suitable dosages, formulations, administration routes, compositions, dosage forms, combinations with other therapeutic agents, pro-drug formulations are also provided in WO2007/031091.

- 5 Oligonucleotides or oligonucleotide conjugates of the invention may be mixed with pharmaceutically acceptable active or inert substances for the preparation of pharmaceutical compositions or formulations. Compositions and methods for the formulation of pharmaceutical compositions are dependent upon a number of criteria, including, but not limited to, route of administration, extent of disease, or dose to be administered.
- 10 These compositions may be sterilized by conventional sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile aqueous carrier prior to administration. The pH of the preparations typically will be between 3 and 11, more preferably between 5 and 9 or between 6 and 8, and most preferably between 7 and 8, such as 7 to 7.5. The resulting
- 15 compositions in solid form may be packaged in multiple single dose units, each containing a fixed amount of the above-mentioned agent or agents, such as in a sealed package of tablets or capsules. The composition in solid form can also be packaged in a container for a flexible quantity, such as in a squeezable tube designed for a topically applicable cream or ointment.
- In some embodiments, the oligonucleotide or oligonucleotide conjugate of the invention is a
- 20 prodrug. In particular with respect to oligonucleotide conjugates the conjugate moiety is cleaved of the oligonucleotide once the prodrug is delivered to the site of action, e.g. the target cell.

Applications

The oligonucleotides of the invention may be utilized as research reagents for, for example, diagnostics, therapeutics and prophylaxis.

- 25 In research, such oligonucleotides may be used to specifically modulate the synthesis of TMEM106B protein in cells (e.g. *in vitro* cell cultures) and experimental animals thereby facilitating functional analysis of the target or an appraisal of its usefulness as a target for therapeutic intervention. Typically the target modulation is achieved by degrading or inhibiting the mRNA producing the protein, thereby prevent protein formation or by degrading or inhibiting
- 30 a modulator of the gene or mRNA producing the protein.

If employing the oligonucleotide of the invention in research or diagnostics the target nucleic acid may be a cDNA or a synthetic nucleic acid derived from DNA or RNA.

The present invention provides an *in vivo* or *in vitro* method for modulating TMEM106B expression in a target cell which is expressing TMEM106B, said method comprising administering an oligonucleotide of the invention in an effective amount to said cell.

In some embodiments the target cell is a neuronal cell. In some embodiments the target cell is a microglial cell.

In some embodiments, the target cell, is a mammalian cell in particular a human cell. The target cell may be an *in vitro* cell culture or an *in vivo* cell forming part of a tissue in a mammal. In preferred embodiments the target cell is present in the CNS, such as the brain, such as in the frontal temporal lobes.

In some embodiments the target cell is a CNS cell, a brain cell, a frontal cortex cell or a frontal temporal lobe cell.

In some embodiments the target cell is a cell which is present in the thalamus, hippocampus, striatum, retina, or spinal cord.

In some embodiments the target cell is a thalamus cell, a hippocampus cell, a striatum cell, a retina cell, or a spinal cord cell.

It will be understood that for *in vitro* use, such as for evaluation of TMEM106B expression or inhibition thereof, or targeting, in a cell, such as a target cell, the cell may be isolated from the tissue or may be derived from the tissue (e.g. an established or immortalized cell line), such as CNS tissue, brain tissue, frontal cortex, frontal temporal lobe tissue, thalamus tissue, hippocampus tissue, striatum tissue, retinal tissue, or spinal cord tissue. Cells which are isolated from the target tissue are referred to as primary cells.

In diagnostics the oligonucleotides may be used to detect and quantitate TMEM106B expression in cell and tissues by northern blotting, *in-situ* hybridisation or similar techniques.

For therapeutics, the oligonucleotides may be administered to an animal or a human, suspected of having a disease or disorder, which can be treated by modulating the expression of TMEM106B.

The invention provides methods for treating or preventing a disease, comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide, an oligonucleotide conjugate or a pharmaceutical composition of the invention to a subject suffering from or susceptible to the disease.

The invention also relates to an oligonucleotide, a composition or a conjugate as defined herein for use as a medicament.

The oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition according to the invention is typically administered in an effective amount.

The invention also provides for the use of the oligonucleotide or oligonucleotide conjugate of the invention as described for the manufacture of a medicament for the treatment of a disorder as referred to herein, or for a method of the treatment of as a disorder as referred to herein.

The disease or disorder, as referred to herein, is associated with expression of TMEM106B. In some embodiments disease or disorder may be associated with a mutation in the TMEM106B gene or a gene whose protein product is associated with or interacts with TMEM106B.

Therefore, in some embodiments, the target nucleic acid is a mutated form of the TMEM106B sequence and in other embodiments, the target nucleic acid is a regulator of the TMEM106B sequence.

The methods of the invention are preferably employed for treatment or prophylaxis against diseases caused by abnormal levels and/or activity of TMEM106B.

The invention further relates to use of an oligonucleotide, oligonucleotide conjugate or a pharmaceutical composition as defined herein for the manufacture of a medicament for the treatment of abnormal levels and/or activity of TMEM106B.

In some aspects, the invention relates to oligonucleotides, oligonucleotide conjugates or pharmaceutical compositions of the invention, for use in the treatment of diseases or disorders selected from neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

In some embodiments the compounds of the invention are used for the treatment of age associated changes in frontal cortex.

In one aspect, the invention relates to oligonucleotides, oligonucleotide conjugates or pharmaceutical compositions, of the invention, for use in the treatment of frontotemporal lobar degeneration (FTLD). The oligonucleotides, oligonucleotide conjugates or pharmaceutical compositions may be advantageous in the treatment of FTLD characterized by intranuclear and/or cytoplasmic accumulations of ubiquitinated proteins (FTLD-U), in particular FTDL-TDP which is characterized by the presence of ubiquitinated TAR DNA binding protein 43 (TDP-43) accumulations in frontal and temporal brain regions and in other TDP-43 proteinopathies.

Administration

The oligonucleotides or pharmaceutical compositions of the present invention may be administered via parenteral (such as, intravenous, subcutaneous, intra-muscular, intracerebral, intracerebroventricular intraocular, or intrathecal administration).

- 5 In some embodiments, the administration is via intrathecal administration.

Advantageously, e.g. for treatment of neurological disorders, the oligonucleotide or pharmaceutical compositions of the present invention are administered intrathecally or intracranially, e.g. via intracerebral or intraventricular administration.

- 10 The invention also provides for the use of the oligonucleotide or conjugate thereof, such as pharmaceutical salts or compositions of the invention, for the manufacture of a medicament wherein the medicament is in a dosage form for subcutaneous administration.

The invention also provides for the use of the oligonucleotide of the invention, or conjugate thereof, such as pharmaceutical salts or compositions of the invention, for the manufacture of a medicament wherein the medicament is in a dosage form for intrathecal administration.

15 Combination therapies

In some embodiments the oligonucleotide, oligonucleotide conjugate or pharmaceutical composition of the invention is for use in a combination treatment with another therapeutic agent. The therapeutic agent can for example be the standard of care for the diseases or disorders described above.

20 EMBODIMENTS

1. An oligonucleotide targeting TMEM106B, which comprises a contiguous nucleotide sequence of 10 – 30 nucleotides in length with at least 90% complementary, such as fully complementary, to a mammalian TMEM106B target nucleic acid.
- 25 2. The oligonucleotide according to embodiment 1, wherein the oligonucleotide is capable of reducing the expression of the mammalian TMEM106B target nucleic acid in a cell.
3. The oligonucleotide according to any one of embodiments 1 to 2, wherein the oligonucleotide is a therapeutic oligonucleotide.
4. The oligonucleotide according to any one of embodiment 1 to 3, wherein the mammalian
- 30 TMEM106B target nucleic acid is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5 and 6, or a naturally occurring variant thereof.
5. The oligonucleotide according to embodiment 4, wherein the naturally occurring variant is selected from the polymorphisms listed in Table 4.

6. The oligonucleotide of embodiment 1 to 5, wherein the target nucleic acid is RNA.
7. The oligonucleotide of embodiment 6, wherein the RNA is mRNA.
8. The oligonucleotide of embodiment 7, wherein the mRNA is pre-RNA or mature RNA
9. The oligonucleotide according to any one of embodiments 1 to 8, wherein the contiguous
5 nucleotide sequence, comprises at least 10 contiguous nucleotides, which are at least 90% complementary to, such as fully complementary, to a sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215,
10 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246, or a group consisting of SEQ ID NO: 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298,
15 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320 and 321.
10. The oligonucleotide according to any one of embodiment 1 to 9, wherein the oligonucleotide or contiguous nucleotide sequence is fully complementary to SEQ ID NO: 1 and/or 2, or a naturally occurring variant thereof.
- 20 11. The oligonucleotide according to any one of embodiments 1 to 10, wherein the contiguous nucleotide sequence comprises at least 10 contiguous nucleotides which are at least 90% complementary, such as is fully complementary, to a region of SEQ ID NO 1, wherein the regions is selected from the group consisting of position 546 - 563; 2122 - 2140; 2143 - 2160; 2165 - 2183; 2300 - 2317; 2392 - 2410; 2548 - 2565; 3507 - 3524; 3678 - 3694;
25 3736 - 3753; 3752 - 3767; 3802 - 3819; 3908 - 3925; 3908 - 6417; 4321 - 4337; 4701 - 4720; 4948 - 4965; 5063 - 5080; 5069 - 5086; 5172 - 5190; 5512 - 5530; 5583 - 5599; 6015 - 6047; 6015 - 6032; 6032 - 6047; 6125-6154; 6125 - 6140; 6136 - 6154; 6172 - 6189; 6200-6231; 6200 - 6216; 6214 - 6231; 6401 - 6417; 6458 - 6476; 6837 - 6853; 8453 - 8472; 8983 - 9001; 9533 - 9549; 9628 - 9644; 11065 - 11083; 11117 - 11134; 11264 - 11281; 12310 - 12325;
30 12870 - 12887; 13050 - 13065; 13397 - 13414; 15061 - 15079; 15249 - 15266; 15318 - 15336; 15368 - 15385; 15440 - 15457; 15632 - 15649; 15823 - 15842; 16496 - 16513; 19090 - 19109; 19198 - 19217; 19211 - 19228; 19699 - 19718; 20217-20243; 20217 - 20236; 20227 - 20243; 20755 - 26403; 20767 - 20786; 20880 - 20896; 21084 - 21101; 21214 - 21231; 21425 - 21442; 22110 - 25406; 22110 - 22128; 23374 - 23393; 23435 - 23452; 23806 -
35 23822; 23874 - 23890; 24045 -24098; 24045 - 24063; 24060 - 24077; 24060 - 24076; 24064

- 24083; 24081 - 24098; 24045-24098; 24801 – 24828; 24801 - 24819; 24812 - 24828; 25050 - 25067; 25372 - 25387; 25392 - 25406; 25773 - 25790; 25796 - 25814; 25969 - 25985; and 29351 – 29367 of SEQ ID NO: 1.

12. The oligonucleotide according to any one of embodiments 1 to 11, wherein the
contiguous nucleotide sequence, comprises at least 10 contiguous nucleotides, which are at
least 90% complementary to, such as fully complementary, to a sequence selected from the
group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178,
179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196,
197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232,
233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246.

13. The oligonucleotide according to any one of embodiment 1 to 12, wherein the
contiguous nucleotide sequence is complementary, such as fully complementary, to SEQ ID
NO: 1 and SEQ ID NO: 3, or a naturally occurring variants thereof.

14. The oligonucleotide according to embodiment 13, wherein the contiguous nucleotide
sequence, comprises at least 10 contiguous nucleotides, which are at least 90%
complementary to, such as fully complementary to a sequence selected from the group
consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197,
198, 199, 200, 201, 202, 203, 204, 206, 208, 209, 210, 211, 213, 214, 215, 216, 217, 218,
219, 220, 221, 222, 223, 224, 225, 226, 227, 229, 230, 231, 232, 236, 237, 238, 239, 240,
241, 243, 244 and 245.

15. The oligonucleotide according to any one of embodiments 1 to 14, which comprises a
contiguous nucleotide sequence of 10 to 30 nucleotides in length with at least 90%
complementary, such as fully complementary, to the 3'UTR of a mammalian TMEM106B
target nucleic acid.

16. The oligonucleotide according to any one of embodiments 1 to 15, wherein the
contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90%
complementary, such as fully complementary to the sequence from position 20227 to 26403
or from position 20227 to 24077 of SEQ ID NO 1.

17. The oligonucleotide according to any one of embodiments 1 to 16, wherein the
contiguous nucleotide sequence is at least 90% complementary, such as fully
complementary, to position 20755 to 26403 of SEQ ID NO: 1.

18. The oligonucleotide according to any one of embodiments 1 to 17, wherein the
contiguous nucleotide sequence of at least 10 nucleotides in length, has at least 90%

complementary, such as fully complementary, to the sequence from position 21084 to 21231, such as from position 21084 to 21213 of SEQ ID NO 1.

19. The oligonucleotide according to any one of embodiments 1 to 17, wherein, the contiguous nucleotide sequence of at least 10 nucleotides in length, has at least 90% complementary, such as fully complementary, to position 22110 to 25406 of SEQ ID NO: 1.
20. The oligonucleotide according to any one of embodiments 1 to 17, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary, to the sequence from position 23086 to 24077 of SEQ ID NO 1.
21. The oligonucleotide according to any one of embodiments 1 to 17, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary to the sequence from position 20227 to 20243 of SEQ ID NO 1.
22. The oligonucleotide according to any one of embodiments 1 to 17, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary to the sequence from position 20227 to 26403 of SEQ ID NO 1.
23. The invention provides an oligonucleotide targeting TMEM106B, which comprises a contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary to the sequence from position 24045 to 24098, of SEQ ID NO 1.
24. The oligonucleotide according to any one of embodiments 1 to 17, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary to a region selected from the group consisting of position 22110 – 22128, 24045 – 24063, 24060 – 24077, 24812 – 24828, and 25392-25406 of SEQ ID NO 1.
25. The oligonucleotide according to any one of embodiments 1 to 14, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length has at least 90% complementary, such as fully complementary to position from 3908 – 6417 of SEQ ID NO: 1.
26. The oligonucleotide according to embodiment 25, wherein the contiguous nucleotide sequence of at least 10 nucleotides in length, has at least 90% complementary, such as fully complementary to a region selected from the group consisting of position 3908 - 3925, 6136 – 6154, 5172 – 5190, 6200 – 6216, and 6401- 6417 of SEQ ID NO: 1.

27. The oligonucleotide according to any one of embodiments 1 – 26, wherein the contiguous nucleotide sequence is fully complementary to SEQ ID NO: 1 or to one of the SEQ ID NO's listed in embodiment 12 or 14.

28. The oligonucleotide according to any one of embodiments 1 to 27, wherein the

oligonucleotide is capable of hybridizing with a ΔG° below -10 kcal to a target nucleic acid of SEQ ID NO: 1 or to a target sequence selected from the group consisting of SEQ ID NO: 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245 and 246.

29. The oligonucleotide according to any one of embodiments 1 to 28, wherein the

contiguous nucleotide sequence comprises at least 10 contiguous, such as at least 12 or at least 14 contiguous nucleotides present in a sequence selected from the group consisting of SEQ ID NO 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86,.

30. The oligonucleotide according to any one of embodiments 1 to 29, wherein the

contiguous nucleotide sequence comprises at least 10 contiguous nucleotides selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 46, 48, 49, 50, 51, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 69, 70, 71, 72, 76, 77, 78, 79, 80, 81, 83, 84 and 85.

31. The oligonucleotide according to any one of embodiments 1 to 9, wherein the

contiguous nucleotide sequence comprises at least 10 contiguous nucleotides selected from the group consisting of SEQ ID NO: 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160 and 161.

32. The oligonucleotide according to any one of embodiments 1 to 31, wherein the

oligonucleotide is shorter than 60 nucleotides in length, such as shorter than 50 nucleotides in length, such as between 10 and 60 or 10 and 50 nucleotides in length.

33. The oligonucleotide of embodiment 1-32, wherein the contiguous nucleotide sequence comprises or consists of at least 10 contiguous nucleotides, particularly 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, or 29 contiguous nucleotides.
34. The oligonucleotide according embodiment 33, wherein the contiguous nucleotide
5 sequence is at least 12 nucleotides in length, such as at least 14 nucleotides in length which are fully complementary to SEQ ID NO 1 or to one of the SEQ ID NO's listed in embodiment 12 or 14.
35. The oligonucleotide according to any one of embodiments 1 to 32, wherein the contiguous nucleotide sequence comprises or consists of from 12 to 22 nucleotides.
- 10 36. The oligonucleotide of embodiment 35, wherein the contiguous nucleotide sequence comprises or consists of from 14-20 nucleotides.
37. The oligonucleotide according to any one of embodiments 1 to 36, wherein the contiguous nucleotide sequence has zero to three mismatches compared to the target nucleic acid it is complementary to.
- 15 38. The oligonucleotide of embodiment 37, wherein the contiguous nucleotide sequence has one mismatch compared to the target nucleic acid.
39. The oligonucleotide of embodiment 37, wherein the contiguous nucleotide sequence has two mismatches compared to the target nucleic acid.
40. The oligonucleotide of embodiment 37, wherein the contiguous nucleotide sequence is
20 fully complementary to the target nucleic acid sequence.
41. The oligonucleotide according to any one of embodiments 1 to 40, wherein the oligonucleotide comprises one or more 2' sugar modified nucleosides.
42. The oligonucleotide according to embodiment 41, wherein the one or more 2'-sugar modified nucleosides are independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.
25
43. The oligonucleotide according to embodiment 42, wherein at least one of the one or more 2'-sugar modified nucleosides is a LNA nucleoside.
44. The oligonucleotide according to embodiment 43, wherein the modified LNA nucleoside
30 is selected from oxy-LNA, amino-LNA, thio-LNA, cET, and ENA.
45. The oligonucleotide according to embodiment 43 or 44, wherein the modified LNA nucleoside is oxy-LNA with the following 2'-4' bridge -O-CH₂-.

46. The oligonucleotide according to embodiment 45, wherein the oxy-LNA is beta-D-oxy-LNA.
47. The oligonucleotide according to embodiment 43 or 44, wherein the modified LNA nucleoside is cET with the following 2'-4' bridge -O-CH(CH₃)-.
- 5 48. The oligonucleotide according to embodiment 47, wherein the cET is (S)cET, i.e. 6'(S)methyl-beta-D-oxy-LNA.
49. The oligonucleotide according to embodiment 43 or 44, wherein the LNA is ENA, with the following 2' - 4' bridge -O-CH₂-CH₂-.
50. The oligonucleotide according to any one of embodiments 1 - 49, wherein the
10 contiguous nucleotide sequence comprises at least one modified internucleoside linkage.
51. The oligonucleotide according to any one of embodiments 1 - 50, wherein the continuous nucleotide sequence comprises at least one phosphorothioate modified internucleoside linkage.
52. The oligonucleotide according to any one of embodiments 1 to 51, wherein the
15 oligonucleotide is a siRNA or shRNA or forms the guide strand of a siRNA or shRNA complex.
53. The oligonucleotide according to embodiment 52, wherein the oligonucleotide is a double stranded siRNA oligonucleotide or shRNA oligonucleotide capable of interacting with the RISC complex.
- 20 54. The oligonucleotide according to any one of embodiments 1 to 51, where the oligonucleotide is an antisense oligonucleotide.
55. The antisense oligonucleotide according to embodiment 54, wherein the oligonucleotide is single stranded.
56. The oligonucleotide according to embodiments 54 or 55, wherein at least 75% or all of
25 the internucleoside linkages between the nucleosides of the contiguous nucleotide sequence are phosphorothioate internucleoside linkages.
57. The oligonucleotide according to any one of embodiments 54 to 56, wherein the oligonucleotide is capable of recruiting RNase H1.
58. The antisense oligonucleotide according to embodiment 57, wherein oligonucleotide is
30 an antisense oligonucleotide gapmer.
59. The antisense oligonucleotide according to embodiment 57 or 58, wherein the antisense oligonucleotide, or contiguous nucleotide sequence thereof, consists or comprises a gapmer of formula 5'-F-G-F'-3', where region F and F' independently comprise 1 - 8 nucleosides, of

which 1-5 independently are 2' sugar modified and defines the 5' and 3' end of the F and F' region, and G is a region between 5 and 18 nucleosides which are capable of recruiting RNaseH, such as a region comprising 5 – 18 DNA nucleosides.

60. The antisense oligonucleotide of embodiment 59, wherein the 2' sugar modified nucleoside independently is selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.
61. The antisense oligonucleotide of embodiment 59 or 60, wherein one or more of the 2' sugar modified nucleosides in region F and F' is a LNA nucleoside
62. The antisense oligonucleotide according to any one of embodiments 60 or 61, wherein the LNA nucleoside is selected from beta-D-oxy-LNA, alpha-L-oxy-LNA, beta-D-amino-LNA, alpha-L-amino-LNA, beta-D-thio-LNA, alpha-L-thio-LNA, (S)cET, (R)cET beta-D-ENA and alpha-L-ENA.
63. The antisense oligonucleotide according to any one of embodiments 54 to 62, wherein the antisense oligonucleotide is selected from the group consisting of a LNA gapmer, a mixed wing gapmer and an alternating flank gapmer.
64. The oligonucleotide of embodiment 59 - 63, wherein
 - a. the F region is between 1 and 5 nucleotides in length and consists of 1-4 identical LNA nucleosides and 0-2 DNA nucleosides; and
 - b. the F' region is between 2 and 5 nucleotides in length and consists of 2-4 identical LNA nucleosides and 0-2 DNA nucleosides; and
 - c. region G is between 8 and 16 DNA nucleotides.
65. The antisense oligonucleotide of embodiment 59 to 62, wherein region F and F' consist of identical LNA nucleosides.
66. The antisense oligonucleotide of embodiment 59 to 62, wherein all the 2' sugar modified nucleosides in region F and F' are oxy-LNA nucleosides.
67. The antisense oligonucleotide according to any one of embodiments 54 to 60, wherein the antisense oligonucleotide is 2'-MOE gapmer.
68. The antisense oligonucleotide of any one of embodiments 54 to 67, wherein the nucleosides in region G is DNA and/or alpha-L-LNA nucleosides.
69. The antisense oligonucleotide of embodiment 68, wherein region G consists of at least 75% DNA nucleosides.

70. The antisense oligonucleotide of embodiment 69, where all the nucleosides in region G are DNA nucleosides.

71. The oligonucleotide according to any one of embodiments 1 – 51 or 54 to 70, wherein the oligonucleotide or contiguous nucleotide sequence thereof, is selected from the motif sequences in combination with the indicated designs as listed in Table 7.

72. The oligonucleotide according to any one of embodiments 1 – 51 or 54 to 71, wherein the oligonucleotide or contiguous nucleotide sequence thereof, is selected from the group consisting of CMP ID NO: 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, 86_1, 87_1, 88_1, 89_1, 90_1, 91_1, 92_1, 93_1, 94_1, 95_1, 96_1, 97_1, 98_1, 99_1, 100_1, 101_1, 102_1, 103_1, 104_1, 105_1, 106_1, 107_1, 108_1, 109_1, 110_1, 111_1, 112_1, 113_1, 114_1, 115_1, 116_1, 117_1, 118_1, 119_1, 120_1, 121_1, 122_1, 123_1, 124_1, 125_1, 126_1, 127_1, 128_1, 129_1, 130_1, 131_1, 132_1, 133_1, 134_1, 135_1, 136_1, 137_1, 138_1, 139_1, 140_1, 141_1, 142_1, 143_1, 144_1, 145_1, 146_1, 147_1, 148_1, 149_1, 150_1, 151_1, 152_1, 153_1, 154_1, 155_1, 156_1, 157_1, 158_1, 159_1, 160_1 and 161_1 as listed in Table 7.

73. The oligonucleotide according to any one of embodiments 1 – 51 or 54 to 72, wherein the oligonucleotide or contiguous nucleotide sequence thereof, is selected from the group consisting of:

ATGTttatcaccaaAATT (SEQ ID NO: 65, CMP ID NO: 65_1)

CTGAaatactaccaTATA (SEQ ID NO: 66, CMP ID NO: 66_1)

TTTAatcataccaATCT (SEQ ID NO: 71, CMP ID NO: 71_1)

TTCTtatttcaaCTCA (SEQ ID NO: 74, CMP ID NO: 74_1)

TCTTatttcaaCTCA (SEQ ID NO: 75, CMP ID NO: 75_1)

wherein a capital letter is a LNA nucleoside, such as a beta-D-oxy-LNA, a lower case letter is a DNA nucleoside, LNA cytosine nucleosides are optionally 5 methyl cytosine LNA, DNA cytosine nucleosides are optionally 5-methyl cytosine DNA, the internucleoside linkages between DNA nucleosides are phosphorothioate internucleoside linkages

74. A conjugate comprising the oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 73, and at least one conjugate moiety covalently attached to said oligonucleotide.

75. The oligonucleotide conjugate according to embodiment 74, wherein the conjugate moiety is selected from carbohydrates, cell surface receptor ligands, drug substances, hormones, lipophilic substances, polymers, proteins, peptides, toxins, vitamins, viral proteins or combinations thereof.
- 5 76. The oligonucleotide conjugate according to embodiment 74 or 75, wherein the conjugate facilitates delivery across the blood brain barrier.
77. The oligonucleotide conjugate according to embodiment 76, wherein the conjugate is an antibody or antibody fragment targeting the transferrin receptor.
- 10 78. A pharmaceutically acceptable salt of the oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72, or the conjugate according to embodiment 74 - 77.
- 15 79. A pharmaceutical composition comprising the oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72 or the conjugate according to embodiment 74 -77 and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.
- 20 80. An *in vitro* or *in vivo* method for modulating TMEM106B expression in a target cell which is expressing TMEM106B, said method comprising administering an oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72, conjugate according to embodiment 74 -77, or the pharmaceutical salt according to embodiment 78 , or pharmaceutical composition according to embodiment 79 in an effective amount to said cell.
- 25 81. A method for treating or preventing a disease comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72, conjugate according to embodiment 74 -77, or the pharmaceutical salt according to embodiment 78, or pharmaceutical composition according to embodiment 79, to a subject suffering from or susceptible to the disease.
82. The oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72, conjugate according to embodiment 74 -77, or the pharmaceutical salt according to embodiment 78, or pharmaceutical composition according to embodiment 79 for use in medicine for treatment or prevention of a disease in a subject.
- 30 83. The oligonucleotide or antisense oligonucleotide according to any one of embodiments 1 – 72, conjugate according to embodiment 74 -77, or the pharmaceutical salt according to embodiment 78, or pharmaceutical composition according to embodiment 79 for use in the treatment or prevention of a disease selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or

parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

84. Use of the oligonucleotide or antisense oligonucleotide according to any one of
embodiments 1 – 72, conjugate according to embodiment 74 -77, or the pharmaceutical salt
according to embodiment 78, or pharmaceutical composition according to embodiment 79,
for the preparation of a medicament for treatment or prevention of a disease.

85. The oligonucleotide for use, or the use or the method according to any one of
embodiments 81 to 84, wherein the disease is associated with overexpression of TMEM106B
and/or abnormal levels of TMEM106B.

86. The oligonucleotide for use, or the use or the method according to any one of
embodiments 81 to 84, wherein the treatment reduces TMEM106B mRNA levels in the
frontal cortex to normal levels.

87. The oligonucleotide for use, or the use or the method according to any one of
embodiments 81 to 84, wherein the disease is selected from the group consisting of
neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or
parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple
system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome,
progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

88. The oligonucleotide for use, or the use or the method according to any one of claims 81
to 87, wherein the disease is frontotemporal lobar degeneration (FTLD).

89. The oligonucleotide for use, or the use or the method according to any one of claims 81
to 84 to 88, wherein the subject is a mammal.

90. The oligonucleotide for use, or the use or the method according to embodiment 89,
wherein the mammal is human.

EXAMPLES

Materials and methods

Oligonucleotide compounds and motif sequences

Table 7 – Compound List

List of oligonucleotide motif sequences (indicated by SEQ ID NO), designs of these, as well as
specific oligonucleotide compounds (indicated by CMP ID NO) designed based on the motif
sequence.

In the examples, the compounds used have the following structure - Capital letters represents beta-D-oxy LNA nucleosides; all LNA cytosines are 5-methyl cytosine; lower case letters represent DNA nucleosides; all internucleoside linkages are phosphorothioate internucleoside linkages.

SEQ ID NO	Motif sequence	Design	CMP ID NO	Oligonucleotide Compound
7	aagctccataaacaacac	4-11-3	7_1	AAGCtccataaacaacAC
8	ctttaaacatttaaacact	4-11-4	8_1	CTTTaaacatttaaaCACT
9	ttccatccttaaatttct	4-12-2	9_1	TTCCatccttaaatttCT
10	tgataaatacaatcaccac	3-12-4	10_1	TGAtaaatacaatcaCCAC
11	tacattctaccttttaac	2-12-4	11_1	TAcattctacctttTAAC
12	gctttcaaacattaacatt	4-11-4	12_1	GCTTtcaaacattaaCATT
13	atgttcaaactacctttt	3-11-4	13_1	ATGttcaaactaccTTTT
14	agatattttacactaatta	4-10-4	14_1	AGATattttacactaATTA
15	gacttcactattaacca	3-11-3	15_1	GACttcactattaaCCA
16	cctgtaaattccacatat	4-12-2	16_1	CCTGtaaattccacatAT
17	tgacactatctcttcc	3-11-2	17_1	TGAcactatctcttCC
18	caataacacataccccta	3-12-3	18_1	CAAtaacacatacccCTA
19	gtttcaactttaattcta	3-11-4	19_1	GTTtcaactttaatTCTA
20	agcttccttacacatta	3-12-2	20_1	AGCttccttacacatTA
21	atctttattattttactta	3-13-4	21_1	ATCtttattattttctaCTTA
22	atcccttcaactacaata	4-12-2	22_1	ATCCcttcaactacaaTA
23	ttcctactttccataatc	4-12-2	23_1	TTCCtactttccataaTC
24	cttgatttcctactttcc	2-14-2	24_1	CTtgatttcctactttCC
25	gacatatacactcaaataa	4-11-4	25_1	GACAtatacactcaaATAA
26	ttcttcacttatcttccat	1-15-3	26_1	TtcttcacttatcttcCAT
27	tcagtcttcacactacc	2-13-2	27_1	TCagtcttcacactaCC
28	cttctctttttattacaa	4-11-3	28_1	CTTctctttttattacCAA
29	gtgtccatactttacc	1-11-4	29_1	GtgtccatacttTACC
30	tcttcgctatcctcat	2-11-3	30_1	TCttcgctatcctCAT
31	aatctttaatatcttcttc	4-11-4	31_1	AATCtttaatatcttCTTC
32	ccaagaccacaattttat	3-11-4	32_1	CCAagaccacaattTTAT
33	ccaagttcatactctca	3-12-2	33_1	CCAagttcatactctCA
34	atcatactacatttcca	4-12-2	34_1	ATCAtactacatttccCA
35	tgtttacatatctcacc	2-11-4	35_1	TGtttacatatctCACC
36	ccatcacacccatatataa	3-14-2	36_1	CCAtcacacccatatataAA
37	tcctgaaacctctatca	3-12-2	37_1	TCctgaaacctctatCA
38	ttttcttctaattctttcca	1-16-3	38_1	TtttcttctaattctttCCA
39	cctaatttccttcatattc	2-13-4	39_1	CCtaatttccttcatATTC
40	tatttgacaactatcct	3-10-4	40_1	TATtgacaactaTCCT
41	catcagtcctctattat	2-11-4	41_1	CATcagtcctctaTTAT
42	gtctccattacaaaattaa	3-12-4	42_1	GTctccattacaaaTTAA

SEQ ID NO	Motif sequence	Design	CMP ID NO	Oligonucleotide Compound
43	tagtatttcattccaaat	4-10-4	43_1	TAGTatttcattccAAAT
44	tgaatccatcataatcta	3-11-4	44_1	TGAatccatcataaTCTA
45	ttacatgatcccctaa	3-9-4	45_1	TTAcatgatcccCTAA
46	atgttaccaaattttcac	4-10-4	46_1	ATGTtaccaaatttTCAC
47	aaacacagccaatcca	4-9-3	47_1	AAACacagccaatCCA
48	agtttattttaccctcct	1-15-2	48_1	AgtttattttaccctcCT
49	gcataccttcaaactatac	3-13-3	49_1	GCAataccttcaaactaTAC
50	tcccttttcttaattcaa	3-13-2	50_1	TCCcttttcttaattcAA
51	aaacaactatcactcttcc	4-12-3	51_1	AAACaactatcactctTCC
52	cagacatctctacctcaa	2-13-3	52_1	CAGacatctctacctCAA
53	tgattccactttaacata	3-11-4	53_1	TGAttccactttaaCATA
54	ataccaacaattcccca	1-15-2	54_1	AtaccaacaattcccCA
55	tattcacatttaaataact	3-13-4	55_1	TATtcacatttaaataTACT
56	acaaagaccctaaactac	4-10-4	56_1	ACAAagaccctaaaCTAC
57	atatacttcataacttcaaa	4-12-4	57_1	ATATacttcataacttCAAA
58	tacataataactcatttcctc	4-14-2	58_1	TACAtataactcatttcTC
59	tcagaacttactacatat	4-10-4	59_1	TCAGaacttactacATAT
60	ttttctatacttcaaacaat	4-12-4	60_1	TTTTctatacttcaaaCAAT
61	aacacccaatttacaaccca	1-16-3	61_1	AacacccaatttacaacCCA
62	cttagataaacacccaat	4-9-4	62_1	CTTAgataaacaccCAAT
63	tatttcttctttaaatccat	2-14-4	63_1	TatttcttctttaaatCCAT
64	tccacatacttttaact	4-9-4	64_1	TCCAcatacttttAACT
65	atgtttatcaccaaaatt	4-10-4	65_1	ATGTttatcaccaaAATT
66	ctgaaatactaccatata	4-10-4	66_1	CTGAaatactaccaTATA
67	agatttcacaaaactata	3-11-4	67_1	AGAtttcacaaaacTATA
68	cgaaattaatctcaaccca	1-14-4	68_1	CgaaattaatctcaaCCCA
69	taatacctatcctattccca	3-15-2	69_1	TAAtacctatcctattccCA
70	gtaacatatctttaccat	2-12-4	70_1	GTaacatatctttaCCAT
71	tttaatacataccaatct	4-9-4	71_1	TTTAatcataccaATCT
72	atgctacaaaatctta	4-9-4	72_1	ATGctacaaaatCTTA
73	ctcaaataaattaatctct	4-11-4	73_1	CTCAaataaattaatCTCT
74	ttcttatttcaaactctca	4-10-4	74_1	TTCTtatttcaaactCTCA
75	tcttatttcaaactctca	4-9-4	75_1	TCTTatttcaaactCTCA
76	atactattcttatttcaaat	4-12-4	76_1	ATACtattcttatttcAAAT
77	gtatctaataattttcata	4-10-4	77_1	GTATctaataattttCATA
78	ttttactccaccatctcaa	1-15-3	78_1	TtttactccaccatctCAA
79	taacagtctttttactc	4-9-4	79_1	TAAcagtctttttACTC
80	tagtaactttaatcactt	4-10-4	80_1	TAGTaactttaatcACTT
81	tagtaatattaccttt	4-8-4	81_1	TAGTaatattacCTTT
82	actataacagtctac	4-7-4	82_1	ACTAtaacagtCTAC
83	tgcccaaacatattttca	2-12-4	83_1	TGcccaaacatattTTCA

SEQ ID NO	Motif sequence	Design	CMP ID NO	Oligonucleotide Compound
84	ctactacataatataaaca	4-11-4	84_1	CTACTacataatataAACA
85	gtcatcacaaactacaa	4-9-4	85_1	GTCAtacacaaactACAA
86	tcgtttttccatattat	4-9-4	86_1	TCGTttttccataTTAT
87	atactacttttaatttaata	4-12-4	87_1	ATACtacttttaatttAATA
88	ctcatttcactcacttaa	4-14-2	88_1	CTCAtttcactcacttaaAT
89	tatgaaaccaaatacct	3-9-4	89_1	TATgaaaccaaataCCT
90	catagccatcttcttta	2-11-4	90_1	CATagccatcttctTTTA
91	caacacgtaccacct	1-10-4	91_1	CaacacgtaccCCTA
92	agtcacttctattact	1-11-4	92_1	AgtcacttctatTACT
93	cttttcttcatacactata	1-14-4	93_1	CttttcttcatacacTATA
94	acccacttaacccaa	2-11-3	94_1	ACccacttaaccCAA
95	acagaaatcctattccca	3-13-2	95_1	ACAgaaatcctattccCA
96	ctacttgccacaatccc	1-14-2	96_1	CtacttgccacaatcCC
97	attcagacccttataca	4-9-3	97_1	ATTCagacccttaCAA
98	cattactcacaccttt	3-9-4	98_1	CATtactcacacCTTT
99	cccataagtacccatct	1-14-2	99_1	CccataagtacccatCT
100	atctatttgctcccat	3-10-3	100_1	ATCtatttgctccCAT
101	ctctgtaccatctatt	1-11-4	101_1	CtctgtaccatcTATT
102	gcaaataacaaaatctct	4-10-4	102_1	GCAAataacaaaatCTCT
103	ccttttatcttcattct	3-12-2	103_1	CCTtttatcttcattCT
104	tgacaatttcaaaactca	2-12-4	104_1	TGacaatttcaaaaCTCA
105	cctagtttacaccct	3-10-2	105_1	CCTagtttacaccCT
106	tttcctagttcacatt	4-8-4	106_1	TTTCctagttcaCATT
107	aactgcaatcactcat	3-9-4	107_1	AACtgcaatcacTCAT
108	atctacagttttccac	4-9-3	108_1	ATCTacagttttcCAC
109	gcttctctcatctaca	2-12-2	109_1	GCTtctctcatctaCA
110	agaatacttctctcctt	1-12-4	110_1	AgaatacttctctCCTT
111	tcacatacgttcttc	4-7-4	111_1	TCACatacgttCTTC
112	taaaatgtccacatatac	4-9-4	112_1	TAAAatgtccacaTATC
113	gattttcaaacccttcaat	3-12-4	113_1	GATtttcaaacccttCAAT
114	tacatttccaattttata	4-10-4	114_1	TACAttccaattttTATA
115	tagctttctttattttc	3-10-4	115_1	TAGctttctttatTTTC
116	tagtctactctcctaa	2-10-4	116_1	TAGtctactctcCTAA
117	tatgcctacaatatatac	4-8-4	117_1	TATGcctacaatATAC
118	atgaacaacaactcccatt	2-13-4	118_1	ATgaacaacaactccCATT
119	ccatctaccttataacat	3-12-3	119_1	CCAtctaccttataaCAT
120	cctgcatttactatcca	2-13-2	120_1	CCTgcatttactatcCA
121	attagaaccctttaca	3-9-4	121_1	ATTagaacccttTACA
122	atagaatccttacata	4-8-4	122_1	ATAGaatccttaCATA
123	ctgattttactccaat	4-8-4	123_1	CTGAttttactcCAAT
124	ctaaatgattcccaat	4-8-4	124_1	CTAAatgattccCAAT

SEQ ID NO	Motif sequence	Design	CMP ID NO	Oligonucleotide Compound
125	tacttgatcttcctaca	4-11-2	125_1	TACTtgatcttcctaCA
126	tcatcatataaactccat	3-11-4	126_1	TCAtcatataaactCCAT
127	caccatgttctttaca	4-10-2	127_1	CACCatgttctttaCA
128	ctactcttcatctcaaca	1-13-4	128_1	CtactcttcatctcAACA
129	caacaactcatttcat	4-8-4	129_1	CAACaactcattTCAT
130	cctctttgaacaaaacca	2-12-3	130_1	CCtctttgaacaaaCCA
131	ccttttactctacctt	1-11-4	131_1	CcttttactctaCCTT
132	tcagcttatttacatta	4-9-4	132_1	TCAGcttatttacATTA
133	tgctttacattcacac	3-10-4	133_1	TGCTttacattcaCAAC
134	ggcttttaccttacat	4-10-2	134_1	GGCTtttaccttacAT
135	acacgatttcataacaatc	4-10-4	135_1	ACACgatttcataacAATC
136	atgttttcaacttcaac	4-9-4	136_1	ATGTtttcaacttCAAC
137	gaatacccatctcaccc	3-12-2	137_1	GAAtaccatctcacCC
138	cctatgtctaaattttc	4-9-4	138_1	CCTAtgtctaaatTTTC
139	tttatctatctatcttat	4-10-4	139_1	TTTAtctatctatCTTAT
140	cactgtcatttacatta	4-8-4	140_1	CACTgtcatttacATTA
141	cctgaactcctacaatc	2-11-4	141_1	CCtgaactcctacAATC
142	tccttaaaattactta	4-8-4	142_1	TCCCTaaaattaCTTA
143	attaattccctaaaattac	4-11-4	143_1	ATTAattccctaaaaTTAC
144	tcggctctaaccaca	3-9-3	144_1	TCGgctctaaccACA
145	tacatgaaacacatact	4-9-4	145_1	TACAtgaaacacaTACT
146	catttgacctttatcaa	4-9-4	146_1	CATTtgacctttaTCAA
147	tccttaaaacattcata	4-10-3	147_1	TCCCTaaaacattcATA
148	attttgcacacctcaca	2-13-2	148_1	ATtttgcacacctcaCA
149	ttaatacctactcttc	4-8-4	149_1	TTAAtacctactCTTC
150	caaagctacaaaaatct	4-9-4	150_1	CAAAGctacaaaaATCT
151	tgtatttcaaactcaca	4-10-4	151_1	TGTAtttaaactcCAAA
152	ctgtatttcaaactcaca	3-10-4	152_1	CTGtatttcaaactCTCA
153	cccacatccttttacac	2-13-2	153_1	CCcacatccttttacAC
154	cccacatccttttaca	2-12-2	154_1	CCcacatccttttaCA
155	atgtactaattttcttt	4-9-4	155_1	ATGTactaattttCTTT
156	ccacactgtatcttca	3-11-2	156_1	CCAcactgtatcttCA
157	agcatataaaaatatcc	4-8-4	157_1	AGCAtataaaaATCC
158	aatcatctttccaactct	3-11-4	158_1	AAAtcatctttccaaCTCT
159	aaccatgtttccctaca	3-12-2	159_1	AACcatgtttccctaCA
160	ttcctatcataacat	4-9-3	160_1	TTCCtatcataacCAT
161	attcttgttcttatca	4-10-2	161_1	ATTCTtgttcttatCA
162	ttgaataagtggatgt	3-10-3	162_1	TTGaataagtggaTGT
163	ccaaatcttataataactac	1-1-3-10-2-1-2	163_1	CcAAAtcttataataACtAC
164	cgtaaactacccttat	2-10-4	164_1	CGtaaactaccctCTAT

Motif sequences represent the contiguous sequence of nucleobases present in the oligonucleotide.

Designs refer to the oligonucleotide design, e.g. gapmer design, F-G-F'. In classic gapmer design e.g. 3-10-3 all the nucleotides in the flanks (F and F') are constituted of the same 2'-sugar modified nucleoside, e.g. LNA, cET, or MOE, and a stretch of DNA in the middle forming the gap (G). In gapmers with

5 alternating flank designs the flanks of oligonucleotide is annotated as a series of integers, representing a number of 2' sugar modified nucleosides (M) followed by a number of DNA nucleosides (D). For example a flank with a 2-2-1 motif represents 5' [M]₂-[D]₂-[M] 3' and a 1-1-1-1-1 motif represents 5' [M]-[D]-[M]-[D]-[M] 3'. Both flanks have a 2' sugar modified nucleoside at the 5' and 3' terminal. The gap region (G), is constituted of a number of DNA nucleosides (typically between 5 and 16), located between the flanks.

10 Oligonucleotide compounds represent specific designs of a motif sequence. Capital letters represent beta-D-oxy LNA nucleosides, lowercase letters represent DNA nucleosides, all LNA C are 5-methyl cytosine, all internucleoside linkages are phosphorothioate internucleoside linkages.

Table 8: Motif List

List of oligonucleotide motif sequences (indicated by SEQ ID NO), of the compounds used in the examples, and their target sequence and location on their nucleic acid target /target sequence (SEQ ID NO 1 – 6), as indicated. Motif sequences represent the contiguous sequence of nucleobases present in the oligonucleotide in the 5' to 3' direction. The RNA target sequence is the complementary sequence of the motif sequence, also in the 5' to 3' direction.

SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1		SEQ ID NO 2		SEQ ID NO 3		SEQ ID NO 4		SEQ ID NO 5		SEQ ID NO 6	
				start	stop	start	stop	start	stop	start	stop	start	stop	start	stop
		Note DNA version is shown (U→T)													
7	aagctccataaacaacac	gtgtgtttatggagctt	167	546	563			565	582						
8	ctttaaacatttaaacact	agtgtttaaatgtttaaag	168	2122	2140			2186	2204						
9	ttccatcctctaaattctt	agaaaatttaaggatggaa	169	2143	2160			2207	2224						
10	tgataaatacaatcaaccac	gtgggattgtatttatca	170	2165	2183			2227	2245						
11	tacattctactctttaac	gttaaaaggtagaatgta	171	2300	2317			2362	2379						
12	gccttcaaacatttaacatt	aatgttaaatgtttgaaagc	172	2392	2410			2454	2472						
13	atgttcaaaactaccctttt	aaaaggtagtttgaacat	173	2548	2565			2596	2613						
14	agatatttacactaatta	taattagtgtaaatatct	174	3507	3524			3564	3581						
15	gactcactatttaacca	tggttaatagtgaaagtc	175	3678	3694	489	505	3735	3751	314	330				
16	cctgtaaattccacat	atatgtggaatttacagg	176	3736	3753	547	564	3793	3810	372	389				
17	tgacactatctcttcc	ggaagagatagtgta	177	3752	3767	563	578	3809	3824	388	403	2166	2181	477	492
18	caataacacatacccccta	taggggtatgtgtattg	178	3802	3819			3859	3876						
19	gtttcaactttaattcta	tagaattaaagttgaaac	179	3908	3925			3968	3985						
20	agcttccttacacattta	taatgtgtaagggaagct	180	4321	4337			4382	4398						
21	atctttatttttctactta	taagtagaataataaaagat	181	4701	4720			4772	4791						
22	atcccttcaactacaata	tattgtagttgaagggt	182	4948	4965			4999	5016						
23	ttcctacttctccataatc	gattatggaagtagggaa	183	5063	5080			5114	5131						

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SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1		SEQ ID NO 2		SEQ ID NO 3		SEQ ID NO 4	SEQ ID NO 5		SEQ ID NO 6																				
24	cttgatttctactttcc	ggaaagtaggaaatcaag	184	5069	5086			5120	5137																								
25	gacatatcacacaataa	ttatttgagtatatgtc	185	5172	5190			5226	5244																								
26	ttcttcacttatctccat	atggaagataagtgaaaga	186	5512	5530			5563	5581																								
27	tcagcttccacactacc	ggtagtgtagaagactga	187	5583	5599			5634	5650																								
28	cttctctttttattacca	ttggtataaaaaagagaag	188	6015	6032			6070	6087																								
29	gtgtccatactttacc	ggtaaaagtatggacac	189	6032	6047			6087	6102																								
30	ttctcgctatcccat	atgaggatagcgaaga	190	6125	6140			6179	6194																								
31	aatctttaatatctcttc	gaagaagatattaaagatt	191	6136	6154			6190	6208																								
32	ccaagaccacaattttat	ataaaattgtggtcttgg	192	6172	6189			6226	6243																								
33	ccaagttcatactctca	tgagagtatgaacttgg	193	6200	6216			6254	6270																								
34	atcatactacatttccca	tgggaaatgtagtatgat	194	6214	6231			6268	6285																								
35	tgtttacatatctcacc	ggtagagatatgtaaaca	195	6401	6417			6446	6462																								
36	ccatcacacccatatataa	ttatatatgggtgtgatgg	196	6458	6476			6513	6531																								
37	tcttgaaaacctctatca	tgatagagggttcaggga	197	6837	6853			6885	6901																								
38	ttttctttaaattcttcca	tggaaagaattagaagaaaa	198	8453	8472			8520	8539																								
39	cctaatttccitcatattc	gaatatgaaggaaaattagg	199	8983	9001			9054	9072																								
40	tatttgacaactatcct	aggatagttgtcaaata	200	9533	9549			9604	9620																								
41	catcagtcctcttattat	ataatagaggagactgatg	201	9628	9644			9699	9715																								
42	gtctccattacaaaattaa	ttaattttgtaattggagac	202	11065	11083			11221	11239																								
43	tagtatttcatccaaat	atttggaaatgaaatacta	203	11117	11134			11273	11290																								
44	tgaatccatcataatacta	tagattatgatggatttca	204	11264	11281			9869	9886																								
45	ttacatgatccccttaa	ttaggggatcatgttaa	205	12310	12325																												
46	atgttaccaaaattttcac	gtgaaaaatttggtaacat	206	12870	12887			13084	13101																								
47	aaacacagccaatcca	tggattggctgtgtttt	207	13050	13065	727	742				8394	8409	641																				
48	agttttattttaccctcct	aggagggttaaaaaataaact	208	13397	13414			13604	13621				656																				

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SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1	SEQ ID NO 2	SEQ ID NO 3		SEQ ID NO 4	SEQ ID NO 5		SEQ ID NO 6								
49	gcacacttcaaacatatac	gtatagtttgaagtgatgc	209	15061	15079	15198	15216												
50	tcccttttctaattcaa	ttgaattaggaaaaggga	210	15249	15266	15386	15403												
51	aaacaactatcaccttcc	ggaagagtgatagtgttt	211	15318	15336	15455	15473												
52	cagacatctctacctcaa	ttgaggtagagatgtctg	212	15368	15385														
53	tgattccactttaacata	tatgttaaagtggaatca	213	15440	15457	15577	15594												
54	ataccaacaattcccca	tggggaattgttgggtat	214	15632	15649	15774	15791												
55	tattcacatttfaatatact	agtatattttaaattggaata	215	15823	15842	15957	15976												
56	acaaagaccctaaactac	glagttagggctcttgt	216	16496	16513	16621	16638												
57	atatacttcataaacttcaaa	tttgaagttatgaagtatat	217	19090	19109	19322	19341												
58	tacataaactcatttctct	gaggaaatgagttatatgta	218	19198	19217	1013	1032	838	857										
59	tcagaacttactacatat	atatgtagtaagttctga	219	19211	19228	19445	19462												
60	ttttctatacttcaacaat	attgtttgaagtatagaaaa	220	19699	19718	19935	19954												
61	aacacccaatttcaaaaacca	tggtttgtaaattgggtgtt	221	20217	20236	20470	20489												
62	cttagataacacccaat	attgggtgttatctaag	222	20227	20243	20480	20496												
63	tatttcttctttaaattccat	atggatttaaagaagaataa	223	20767	20786	1238	1257	1063	1082										
64	tccacatacttttaact	agttaaaaagtatgtgga	224	20880	20896	1351	1367	1181	1197										
65	atgtttatcaccaaaaatt	aattttggtgataaacat	225	21084	21101	1555	1572	1385	1402										
66	ctgaaatactactacatata	tatatggtagtatttcag	226	21214	21231	1685	1702	1512	1529										
67	agatttcacaaaaactata	tatagtttttgaaatct	227	21425	21442	1896	1913	1719	1736										
68	cgaaaattaatctcaaccca	tgggttgagattaatttcg	228	22110	22128	2581	2599												
69	taatacctatcttattccca	tgggaataggataggtatta	229	23374	23393	3845	3864	23992	24011										
70	gtaacatatctttaccat	atggtaaagatatgtttac	230	23435	23452	3906	3923	24053	24070										
71	tttaatcataccaatct	agattggtagtattaaa	231	23806	23822	4277	4293	24430	24446										
72	atgctacaaaacttta	taagattttggtagcat	232	23874	23890	4345	4361	24498	24514										
73	ctcaaatataatataatct	agagattaattttatttgag	233	24045	24063	4516	4534												

SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1		SEQ ID NO 2		SEQ ID NO 3		SEQ ID NO 4	SEQ ID NO 5		SEQ ID NO 6
74	ttctatttcaaatctca	tgagatttgaaataagaa	234	24060	24077	4531	4548						
75	ttctatttcaaatctca	tgagatttgaaataaga	235	24060	24076	4531	4547						
76	atcactatttctatttcaaat	attgaaataagaataagtagtat	236	24064	24083	4535	4554	24675	24694				
77	gtatcctaataattttcata	tatgaaaaataattagatcac	237	24081	24098	4552	4569	24692	24709				
78	tttttactocaccatctcaa	ttgagatgtgtggagtaaaaa	238	24801	24819	5272	5290	25418	25436				
79	taacagctcttttactc	gagtaaaaagagactgtta	239	24812	24828	5283	5299	25429	25445				
80	tagtaacctttaatcacatt	aagtgtattaaggttacta	240	25050	25067	5521	5538	25666	25683				
81	tagtaatatattaccttt	aaaggtaataattacta	241	25372	25387	5843	5858	25984	25999		18910	18925	5466
82	actataacacagctcac	gtagactgtttatagt	242	25392	25406	5863	5877						5481
83	tgcccaaacacatttttca	tgaaaatatgtttgggca	243	25773	25790	6244	6261	26388	26405				
84	ctactacataataataaaca	tgtttatattatgtagtag	244	25796	25814	6267	6285	26411	26429				
85	gtcatcacacaactacaa	ttgtagttgtgtatgac	245	25969	25985	6440	6456	26583	26599				
86	tcgtttttccatattat	ataatatgtgaaaaacga	246	29351	29367								
87	atactacttttaatttaata	tattaaattaaaagtagtat	247								1336	1355	
88	ctcatttcactcacttaaat	atttaagtgagtgaaaatgag	248								1555	1574	
89	tatgaaacccaatcct	aggatttggtttcata	249								1795	1810	
90	catagocattctcttta	taaagaagatggcctatg	250								2039	2055	366
91	caacacgtacoccta	taggggtacgtgttg	251								2216	2230	
92	agtcactcttattact	agtaatagaagtgact	252								2383	2398	
93	cttttcttcatacactata	tatagtgatgaagaaaag	253								2606	2624	
94	acccacttaacccaa	ttgggttaagtgggggt	254								2851	2866	
95	acagaaaaatccatttccca	tgggaataggatttctgt	255								2961	2978	
96	ctacttgccacaatccc	gggatttgccaagtag	256								3033	3049	
97	attcagacccttcaaa	ttgtaagggtctgaat	257								3242	3257	
98	cattactcacacacctt	aaagggtgtgagtaatg	258								3918	3933	

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SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1	SEQ ID NO 2	SEQ ID NO 3	SEQ ID NO 4	SEQ ID NO 5		SEQ ID NO 6
99	cccataagtaaccatct	agatgggtacttatggg	259					4076	4092	
100	atctattgtctccat	atgggagcaaatagat	260					4088	4103	
101	ctctgtaccatctatt	aatagatggtacagag	261					4097	4112	
102	gcaaaataacaaaatctct	agagattttgtatttgc	262					4481	4498	
103	ccctttatcttctct	agaaatgaagataaaaagg	263					4734	4750	
104	tgacaatttcaaaaactca	tgagttttgaaatgtca	264					4778	4795	
105	cctagtttacacct	aggggttaaaactagg	265					4800	4814	
106	tttcctagttcacatt	aatgtgaactaggaaa	266					4816	4831	
107	aactgcaatcactcat	atgagtgattgcagtt	267					4831	4846	
108	atctacagttttccac	gtggaaaaactgtagat	268					4978	4993	
109	gcttctctcatcaca	tgtagatgagagaagc	269					4987	5002	
110	agaataactctctcct	aaggagagaagatttct	270					5186	5202	
111	tcacatacgtttcttc	gaagaacgtatgtga	271					5350	5364	
112	taaaatgtccacatc	gatatgtggacatttta	272					5508	5524	
113	gatttctaaacccitcaat	attgaagggtttagaaatc	273					5877	5895	
114	tacatttccaatttata	tataaaattggaaatgta	274					5965	5982	
115	tagctttctttatttc	gaaaaataaagaaaagcta	275					6439	6455	
116	tagtctactctctaa	ttaggagagtagacta	276					6901	6916	
117	tatgccctacaatalac	gtatatgttaggcata	277					7356	7371	
118	atgaacaacaacitcccatt	aatgggagtggtgttctcat	278					7375	7393	
119	ccatctactcttataacat	atgttataaggtagatgg	279					7602	7619	
120	cctgcatttactatcca	tggatagtaaatgcagg	280					7823	7839	
121	attagaaccccttaca	tgtaaaaggggttctaat	281					8051	8066	
122	atagaatccttacata	tatgtaaggattctat	282					8322	8337	
123	ctgatttttactccaat	attggagtaaaaatcag	283					8443	8458	705

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SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1	SEQ ID NO 2	SEQ ID NO 3	SEQ ID NO 4	SEQ ID NO 5	SEQ ID NO 6
124	ciaaatgattccaat	atgggaatcattag	284					8695 8710	
125	tactgatcttctaca	ttaggaagatcaagta	285					8727 8743	
126	tcatcatataaactccat	atggagtttatatgatga	286					8925 8942	
127	caccatgttctttaca	tgtaaagaacaatgggtg	287					9075 9090	
128	ctactcttctatcaaca	tgttagatgaagagtag	288					9348 9365	
129	caacaactcattcat	atgaaatgagttgttg	289					9584 9599	
130	cctctttgaacaaacca	tggtttgttcaaaagagg	290					10182 10198	
131	ccttttacttacctt	aaggtagagtaaaaagg	291					10234 10249	
132	tcagcttatttaccatta	taatgtaaaataaagctga	292					10413 10429	
133	tgctttacattcacaac	gttgtaaatgtaaagca	293					10775 10791	
134	ggcttttaccttacct	atgtaaggtaaaaagcc	294					11179 11194	
135	acacgatttcatacaatc	gattgtatgaaatcgtgt	295					11393 11410	
136	atgttttcaacttcaac	gttgaagttgaaaacat	296					11833 11849	808
137	gaataccccatttcaccc	gggtgaaatgggtatttc	297					11961 11977	
138	cctaigtctlaaaatttctc	gaaaatttagacatagg	298					12579 12595	
139	tttatctatctatcttat	ataagatagatagataaaa	299					12871 12888	
140	cactgtcatttaccatta	taatgtaatgacagtg	300					13583 13598	
141	ccgtgaactcctacaatc	gattgtaggagttcagg	301					13875 13891	
142	tccctaaaaatttactta	taagtaatttttaggga	302					14319 14334	
143	attaattccctaaaaatttacc	gtaatttttagggaaattaat	303					14322 14340	
144	tgggtcttaaccaca	tgtggttagagccga	304					14597 14611	1167
145	tacatgaaacacataact	agtatgtgttttcatgta	305					15223 15239	1795
146	catttgacctttatcaa	ttgataaaaggctcaaatg	306					15326 15342	1898
147	tccctaaaaacatttcata	tatgaatgttttagggga	307					15544 15560	2116
148	attttgcacacctcaca	tgtgagggtgtgcaaaat	308					16363 16379	2919 2935

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SEQ ID NO	motif sequence	RNA TARGET SEQUENCE	RNA SEQ ID	SEQ ID NO 1	SEQ ID NO 2	SEQ ID NO 3	SEQ ID NO 4	SEQ ID NO 5	SEQ ID NO 6
149	ttaataccactctc	gaagagtaggtattaa	309					16841 16856	3397 3412
150	caaagctacaaaactct	agatttggtagctttg	310					17465 17481	4021 4037
151	tgtattcaaatctcaaa	ttgagatttgaaataca	311					17649 17666	4205 4222
152	cgtatttcaaatctca	tgagatttgaaatacacg	312					17651 17667	4207 4223
153	cccacatcttttacac	gtgtaaaaggatgtggg	313					17892 17908	4448 4464
154	cccacatcttttaca	tgtaaaaaggatgtggg	314					17893 17908	4449 4464
155	atgtactaatctttt	aaagaaaaattagtagcat	315					18346 18362	4902 4918
156	ccacactgtatctca	tgaagatacacagtgtgg	316					18698 18713	5254 5269
157	agcatacaaaatatcc	ggatattttgtatgct	317					18858 18873	5414 5429
158	aaatcatttccaactct	agagttggaaaatgattt	318					19193 19210	5749 5766
159	aaccatgtttccctaca	tgtagggaacaacatggtt	319					19369 19385	5925 5941
160	ttcctatcataaaccat	atggttatgataggaa	320					19380 19395	5936 5951
161	attctgttctctatca	tgataggaaacaagaat	321					19387 19402	5943 5958
162	ttgaataagtggaagt	None – negative control							
163	ccaaatcttataataaactac	None – negative control							
164	cgtaaaactacccttat	None – negative control							
165	tgaggctctgcactgg*	SOD1							
166	gtcagtatcccagtg*	FXI							

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*Corresponds to ASO ID 569721 and 569720 in Burel et al 2016 Nucleic Acid Res 44(5); 2093-109 – they be used as positive controls for hepatotoxicity.

Oligonucleotide synthesis

Oligonucleotide synthesis is generally known in the art. Below is a protocol which may be applied. The oligonucleotides of the present invention may have been produced by slightly varying methods in terms of apparatus, support and concentrations used.

- 5 Oligonucleotides are synthesized on uridine universal supports using the phosphoramidite approach on an Oligomaker 48 at 1 μ mol scale. At the end of the synthesis, the oligonucleotides are cleaved from the solid support using aqueous ammonia for 5-16 hours at 60°C. The oligonucleotides are purified by reverse phase HPLC (RP-HPLC) or by solid phase extractions and characterized by UPLC, and the molecular mass is further confirmed by ESI-MS.
- 10 *Elongation of the oligonucleotide:*
The coupling of β -cyanoethyl- phosphoramidites (DNA-A(Bz), DNA- G(ibu), DNA- C(Bz), DNA- T, LNA-5-methyl-C(Bz), LNA-A(Bz), LNA- G(dmf), or LNA-T) is performed by using a solution of 0.1 M of the 5'-O-DMT-protected amidite in acetonitrile and DCI (4,5-dicyanoimidazole) in acetonitrile (0.25 M) as activator. For the final cycle a phosphoramidite with desired
15 modifications can be used, e.g. a C6 linker for attaching a conjugate group or a conjugate group as such. Thiolation for introduction of phosphorothioate linkages is carried out by using xanthane hydride (0.01 M in acetonitrile/pyridine 9:1). Phosphodiester linkages can be introduced using 0.02 M iodine in THF/Pyridine/water 7:2:1. The rest of the reagents are the ones typically used for oligonucleotide synthesis.
- 20 For post solid phase synthesis conjugation a commercially available C6 aminolinker phosphoramidite can be used in the last cycle of the solid phase synthesis and after deprotection and cleavage from the solid support the aminolinked deprotected oligonucleotide is isolated. The conjugates are introduced via activation of the functional group using standard synthesis methods.
- 25 *Purification by RP-HPLC:*
The crude compounds are purified by preparative RP-HPLC on a Phenomenex Jupiter C18 10 μ 150x10 mm column. 0.1 M ammonium acetate pH 8 and acetonitrile is used as buffers at a flow rate of 5 mL/min. The collected fractions are lyophilized to give the purified compound typically as a white solid.
- 30 *Abbreviations:*
DCI: 4,5-Dicyanoimidazole
DCM: Dichloromethane
DMF: Dimethylformamide
DMT: 4,4'-Dimethoxytrityl
35 THF: Tetrahydrofurane

Bz: Benzoyl

Ibu: Isobutyryl

RP-HPLC: Reverse phase high performance liquid chromatography

***T_m* Assay:**

- 5 Oligonucleotide and RNA target (phosphate linked, PO) duplexes are diluted to 3 mM in 500 ml RNase-free water and mixed with 500 ml 2x *T_m*-buffer (200mM NaCl, 0.2mM EDTA, 20mM Naphosphate, pH 7.0). The solution is heated to 95°C for 3 min and then allowed to anneal in room temperature for 30 min. The duplex melting temperatures (*T_m*) is measured on a Lambda 40 UV/VIS Spectrophotometer equipped with a Peltier temperature programmer PTP6 using PE
- 10 Templab software (Perkin Elmer). The temperature is ramped up from 20°C to 95°C and then down to 25°C, recording absorption at 260 nm. First derivative and the local maximums of both the melting and annealing are used to assess the duplex *T_m*.

Example 1: *In vitro* reduction of TMEM106b in Neuro2a mouse cell line using oligonucleotides

- 15 LNA modified oligonucleotides targeting mouse *Tmem106b* were tested for its ability to reduce *Tmem106b* mRNA expression in mouse Neuro-2a neuroblastoma cell acquired from ATCC (CCL-131).

Neuro2a cells were grown in cell culturing media (DMEM AQ media [Sigma, cat. D0819] supplemented with 10% fetal bovine serum [Sigma, cat.no F7524], 1x Glutamax™ [Sigma, cat.no 3050-038], 1 mM Na-pyruvate and 25 µg/ml gentamicin) in a cell incubator at 37°C in

20 atmosphere with 5% CO₂. Cells were trypsinized upon reaching 80% confluency, by washing with Phosphate Buffered Saline (PBS), [Sigma cat.no 14190-094] followed by addition of 0.25% Trypsin-EDTA solution (Sigma, T3924), 2-3 minutes incubation at 37°C, and trituration before cell seeding. Cells were maintained in culture for up to 15 passages.

- 25 For experimental use, 2400 cells per well were seeded in 96 well plates (Nunc cat.no 167008) in 95µL growth media. Oligonucleotides were prepared from a 500µM stock. 5 µl of ASOs dissolved in PBS were added approximately 24 hours after the cells were seeded to a final concentration in cell media of 5 µM or 25µM. Cells were incubated for 3 or 6 days without any media change. Cells used for 3 days and for 6 days long incubation with ASOs were derived
- 30 from different frozen stock and were at a different passage number during the experiment.

After incubation, cells were harvested by removal of media followed by cell lysis and RNA purification using QIAGEN RNeasy 96 Kit (cat 74181), following manufacturers protocol. RNA was diluted 10 fold in water prior to the one-step qPCR reaction. For one-step qPCR reaction qPCR-mix (qScript™ XLT One-Step RT-qPCR ToughMix® Low ROX from QuantaBio, cat.no

35 95134-500) was mixed with two Taqman probes in a ratio 10:1:1 (qPCR mix: probe1:probe2) to

generate the mastermix. Taqman probes were acquired from LifeTechnologies:

Mm00510952_m1, Mm00510954_m1, Mm01134666_m1 (Thermo Fisher Scientific, cat. 4351368, 4351368 and 4351370, respectively); GAPDH (cat. 4352339E) and ACTB (cat.

4352341E). Each experiment with Neuro2a cells included measurement of both GAPDH and

5 ACTB and one (Mm00510952_m1) or all three of the *Tmem106b* specific probes, in such a way that in a given well one *Tmem106b* and one control probe set was included. Mastermix (6μL) and RNA (4μL) were then mixed in a qPCR plate (MICROAMP®optical 384 well, 4309849).

After sealing, the plate was given a quick spin, 1000g for 1 minute at RT, and transferred to a ViiATM 7 system (Applied Biosystems, Thermo), and the following PCR conditions used: 50°C

10 for 15 minutes; 95°C for 3 minutes; 40 cycles of: 95°C for 5 sec followed by a temperature decrease of 1.6 °C/sec followed by 60 °C for 45 sec. The data was analyzed using the

QuantStudioTM Real_time PCR Software. Presented results are normalized to the different

housekeeping genes. The results are shown in Table 9 below as control samples (PBS-treated cells) i.e. the lower the value the larger the inhibition. The results are also plotted in Figure 1

15 and Figure 2. Almost all of the tested compounds (black dots) were found to inhibit target expression at 5 μM and 25 μM as compared to the negative control gapmers (white dots), highlighting that TMEM106B is surprisingly susceptible to oligonucleotide directed inhibition.

Table 9: *in vitro* efficacy of oligonucleotides targeting TMEM106B mRNA in Neuro2a mouse cells. The experiment was performed in duplex for day 3 (replicate A and B) and as a single
20 experiment on day 6.

CMP ID NO	Day 3						Day 6	
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM	mRNA (%PBS) 25uM
Replicate	A	B	AVG	A	B	AVG		
17_1	66	75	71	39	50	44	25	7
47_1	78	78	78	57	65	61	46	25
81_1	92	95	93	99	101	100	79	70
87_1	102	100	101	102	104	103	95	96
88_1	89	89	89	61	68	65	32	23
89_1	96	94	95	91	85	88	70	48
90_1	89	82	86	80	79	79	75	50
91_1	101	109	105	102	104	103	110	103
92_1	94	99	97	94	97	96	70	66
93_1	108	96	102	105	94	100	111	103
94_1	103	97	100	105	99	102	105	116
95_1	105	104	104	101	95	98	104	115
96_1	108	93	100	105	105	105	102	112
97_1	89	92	91	74	78	76	58	37

CMP ID NO	Day 3						Day 6	
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM	mRNA (%PBS) 25uM
Replicate	A	B	AVG	A	B	AVG		
98_1	91	89	90	80	92	86	52	35
99_1	100	108	104	102	99	100	111	112
100_1	98	90	94	90	88	89	89	68
101_1	100	98	99	104	100	102	84	86
102_1	92	96	94	90	71	80	48	31
103_1	108	95	101	99	99	99	115	108
104_1	93	103	98	95	101	98	121	95
105_1	92	99	96	95	87	91	81	59
106_1	102	105	104	101	105	103	76	68
107_1	95	99	97	89	91	90	55	37
108_1	103	89	96	94	92	93	86	71
109_1	88	85	87	72	77	74	61	44
110_1	97	97	97	91	89	90	82	66
111_1	103	111	107	97	104	100	90	94
112_1	86	92	89	84	78	81	77	48
113_1	99	99	99	93	87	90	67	49
114_1	74	91	82	63	69	66	47	37
115_1	70	76	73	49	58	53	28	15
116_1	101	104	102	104	101	102	96	98
117_1	100	104	102	98	97	97	113	107
118_1	102	99	101	105	99	102	98	81
119_1	104	106	105	99	87	93	95	107
120_1	103	94	98	104	96	100	87	79
121_1	101	94	97	102	90	96	82	73
122_1	103	113	108	104	108	106	95	114
123_1	80	72	76	58	56	57	40	21
124_1	93	90	91	79	79	79	68	46
125_1	79	97	88	65	72	69	49	36
126_1	93	98	95	77	95	86	49	26
127_1	98	85	91	94	86	90	80	74
128_1	102	97	100	92	102	97	76	60
129_1	81	87	84	64	67	66	38	21
130_1	93	93	93	91	85	88	73	54
131_1	88	97	92	74	74	74	69	37
132_1	95	101	98	81	91	86	60	38
133_1	78	84	81	56	60	58	32	15
134_1	94	103	99	90	94	92	66	53
135_1	95	101	98	87	92	90	61	53

CMP ID NO	Day 3						Day 6	
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM	mRNA (%PBS) 25uM
Replicate	A	B	AVG	A	B	AVG		
136_1	88		88	71	80	75	53	33
137_1	99	105	102	107	96	102	113	106
138_1	95	97	96	91	96	93	75	62
139_1	105	105	105	101	NA	101	105	74
140_1	93	99	96	93	101	97	82	85
141_1	95	112	103	99	97	98	79	62
142_1	112	95	103	101	111	106	88	99
143_1	109	97	103	113	94	104	121	135
144_1	65	77	71	58	64	61	55	29
145_1	70	80	75	58	64	61	39	19
146_1	82	96	89	72	75	73	76	70
147_1	105	112	109	104	95	100	86	86
148_1	100	98	99	101	92	97	61	49
149_1	91	98	94	90	91	91	73	NA
150_1	100	99	99	90	85	87	59	42
151_1	71	78	75	57	59	58	42	29
152_1	58	59	59	35	40	37	38	22
153_1	98	101	100	94	97	95	85	74
154_1	95	102	99	87	93	90	73	52
155_1	63	69	66	42	47	45	31	20
156_1	59	56	58	38	42	40	28	19
157_1	72	82	77	57	62	59	41	27
158_1	88	84	86	71	75	73	65	47
159_1	98	87	92	86	91	89	73	61
160_1	88	99	94	84	92	88	75	63
161_1	70	78	74	53	57	55	31	27
162_1	102	103	102	110	100	105	89	115
163_1	103	103	103	104	98	101	111	134
164_1	99	100	100	107	103	105	96	112

Example 2: *In vitro* reduction of TMEM106B in a human SK-N-BE(2) cells using oligonucleotides

5 Oligonucleotides targeting TMEM106B was tested for its ability to reduce TMEM106B mRNA expression in human SK-N-BE(2) neuroblastoma cell acquired from ATCC (CRL-2271).

SK-N-BE(2) cells were grown in cell culturing media (MEM [Sigma, cat.no M2279] supplemented with 10% Fetal Bovine Serum [Sigma, cat.no F7524], 1x GlutamaxTM [Sigma,

cat.no 3050-038] 1x MEM Non-essential amino acid solution [Sigma, cat.no M7145] and 0.025mg/ml Gentamycin [Sigma, cat.no G1397]). Cells were trypsinized every 5 days, by washing with Phosphate Buffered Saline (PBS), [Sigma cat.no 14190-094] followed by addition of 0.25% Trypsin-EDTA solution (Sigma, T3924), 2-3 minutes incubation at 37°C, and trituration before cell seeding. Cells were maintained in culture for up to 15 passages.

For experimental use, 15,000 (day 3) or 25,000 (day 6) cells per well were seeded in 96 well plates (Nunc cat.no 167008) in 100µL growth media. Oligonucleotides were prepared from a 750µM stock. Oligonucleotide dissolved in PBS was added approximately 24 hours after the cells were seeded to a final concentration of 5 µM or 25µM. Cells were incubated for 3 or 6 days without any media change.

After incubation, cells were harvested by removal of media followed by addition of 125µL PureLink®Pro 96 Lysis buffer (Invitrogen 12173.001A) and 125µL 70% ethanol. RNA was purified according to the manufacture's instruction and eluted in a final volume of 50µL water resulting in an RNA concentration of 10-20ng/µL. RNA was diluted 10 fold in water prior to the one-step qPCR reaction. For one-step qPCR reaction qPCR-mix (qScript™XLE 1-step RT-qPCR TOUGHMIX®Low ROX from QauntaBio, cat.no 95134-500) was mixed with two Taqman probes in a ratio 10:1:1 (qPCR mix: probe1:probe2) to generate the mastermix. Taqman probes were acquired from LifeTechnologies: TMEM_Hs00998849_m1; GAPDH 4325792. Mastermix (6µL) and RNA (4µL, 1-2 ng/µL) were then mixed in a qPCR plate (MICROAMP®Optical 384 well, 4309849). After sealing, the plate was given a quick spin, 1000g for 1 minute at RT, and transferred to a Viia™ 7 system (Applied Biosystems, Thermo), and the following PCR conditions used: 50°C for 15 minutes; 95°C for 3 minutes; 40 cycles of: 95°C for 5 sec followed by a temperature decrease of 1.6 °C/sec followed by 60 °C for 45 sec.

The data was analyzed using the QuantStudio™ Real_time PCR Software. Presented results are normalized to GAPDH. The results are shown in Table 10 below as % of control samples (PBS-treated cells) i.e. the lower the value the larger the inhibition. The results are also plotted in Figure 4 and Figure 5. Almost all of the tested compounds (black dots) were found to inhibit target expression at 5 µM and 25 µM as compared to the negative control gapmers (white dots), highlighting that TMEM106B is surprisingly susceptible to oligonucleotide directed inhibition. Notably compounds targeting the 3'UTR were found to be particularly effective, for example compounds 68_1, 73_1, 74_1, 79_1 and 82_1.

Table 10: *in vitro* efficacy of oligonucleotides targeting TMEM106B mRNA in SK-N-BE(2) human cells. The experiment was performed in duplex (sample A and B)

CMP ID NO	Day 3						Day 6					
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM			mRNA (%PBS) 25uM		
Replicate	A	B	AVG	A	B	AVG	A	B	AVG	A	B	AVG
7_1	82	67	75	59	43	51	57	59	58	34	36	35
8_1	40	44	42	20	22	21	28	31	29	16	16	16
9_1	57	57	57	21	24	22	48	56	52	16	17	16
10_1	68	54	61	27	29	28	42	45	44	19	19	19
11_1	80	79	80	58	56	57	70	68	69	46	44	45
12_1	40	43	41	20	23	22	31	31	31	16	15	16
13_1	25	25	25	10	10	10	14	13	14	5	5	5
14_1	53	54	54	33	33	33	44	46	45	23	22	22
15_1	53	55	54	27	28	27	56	55	56	34	32	33
16_1	28	26	27	12	10	11	17	17	17	6	6	6
17_1	34	33	33	13	12	12	24	25	24	8	9	9
18_1	88	103	95	85	90	88	104	97	100	81	79	80
19_1	15	14	14	5	5	5	7	7	7	2	3	2
20_1	30	27	28	14	13	13	19	17	18	7	7	7
21_1	25	26	26	10	10	10	16	16	16	5	6	6
22_1	112	85	99	81	63	72	75	74	74	49	50	49
23_1	74	60	67	40	31	36	45	47	46	18	18	18
24_1	75	77	76	52	55	53	66	72	69	42	43	42
25_1	18	18	18	4	5	4	8	8	8	2	2	2
26_1	91	89	90	85	78	81	85	88	87	77	76	77
27_1	55	45	50	30	21	25	37	35	36	18	18	18
28_1	87	69	78	59	52	55	60	60	60	38	45	42
29_1	32	34	33	13	14	13	23	25	24	9	10	9
30_1	53	58	56	27	30	28	47	47	47	21	21	21
31_1	15	15	15	4	4	4	6	7	7	2	2	2
32_1	39	31	35	14	11	13	19	19	19	8	8	8
33_1	18	18	18	5	5	5	13	13	13	3	3	3
34_1	26	25	25	7	8	8	15	15	15	4	4	4
35_1	14	15	14	5	5	5	6	7	6	2	2	2
36_1	74	77	76	47	50	49	60	60	60	44	41	43
37_1	76	67	71	34	36	35	53	58	55	27	30	29
38_1	95	91	93	84	94	89	93	97	95	88	87	87
39_1	48	52	50	25	25	25	37	38	38	18	22	20
40_1	38	37	38	15	15	15	30	30	30	8	10	9

CMP ID NO	Day 3						Day 6					
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM			mRNA (%PBS) 25uM		
Replic ate	A	B	AVG	A	B	AVG	A	B	AVG	A	B	AVG
41_1	51	50	50	20	22	21	32	33	32	12	13	12
42_1	36	42	39	22	23	23	29	33	31	20	20	20
43_1	33	36	35	15	17	16	23	25	24	12	11	12
44_1	73	69	71	52	54	53	61	60	60	36	38	37
45_1	59	56	57	30	31	30	46	43	44	20	20	20
46_1	29	32	30	20	17	19	20	22	21	9	9	9
47_1	36	37	36	11	11	11	29	28	28	8	8	8
48_1	65	67	66	42	46	44	59	58	58	37	38	38
49_1	66	67	67	47	51	49	56	59	57	42	41	42
50_1	53	64	58	40	42	41	54	55	55	34	35	35
51_1	82	82	82	61	63	62	66	69	68	48	50	49
52_1	85	85	85	69	69	69	83	75	79	59	55	57
53_1	42	32	37	20	15	17	24	25	25	12	13	13
54_1	100	78	89	44	53	49	66	68	67	41	43	42
55_1	82	87	85	64	69	67	77	77	77	60	60	60
56_1	82	84	83	63	62	63	80	77	78	50	53	52
57_1	48	48	48	28	28	28	37	38	38	22	21	22
58_1	42	48	45	22	23	23	33	31	32	15	16	15
59_1	45	49	47	29	33	31	40	37	39	24	24	24
60_1	35	33	34	13	14	14	26	23	24	9	9	9
61_1	64	69	66	34	38	36	53	55	54	26	27	27
62_1	8	8	8	2	2	2	4	5	5	1	1	1
63_1	76	85	80	65	70	68	78	83	81	59	61	60
64_1	68	67	67	42	40	41	58	60	59	36	35	35
65_1	7	7	7	2	2	2	3	3	3	1	1	1
66_1	10	9	10	2	2	2	4	4	4	1	1	1
67_1	54	59	56	29	31	30	48	46	47	20	20	20
68_1	24	23	24	8	8	8	12	13	13	4	5	4
69_1	73	71	72	52	50	51	61	62	61	38	37	38
70_1	20	17	19	6	6	6	8	8	8	3	3	3
71_1	7	9	8	3	3	3	4	4	4	1	2	1
72_1	26	28	27	10	11	11	14	16	15	6	7	6
73_1	14	15	15	5	6	5	9	10	10	4	4	4
74_1	2	2	2	1	1	1	1	1	1	2	1	1
75_1	4	4	4	2	2	2	2	2	2	3	2	3
76_1	75	71	73	56	50	53	64	65	65	42	42	42

CMP ID NO	Day 3						Day 6					
	mRNA (%PBS) 5uM			mRNA (%PBS) 25uM			mRNA (%PBS) 5uM			mRNA (%PBS) 25uM		
Replic ate	A	B	AVG	A	B	AVG	A	B	AVG	A	B	AVG
77_1	35	38	37	18	18	18	25	25	25	11	13	12
78_1	25	24	24	9	9	9	15	15	15	7	6	6
79_1	26	31	29	14	15	14	25	26	26	13	13	13
80_1	89	89	89	75	77	76	83	83	83	52	67	60
81_1	74	71	73	56	56	56	59	63	61	44	44	44
82_1	36	39	37	18	18	18	30	31	31	15	14	14
83_1	12	14	13	5	5	5	8	8	8	4	4	4
84_1	47	53	50	26	25	26	39	40	39	17	17	17
85_1	30	30	30	15	16	15	21	20	20	10	11	11
86_1	40	38	39	36	37	36	40	41	40	41	41	41
162_1	98	98	98	94	98	96	91	93	92	90	91	90
163_1	98	105	101	95	97	96	110	103	106	100	101	101

Example 3: Cellular toxicity of oligonucleotides

To measure if LNA modified oligonucleotides induce apoptosis of the cells a caspase assay was applied as described here. NIH 3T3 cells (ECACC cat. 93061524) were transfected with 100 nM or 30 nM LNA oligonucleotides using Lipofectamine™ 2000 and Caspase 3 and Caspase 7 activation was measured after 24 hours, following protocol described below, adapted from Dieckmann et al. (Molecular Therapy: Nucleic Acids Vol. 10 March 2018). The experiment was performed in two replicates with slightly different protocols. Each replicate was performed in two 96 well plate. Each LNA oligonucleotide at a given transfection concentration was measured in total four times in each replicate.

For the first replicate, mouse embryo fibroblasts cell line NIH 3T3 were grown in m3T3 media (DMEM AQ (Sigma: D0819) supplemented with 10% FBS and 25 µg/ml gentamicin) at 37°C with 5% CO₂. Cells were trypsinized and seeded in 96-well plates (ViewPlate-96, PerkinElmer, cat 6005181), at a density of 4000 cells per well in 100 µl of m3T3 media and grown for 24 hours. LNA oligonucleotides were diluted with DPBS (Thermo Fisher Scientific, cat. 14190250) to a final concentration of 5 µM or 1.5 µM (also included negative controls with 0 µM concentration of oligonucleotide). Each diluted LNA oligonucleotide was mixed with Opti-MEM (Thermo Fisher Scientific cat. 31985047) in a ratio of 1 to 24 (volume), and to 30 µl of such a mixture 30 µl of LOM solution (Lipofectamine™ 2000 (Thermo Fisher Scientific cat. 11668019) mixed with Opti-MEM (Thermo Fisher Scientific cat. 31985047) in a ratio of 1 to 99 (volume), used immediately after preparation) was added followed by 20 min incubation. Media was

removed from the NIH 3T3 cell culture and 50 µl of LNA oligonucleotide in LOM solution was added. After four hours, 50 µl of m20F media (mix 800 ml DMEM AQ (Sigma: D0819) with 200 ml FBS and 10 ml 200 mM L-alanyl-L-glutamine and 500 µl 50 mg/ml gentamicin) was added to each well. After 24 hours from adding LNA oligonucleotide to cells 100 µl of the Caspase-Glo®

5 3/7 reagent (Promega, cat. G8093, prepared as prescribed by the manufacturer) was added to the cells, plates were shaken 500 rpm for 30 seconds and incubated 1 hour at room temperature, followed by blocking back of the plates with BackSeal (PerkinElmer cat. 6005199) and measurement of luminescence with EnSight Multimode Plate Reader (PerkinElmer cat. HH34000000).

10 For the second replicate similar protocol was followed with following modifications: (1) diluted LNA oligonucleotides were mixed with Opti-MEM in a ratio of 2 to 23 instead of 1 to 24; (2) immediately prior to addition of 50 µl of a mixture of LNA oligonucleotides with opti-MEM and LOM solution to cells, 50 µl of Opti-MEM was added to cells; (3) instead of m20F, 50 µl of m30F (mix 700 ml DMEM AQ (Sigma: D0819) with 300 ml FBS and 10 ml 200 mM L-alanyl-L-

15 glutamine and 500 µl 50 mg/ml gentamicin) was added; (4) immediately prior to addition of Caspase-Glo® 3/7 reagent, 50 µl of media from cells was removed.

Luminescence signal as measured by the EnSight reader was divided by the average luminescence signal of the negative control wells within given 96 well plate. Signal for different compounds at a given concentration was averaged across plates and across replicates

20 (outliers, defined as data points that are more or less than 1.5 interquartile ranges from the mean signal within a replicate, were removed). The results are shown in Table 11, and illustrated in Figure 3.

Table 11: Caspase activation in NIH 3T3 cells treated with oligonucleotides (replicates of 4)

CMP ID NO	30 nM, average, replicate 1	30 nM, st dev, replicate 1	30 nM, average, replicate 2	30 nM, st dev, replicate 2	30 nM, average of replicate1 and 2 avg	100 nM, average, replicate 1	100 nM, st dev, replicate 1	100 nM, average, replicate 2	100 nM, st dev, replicate 2	100 nM, average of replicate1 and 2 avg
017_1	102%	7%	115%	4%	109%	171%	25%	199%	31%	185%
047_1	113%	1%	103%	6%	108%	229%	48%	166%	30%	198%
088_1	113%	7%	103%	2%	108%	236%	7%	188%	49%	212%
114_1	105%	9%	124%	13%	115%	232%	4%	405%	55%	319%
115_1	108%	10%	116%	14%	112%	240%	52%	447%	24%	344%
123_1	105%	9%	119%	19%	112%	204%	15%	245%	74%	224%
129_1	88%	18%	108%	10%	98%	102%	2%	105%	11%	103%
133_1	96%	19%	105%	2%	101%	139%	26%	131%	4%	135%

CMP ID NO	30 nM, average, replicate 1	30 nM, st dev, replicate 1	30 nM, average, replicate 2	30 nM, st dev, replicate 2	30 nM, average of replicate1 and 2 avg	100 nM, average, replicate 1	100 nM, st dev, replicate 1	100 nM, average, replicate 2	100 nM, st dev, replicate 2	100 nM, average of replicate1 and 2 avg
144_1	105%	8%	111%	8%	108%	98%	2%	94%	1%	96%
145_1	98%	2%	92%	4%	95%	179%	52%	161%	37%	170%
151_1	102%	1%	94%	4%	98%	121%	13%	110%	20%	116%
152_1	94%	8%	105%	11%	100%	111%	12%	142%	15%	127%
155_1	102%	6%	106%	10%	104%	110%	6%	106%	4%	108%
156_1	106%	2%	102%	15%	104%	121%	0%	125%	10%	123%
157_1	106%	4%	114%	2%	110%	139%	21%	138%	23%	139%
161_1	89%	4%	101%	15%	95%	141%	21%	174%	11%	158%
162_1	96%	0%	106%	4%	101%	107%	8%	106%	9%	107%
163_1	100%	4%	94%	7%	97%	107%	11%	101%	9%	104%
165_1	113%	16%	105%	4%	109%	344%	15%	457%	63%	400%
166_1	116%	15%	174%	48%	145%	188%	42%	476%	11%	332%

Example 4: *In vivo* reduction of TMEM106B in mice

The present example tests the ability of selected oligonucleotides from Example 1 to reduce TMEM106B *in vivo* in mouse brain as well as the acute and non-acute toxicity potential of the oligonucleotides.

C57BL/6J male mice (23-32 g) were freehand injected with 5 µl of 20 mg/ml saline formulated LNA oligonucleotides into right lateral ventricles (0.3 AP, 1.0 ML, 3.0 DV; six animals per group for TMEM106B reactive compounds; fifteen saline treated animals; fifteen animals treated with MAPT reactive compound and six animals treated with a negative control oligo) under isoflurane anesthesia.

After the administration the acute response was scored in four levels: (1) normal behavior, (2) mild response (slight change in activity/posture/gait for 30min-1hr), (3) moderate response (prolonged pronounced change in activity/posture for 2-4hrs), (4) severe (no activity, shallow breathing, moribund). The weight of the mice was measured immediately prior to administration of an oligonucleotide and six days after the administration. Significant loss of body mass is an indicator of potential non-acute toxicity. The results are shown in Table 13 below.

Seven days after the injection, mice were sacrificed with isoflurane overdose followed by rapid decapitation, and the brain was placed in an ice-cold mouse brain slicer matrix (Stoelting) and sectioned into two (2mm) coronal sections (starting at 0.26mm from Bregma) weighing

approximately 30-40 mg. The tissue was immersed in RNALater solution (ThermoFisher Scientific, cat. AM7021) and stored at 4°C. RNA was isolated using RNeasy Mini Kit (Qiagen, cat. 74116) using QIAcube robotic workstation (Qiagen). Briefly, brain fragment was transferred from the RNALater solution to 1 mL RLT buffer in 1.5 mL Eppendorf tube containing 3mm tungsten carbide bead (Qiagen, cat 69997). Tissue was lysed using TissueLyser II (Qiagen) (3min at 30Hz) and centrifuged 3 minutes at 20000g. 550 µl of the lysate (no foam, no sediment) was transferred to 2 mL Eppendorf tube and placed in QIAcube pre-filled with all the required reagents. RNA was purified according to a program "RNeasy Mini - Animal tissues and cells - Large samples (version 2)" with elution with 50 µl of H₂O. RNA concentration was measured using NanoDrop 8000 (ThermoFisher Scientific) spectrophotometer and the concentration was adjusted with H₂O to 2 ng/µl.

Expression levels on sections from the right hemisphere were essentially measured as described in Example 1, using TMEM106B Mm00510952_m1 (Thermo Fisher Scientific, cat. 4351370) as probe and a GAPDH probe (cat. 4352339E, Thermo Fisher Scientific) for normalization. The data was analyzed using the QuantStudio™ Real-time PCR Software, and the readouts of the technical duplicates were averaged. The results are shown in Table 12 as % of average control samples (PBS-treated mice) i.e. the lower the value the larger the inhibition.

Table 12: *In vivo* efficacy of oligonucleotides targeting TMEM106B.

CMP ID NO	TMEM106B mRNA (%saline)	SD
156_1	34%	10%
152_1	34%	13%
155_1	53%	14%
17_1	59%	18%
144_1	67%	27%
157_1	67%	11%
133_1	49%	17%
151_1	63%	8%
163_1	96%	3%

Table 13: Acute response and body mass change observed in mice injected with oligonucleotides targeting TMEM106B.

CMP ID NO	Acute response				Body mass	
	Normal	Mild	Moderate	Severe	Average change [g]	SD
156_1		5	1		-0.03	0.90
152_1	1	5			0.08	0.51
155_1	6				0.82	1.06

CMP ID NO	Acute response				Body mass	
	Normal	Mild	Moderate	Severe	Average change [g]	SD
17_1	2	4			-0.40	0.74
144_1	6				-2.27	2.33
157_1	6				0.83	0.40
133_1	6				0.63	0.54
151_1	6				0.67	0.45
161_1				3	0.22	0.18
163_1	6				0.65	0.74
Saline	14	1				

From Table 12 and 13 it can be seen that all the TMEM106B targeting oligonucleotides were capable of reducing TMEM106B mRNA after a single injection. Of the 10 oligonucleotides tested one was found to cause severe acute toxicity. Compound ID NO 161 was administered to only three animals, which were euthanized immediately following observation of severe response, consequently there is not TMTM106B reduction measured for this compound. Some animals administered with compound 144_1 showed signs of significant body mass loss, which could be due to non-acute toxicity of this compound. All the remaining oligonucleotide compounds seemed to be well tolerated 7 days after treatment.

10 **Example 5: Treatment of human iPSC neurons and astrocytes mix culture**

In Example 2, human TMEM106b were initially screened in the human neuroblastoma cell line. To assess the ability of these ASO's to reduce the target in human neurons, the efficacy of five human TMEM106b ASOs: CMP ID 74_1, 65_1, 75_1, 71_1, 66_1, were evaluated in a cell culture mixture of human iPSC neurons and astrocytes.

- 15 Human iPSC-derived neural stem cells (MTI-GlobalStem, GSC-4311) were maintained in NSC Maintenance Medium (DMEM/F12 (Genentech)/Neurobasal (ThermoFisher Scientific, 21103049), 1X GS22 (MTI-Global STEM, GSM-3200), 20 ng/ml BDNF (Peprotech, 450-02), 20 ng/ml FGF-basic (Peprotech, 100-18b), 20 ng/ml EGF (Peprotech, AF-100-15), 0.5 mM Glutamax (Gibco, 35050061), 0.11mM β -Mercaptoethanol (Sigma-Aldrich CHECKCAT) , 1X
- 20 Normocin (InvivoGen, ant-nr-1), 50 U/ml Penicillin-Streptomycin (ThermoFisher 15160122)) in a 37°C CO₂ cell culture incubator; NSC Maintenance Medium was changed every 3-4 days until cells were confluent. For neuronal differentiation, the cells were plated onto a 50 μ g/ml PDL (Sigma-Aldrich, P6407) and 10 μ g/ml Recombinant Human Laminin (Sigma-Aldrich, St Louis, MO, USA) T-650 cell culture flask at an approximate concentration of 0.7×10^6 –
- 25 1.0×10^6 cells/ml. Cells were plated in Neuron Differentiation Media ((DMEM/F12 (Genentech)/Neurobasal (ThermoFisher Scientific 21103049), 1X GS21 (MTI-Global STEM

GSM-3100), 1X N2 (MTI-GlobalStem GSM3300), 5 µg/ml Cholesterol (Sigma-Aldrich C3045), 1 mM Creatine (Sigma-Aldrich C0780), 100 µM Ascorbic Acid (Sigma-Aldrich A8960), 0.5 mM cAMP (Sigma-Aldrich D0627), 20 ng/ml BDNF (Peprotech, 450-02), 20 ng/ml GDNF (Peprotech, 450-10), 1 µg/ml Mouse Laminin (Invitrogen, 23017-015), 0.5 mM Glutamax (Gibco, 35050061), 1X Normocin (InvivoGen, ant-nr-1), 50 U/ml Penicillin-Streptomycin (ThermoFisher, 15160122)) supplemented with Y27632 (Tocris, 1254), SU9516 (Tocris, 2907), and Cumate (System Biosciences AM100A-1). The plated cells were differentiated for 1 week; one half volume differentiation media was changed every 3-4 days. After differentiation, cells were plated onto 384-well or 96-well, PDL-Laminin coated plates at an approximate concentration of $2.5 \times 10^5 - 5.5 \times 10^5$ in pre-warmed differentiation medium supplemented with Y27632 Rock inhibitor (Tocris, 1254) and 1X RevitaCell (Gibco, A2644501) and maintained for 1 week; one half volume differentiation media was changed every 3-4 days.

Primary human astrocytes (LifeTechnologies, N7805100) were maintained in Astrocyte Medium (DMEM High Glucose (Genentech), 10% FBS (VWR, 89510-198), 1X N2 (MTI-GlobalStem GSM3300), 1X Normocin (InvivoGen, ant-nr-1), 50 U/ml Penicillin-Streptomycin (ThermoFisher, 15160122)) in a 37°C CO₂ cell culture incubator; medium was change every 3-4 days until cells were confluent. Astrocytes were subsequently added to the human iPSC neurons (described in the previous paragraph) in 384-well or 96-well plates at an approximate concentration of $3.0 \times 10^4 - 8.0 \times 10^4$ cells/ml in BrainPhys Maintenance Medium (BrainPhys Basal (STEMCELL Technologies, 05790), 1X GS21 (MTI-Global STEM GSM-3100), 1X N2 (MTI-GlobalStem GSM3300), 5 µg/ml Cholesterol (Sigma-Aldrich C3045), 1 mM Creatine (Sigma-Aldrich C0780), 10 nM β-estradiol (Sigma-Aldrich E2758), 200 nM Ascorbic Acid (Sigma-Aldrich A8960), 1 mM cAMP (Sigma-Aldrich D0627), 20 ng/ml BDNF (Peprotech, 450-02), 20 ng/ml GDNF (Peprotech, 450-10), 1 µg/ml Mouse Laminin (Invitrogen, 23017-015), 0.5mM Glutamax (Gibco, 35050061), 1X Normocin (InvivoGen, ant-nr-1), 50 U/ml Penicillin-Streptomycin (ThermoFisher, 15160122), 1 ng/ml TGFβ1 (Peprotech, 100-21); one half volume of the BrainPhus Maintenance Medium was changed every 3-4 days for 6-8 weeks.

For ASO treatment of the human iPSC neurons CMP ID 74_1, 65_1, 75_1, 71_1, 66_1 were diluted from stock in an intermediate 96 well plate in a 9 point 3 fold serial dilution (10 µM, 3.3 µM, 1.1 µM, 0.37 µM, 0.12 µM, 0.04 µM, 0.0137 µM, 0.0045 µM, 0.0015 µM) or a 5 point 10 fold serial dilution (10 µM, 1 µM, 0.1 µM, 0.01 µM, 0.001 µM).

In a continuous 10 days incubation experiment, the ASO's were added the human iPSC neurons and astrocytes mix after 2 months of culture at the ASO concentrations indicated above (5 point 10 fold). On day 3 and day 7, 50% of media were changed to maintain optimal cell health (no additional ASO was added). 10 days after ASO treatment was initiated, cells were harvested for Taqman assay following the manufacturer's instructions from TaqMan Gene

Expression Cells-to-Ct Kit (ThermoFisher Scientific, AM1728). The human neuron TMEM106b Taqman assay was performed following the manufacturer's instruction with specific gene expression assay probes for human TMEM106b and POL2RB as housekeeping gene normalizer (assay ID Hs00998849_m1 and Hs00946293_m1, respectively). The TMEM106b expression levels were normalized to the POL2RB housekeeping gene and the relative expression in relation to the media control (100%) was calculated (i.e. lower numbers indicate high TMEM106b reduction). Graph Pad Prism software was used to conduct the IC50 analysis using the software curve fit option. The results are shown in Tables 14 and 15, and Figures 7A and 7B. The structural formulas of CMP IDs 74_1, 65_1, 75_1, 71_1, 66_1 are shown in Figures 9-13.

Table 14: % TMEM106b mRNA reduction in relation to saline in human iPSC neurons and astrocytes mix culture following 10 days consecutive treatment with serial dilution of ASOs (n=3).

ASO Conc	CMP ID 74_1		CMP ID 65_1		CMP ID 75_1		CMP ID 71_1		CMP ID 66_1	
μ M	Avg	SD	Avg	SD	Avg	SD	Avg	SD	Avg	SD
10.0000	2	0.0	1	0.6	2	1.0	5	0.6	6	2.0
3.3333	2	0.0	3	0.6	4	1.0	8	5.3	10	2.9
1.1111	2	0.6	5	1.0	7	2.6	14	6.0	18	3.5
0.3704	5	0.6	11	0.6	11	1.5	19	7.9	32	12.1
0.1235	8	0.0	21	2.5	17	2.6	27	10.0	50	3.0
0.0412	16	1.5	46	5.1	32	1.5	44	14.2	61	12.5
0.0137	29	7.0	68	4.6	60	16.1	59	6.4	83	10.6
0.0046	61	12.5	79	11.4	76	7.9	77	1.7	111	11.4
0.0015	100	0.0	100	0.0	110	7.0	96	4.0	112	14.4
IC50/nM	7.6		31.4		21.6		30.7		128.7	

It can be taken from the data that the ASOs show high potency in the range of 7.6 nM to 128.7 nM (Table 14, Figure 7A). Furthermore, it can be seen that the near complete elimination of human neuronal TMEM106b mRNA.

The ASOs were furthermore evaluated in a 24 hour pulse experiment to assess whether short term ASO treatment can have a long-lasting effect. The five human TMEM106b ASOs CMP ID 74_1, 65_1, 75_1, 71_1, 66_1, were added to human iPSC neurons and astrocytes mix after 2 months of culture at the ASO concentrations indicated above (9 point 3 fold dilutions). The ASO treatment was only for 24 hrs then cells were washed with neuronal culture media 3X. On day 3 and day 7, 50% of media were changed to maintain optimal cell health. 10 days after ASO treatments, cells were harvest and TMEM106B mRNA were accessed with the Taqman assay described above. The results are shown in Table 15 and Figure 7B.

Table 15: % TMEM106b mRNA reduction in relation to saline in human iPSC neurons and astrocytes mix culture after 24 hour pulse treatment with serial dilution of ASOs (n=3).

ASO Conc	CMP ID 74_1		CMP ID 65_1		CMP ID 75_1		CMP ID 71_1		CMP ID 66_1	
μM	Avg	SD	Avg	SD	Avg	SD	Avg	SD	Avg	SD
10	16	3.0	10	2.5	14	4.4	9	0.7	15	2.1
1	28	9.6	34	3.5	32	3.6	21	3.5	48	7.5
0.1	45	6.0	76	1.0	68	9.0	56	5.7	90	11.5
0.01	62	3.8	102	2.0	113	15.1	94	8.5	109	13.0
0.001	87	7.8	112	9.6	126	12.0	114	1.4	117	10.7
IC50/nM	62.5		468.9		397.2		163.3		1041	

These results show IC50 in the range of 62.5 nM to 1 μM (Table 15, Figure 7B), and that with only 24 hrs incubation, all five human TMEM106b ASOs at 10 μM can effectively and nearly completely eliminate human TMEM106b mRNA and have a long lasting effect for at least 10 days similar to long term incubation (Table 14, Figure 7A).

It was further investigated if the ASO treatment of the human iPSC neurons and astrocytes results in reduction of TMEM106b protein levels. In a continuous 10 days incubation experiment, the ASO's were added to the human iPSC neurons and astrocytes mix after 2 months of culture at a final ASO concentration of 10 μM . On day 3 and day 7, 50% of media were changed to maintain optimal cell health (no additional ASO was added). 10 days after ASO treatment was initiated, cells were harvested with RIPA buffer (Pierce 89900) with proteinase inhibitors (Roche 11836153001) for protein analysis. BCA micro protein concentration analysis was performed according to the manufacture's instruction on all lysates to measure total protein concentration (Thermo Fisher Scientific, 23235). Protein analysis was performed on the Peggy Sue automated western instrument (Protein Simple) following manufacturer's instruction using Peggy Sue kit (SM-S001). Equal amount of total protein was loaded. Antibody for TMEM106b is from Bethyl (A303-439A) and GAPDH for housekeeping gene normalization is from Novus (NB100-56875).

Figure 7C shows the automated western blot result. On the left panel the neuronal lysates after 10 days treatment with control and CMP ID 65_1 ASO 10 μM were load in the indicated lanes. Then the lanes were probed with anti TMEM106b antibodies. The right panel shows the same sample lanes probed with anti GAPDH antibodies. It can be seen that CMP ID 65_1 is able to reduce human TMEM106b protein level after 10 days of treatment.

Example 6: Time course for *in vivo* reduction in mice of TMEM106b mRNA and protein

The present example tests the ability of selected mouse ASOs, also used in Example 4 above, for long term reduction of mRNA and protein 1, 2, 4, 8, and 12 weeks after a single ICV injection.

The data generated in Example 4 related to the reduction of mRNA 1 week after a single ICV injection has been taken over in this Example. Additional data were generated on the mRNA and protein reduction 1, 2, 4, 8, and 12 weeks after a single ICV injection.

C57BL/6J males from Jackson Laboratory, age 3-6 months, were used in these experiments.

5 Mice were housed on a regular light/dark cycle (14:10 hours) with *ad libitum* access to food (LabDiet 5010) and water. All injections and tissue collections were conducted during the light phase. All protocols for mouse experiments were approved by the Institutional Animal Care and Use Committee and were conducted in accordance with the NIH Guide for the Care and Use of Laboratory Animals.

10 Animals were anesthetized with isoflurane, the hair above the parietal region of the skull was removed by shaving and skin cleaned with either antimicrobial betadine solution and 70% ethanol or Cloraprep solution. A midline incision of the skin was made between the occiput and forehead to identify Bregma. Mice were injected 100 µg of ASO in a volume of 5 µl (saline) into the right lateral ventricle (-0.5 AP, 1.0 ML, 3.0 DV) at a rate of 1 µl/sec, using a 26-gauge 10 µl
15 Hamilton syringe. One minute after the injection the needle was slowly withdrawn. The incision was closed with tissue glue and buprenorphine was given for up to 3 days to reduce any pain caused by the procedure.

At 1 (for mRNA original data from Example 4), 2, 4, 8, and 12 weeks after the injection, mice were euthanized by decapitation under a constant flow of inhalant anesthetic (isoflurane).

20 Brains were placed on an ice cold brain matrix and the right hemibrain was sectioned into two 2 mm sections. One section was immediately place into RNALater (Ambion), and stored at 4°C for qPCR. The second 2 mm slice was weighed, immediately flash frozen in liquid nitrogen and stored at -80°C for protein analysis.

For qPCR, tissues were then transferred to RLT Buffer (Qiagen) lysis reagent and lysed using a
25 TissueLyser (Qiagen). RNA was extracted using RNeasy Mini QIAcube Kit (cat. 74116) with QIACUBE workstation. RNA concentrations were checked on Nanodrop (as RNA-40, blank H2O) and then each sample was diluted with water to yield 2 ng/µl solutions. RNA was heat denatured at 90°C for 40 seconds. qPCR assay was performed on Applied Biosystems ViiA7 thermal cycler using qScript™ XLT One-Step RT-qPCR ToughMix® Low ROX (QuantaBio,
30 cat. 95134-02K), using TMEM106b (cat. 4351368, ThermoFisher Scientific) as the probe and GAPDH (cat. 4352339E, ThermoFisher Scientific) probe for normalization. Results are shown in Table 16 and Figure 8A.

Table 16: Long term reduction of TMEM106b mRNA *in vivo*

Weeks Post-Injection	CMP ID NO: 152_1 (%saline)	SD	CMP ID NO: 155_1 (%saline)	SD
1	34%	13%	51%	14%
2	41%	19%	46%	14%
4	35%	7%	43%	19%
8	57%	5%	56%	6%
12	68%	11%	67%	10%

As can be taken from Table 16 and Figure 8A, reductions of TMEM106b mRNA for both CMP ID NO:152_1 and 155_1 were maximal between 1 and 4 weeks post-injection. Compared to saline controls (n=3-6/group), TMEM106b mRNA in the ASO treated animals did not return to baseline (saline control animals) 12 weeks post-injection, with 30-35% mRNA reduction detected for both CMP ID NO:152_1 and 155_1 (n=6-7/group) after 12 week.

For western blot, the second flash frozen slice was homogenized in 10 volumes of RIPA buffer with Complete Roche protease inhibitor cocktail (Roche) and PhosStop (Roche) using a TissueLyser (Qiagen, 3min at 30cycles/s). Samples were then rotated for 20 min at 4°C, then centrifuged at 14,000 rpm (Gs) at 4°C for 20 min. Supernatants were collected and stored at -80°C. Protein samples were diluted 1/5 in LDS loading buffer (4x, Invitrogen) with Reducing agent (10x, Invitrogen) and heat denatured for 5 min at 95°C. Samples were then kept on ice and stored at -20°C. Equal volumes of sample were separated on a 10% Bis-Tris gel with 1x MOPS running buffer, transferred to nitrocellulose membrane (iBlot2, ThermoFisher) and blocked at room temperature with 5% non-fat dried milk in TBS-Tween. Blots were probed with Rabbit anti-TMEM106b (A303-439; Bethyl, 1:500) or beta-Tubulin in 5% BSA overnight at 4°C. Blots were washed with TBST and incubated with HRP-conjugated secondary antibodies at room temperature for 2 h, then developed using Supersignal West Dura ECL (ThermoFisher) on a ChemiDoc (Bio-Rad). Blots were quantified using Image Lab 5.2 (BioRad) and each lane was normalized to beta-Tubulin, then to control samples. The results are shown in Table 17 and Figure 8B.

Table 17: Long term reduction of TMEM106b protein *in vivo*

Weeks Post-Injection	CMP ID NO: 152_1 (%saline)	SD	CMP ID NO: 155_1 (%saline)	SD
1	66%	7%	64%	18%
2	62%	9%	72%	10%
4	53%	11%	68%	20%
8	65%	14%	67%	22%

Weeks Post- Injection	CMP ID NO: 152_1 (%saline)	SD	CMP ID NO: 155_1 (%saline)	SD
12	61%	7%	86%	14%

Similarly, as can be taken from Table 17 and Figure 8B, TMEM106b protein was maximally reduced by 40-50% between 2-4 weeks post-injection. Compared to saline controls (n=2-6/group), TMEM106b protein did not return to baseline during the 12 weeks post-injection, with 39% reduction in CMP ID NO:152_1-treated animals (n=6-7/group) and 14% reduction in CMP ID NO:155_1-treated (n=5-7/group) animals.

5

CLAIMS

1. A therapeutic oligonucleotide of 10 to 50 nucleotides in length, which comprises a contiguous nucleotide sequence of 10 – 30 nucleotides in length with at least 90% complementary, such as fully complementary, to a mammalian TMEM106B target nucleic acid.
2. The oligonucleotide according to claim 1, wherein the mammalian TMEM106B target nucleic acid is selected from the group consisting of SEQ ID NO: 1, 2, 3, 4, 5 and 6, or a naturally occurring variant thereof.
3. The oligonucleotide according to claim 1 or 2, wherein the contiguous nucleotide sequence comprises at least 10 contiguous nucleotides, which are at least 90% complementary to, such as fully complementary, to a region of SEQ ID NO: 1, wherein the region is selected from the group consisting of position 546 - 563; 2122 - 2140; 2143 - 2160; 2165 - 2183; 2300 - 2317; 2392 - 2410; 2548 - 2565; 3507 - 3524; 3678 - 3694; 3736 - 3753; 3752 - 3767; 3802 - 3819; 3908 - 3925; 3908 - 6417; 4321 - 4337; 4701 - 4720; 4948 - 4965; 5063 - 5080; 5069 - 5086; 5172 - 5190; 5512 - 5530; 5583 - 5599; 6015 - 6047; 6015 - 6032; 6032 - 6047; 6125 - 6154; 6125 - 6140; 6136 - 6154; 6172 - 6189; 6200 - 6231; 6200 - 6216; 6214 - 6231; 6401 - 6417; 6458 - 6476; 6837 - 6853; 8453 - 8472; 8983 - 9001; 9533 - 9549; 9628 - 9644; 11065 - 11083; 11117 - 11134; 11264 - 11281; 12310 - 12325; 12870 - 12887; 13050 - 13065; 13397 - 13414; 15061 - 15079; 15249 - 15266; 15318 - 15336; 15368 - 15385; 15440 - 15457; 15632 - 15649; 15823 - 15842; 16496 - 16513; 19090 - 19109; 19198 - 19217; 19211 - 19228; 19699 - 19718; 20217 - 20243; 20217 - 20236; 20227 - 20243; 20755 - 26403; 20767 - 20786; 20880 - 20896; 21084 - 21101; 21214 - 21231; 21425 - 21442; 22110 - 25406; 22110 - 22128; 23374 - 23393; 23435 - 23452; 23806 - 23822; 23874 - 23890; 24045 - 24098; 24045 - 24063; 24060 - 24077; 24060 - 24076; 24064 - 24083; 24081 - 24098; 24801 - 24828; 24801 - 24819; 24812 - 24828; 25050 - 25067; 25372 - 25387; 25392 - 25406; 25773 - 25790; 25796 - 25814; 25969 - 25985; and 29351 - 29367 of SEQ ID NO: 1.
4. The oligonucleotide according to any one of claims 1 to 3, wherein the contiguous nucleotide sequence comprises at least 10 contiguous nucleotides which are at least 90% complementary, such as fully complementary, to the 3'UTR of a mammalian TMEM106B target nucleic acid.
5. The oligonucleotide according to any one of claims 1 – 4, wherein the contiguous nucleotide sequence is at least 90% complementary, such as fully complementary, to position 20755 to position 26403 of SEQ ID NO: 1.
6. The oligonucleotide according to any one of claims 1 – 5, wherein the contiguous nucleotide sequence is 100% complementary to SEQ ID NO: 1 or to one of the regions of SEQ ID NO: 1 listed in claim 3 or 5.

7. The oligonucleotide according to any one of claims 1 to 6, wherein the contiguous nucleotide sequence is at least 12 nucleotides in length, such as at least 14 nucleotides in length, which are fully complementary to SEQ ID NO 1, or to one of the regions of SEQ ID NO: 1 listed in claim 3 or 5.
8. The oligonucleotide according to any one of claims 1 – 7, wherein the contiguous nucleotide sequence comprises 12 nucleotides in length, such as at least 14 contiguous nucleotides in length, which are 100% identical, to a sequence selected from the group consisting of SEQ ID NO: 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85 and 86.
9. The oligonucleotide according to any one of claim 1 to 8, wherein the contiguous nucleotide sequence comprises or consists of from 12 to 22 nucleotides.
10. The oligonucleotide according to any one of claims 1 – 9, wherein the oligonucleotide comprises one or more 2' sugar modified nucleosides.
11. The oligonucleotide according to claim 10, wherein the one or more 2'-sugar modified nucleosides are independently selected from the group consisting of 2'-O-alkyl-RNA, 2'-O-methyl-RNA, 2'-alkoxy-RNA, 2'-O-methoxyethyl-RNA, 2'-amino-DNA, 2'-fluoro-DNA, arabino nucleic acid (ANA), 2'-fluoro-ANA and LNA nucleosides.
12. The oligonucleotide according to claim 11, wherein at least one of the one or more 2'-sugar modified nucleosides is a LNA nucleoside.
13. The oligonucleotide according to any one of claims 1 – 12, wherein the contiguous nucleotide sequence comprises at least one modified internucleoside linkage.
14. The oligonucleotide according to any one of claims 1 – 13 wherein the continuous nucleotide sequence comprises at least one phosphorothioate modified internucleoside linkage.
15. The oligonucleotide according to any one of claims 1 – 14, wherein the oligonucleotide is an siRNA or shRNA or forms the guide strand of an siRNA or shRNA complex.
16. The oligonucleotide according to any one of claims 1 – 15, where the oligonucleotide is a single stranded antisense oligonucleotide.
17. The antisense oligonucleotide according to claim 16, wherein at least 75% or all of the internucleoside linkages between the nucleosides of the contiguous nucleotide sequence are phosphorothioate internucleoside linkages.
18. The antisense oligonucleotide according to claim 16 or 17, wherein oligonucleotide is capable of recruiting RNase H1.

19. The antisense oligonucleotide according to claim 16 to 18, wherein the antisense oligonucleotide, or contiguous nucleotide sequence thereof, consists or comprises a gapmer of formula 5'-F-G-F'-3', where region F and F' independently comprise 1 - 8 nucleosides, of which 1-5 independently are 2' sugar modified and defines the 5' and 3' end of the F and F' region, and G is a region between 5 and 18 nucleosides which are capable of recruiting RNaseH, such as a region comprising 5 – 18 DNA nucleosides.

20. The antisense oligonucleotide according to any one of claims 16 - 19, wherein the antisense oligonucleotide is selected from the group consisting of a 2'-MOE gapmer, a LNA gapmer, a mixed wing gapmer; and an alternating flank gapmer.

21. The oligonucleotide according to any one of claims 1 - 14 or 16 – 20, wherein the oligonucleotide or contiguous nucleotide sequence thereof, is selected from the group consisting of CMP ID NO: 7_1, 8_1, 9_1, 10_1, 11_1, 12_1, 13_1, 14_1, 15_1, 16_1, 17_1, 18_1, 19_1, 20_1, 21_1, 22_1, 23_1, 24_1, 25_1, 26_1, 27_1, 28_1, 29_1, 30_1, 31_1, 32_1, 33_1, 34_1, 35_1, 36_1, 37_1, 38_1, 39_1, 40_1, 41_1, 42_1, 43_1, 44_1, 45_1, 46_1, 47_1, 48_1, 49_1, 50_1, 51_1, 52_1, 53_1, 54_1, 55_1, 56_1, 57_1, 58_1, 59_1, 60_1, 61_1, 62_1, 63_1, 64_1, 65_1, 66_1, 67_1, 68_1, 69_1, 70_1, 71_1, 72_1, 73_1, 74_1, 75_1, 76_1, 77_1, 78_1, 79_1, 80_1, 81_1, 82_1, 83_1, 84_1, 85_1, 86_1, 87_1, 88_1, 89_1, 90_1, 91_1, 92_1, 93_1, 94_1, 95_1, 96_1, 97_1, 98_1, 99_1, 100_1, 101_1, 102_1, 103_1, 104_1, 105_1, 106_1, 107_1, 108_1, 109_1, 110_1, 111_1, 112_1, 113_1, 114_1, 115_1, 116_1, 117_1, 118_1, 119_1, 120_1, 121_1, 122_1, 123_1, 124_1, 125_1, 126_1, 127_1, 128_1, 129_1, 130_1, 131_1, 132_1, 133_1, 134_1, 135_1, 136_1, 137_1, 138_1, 139_1, 140_1, 141_1, 142_1, 143_1, 144_1, 145_1, 146_1, 147_1, 148_1, 149_1, 150_1, 151_1, 152_1, 153_1, 154_1, 155_1, 156_1, 157_1, 158_1, 159_1, 160_1 and 161_1.

22. A conjugate comprising the oligonucleotide or antisense oligonucleotide according to any one of claims 1 – 21, and at least one conjugate moiety covalently attached to said oligonucleotide.

23. A pharmaceutically acceptable salt of the oligonucleotide or antisense oligonucleotide according to any one of claims 1 – 21, or the conjugate according to claim 22.

24. A pharmaceutical composition comprising the oligonucleotide or antisense oligonucleotide of any one of claims 1 – 21 or the conjugate of claim 22 and a pharmaceutically acceptable diluent, solvent, carrier, salt and/or adjuvant.

25. An *in vitro* or *in vivo* method for modulating TMEM106B expression in a target cell which is expressing TMEM106B, said method comprising administering a oligonucleotide or antisense oligonucleotide of any one of claims 1 – 21, conjugate according to claim 22, or the

pharmaceutical salt of claim 24, or pharmaceutical composition of claim 25 in an effective amount to said cell.

26. A method for treating or preventing a disease comprising administering a therapeutically or prophylactically effective amount of an oligonucleotide or antisense oligonucleotide of any one of claims 1 – 21, conjugate according to claim 22, or the pharmaceutical salt of claim 24, or pharmaceutical composition of claim 25, to a subject suffering from or susceptible to the disease.

27. The method of claim 26, wherein the disease is selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

28. The oligonucleotide or antisense oligonucleotide of any one of claims 1 – 21, conjugate according to claim 22, or the pharmaceutical salt of claim 24, or pharmaceutical composition of claim 25 for use in medicine.

29. The oligonucleotide or antisense oligonucleotide of any one of claims 1-23, conjugate according to claim 22, or the pharmaceutical salt of claim 25, or pharmaceutical composition of claim 26 for use in the treatment or prevention of a disease selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

30. Use of the oligonucleotide or antisense oligonucleotide of any one of claims 1 – 21, conjugate according to claim 22, or the pharmaceutical salt of claim 24, or pharmaceutical composition of claim 25, for the preparation of a medicament for treatment or prevention of a disease selected from the group consisting of neurodegeneration, frontotemporal lobar degeneration (FTLD), Parkinson's disease (or parkinsonism), hypomyelinating leukodystrophies, amyotrophic lateral sclerosis and multiple system atrophy, Alzheimer's disease, motor neuron disease, corticobasal syndrome, progressive supranuclear palsy, and neuronal ceroid lipofuscinosis (NCL).

31. The use or method according to any one of claims 26 – 30, wherein the disease is frontotemporal lobar degeneration (FTLD).

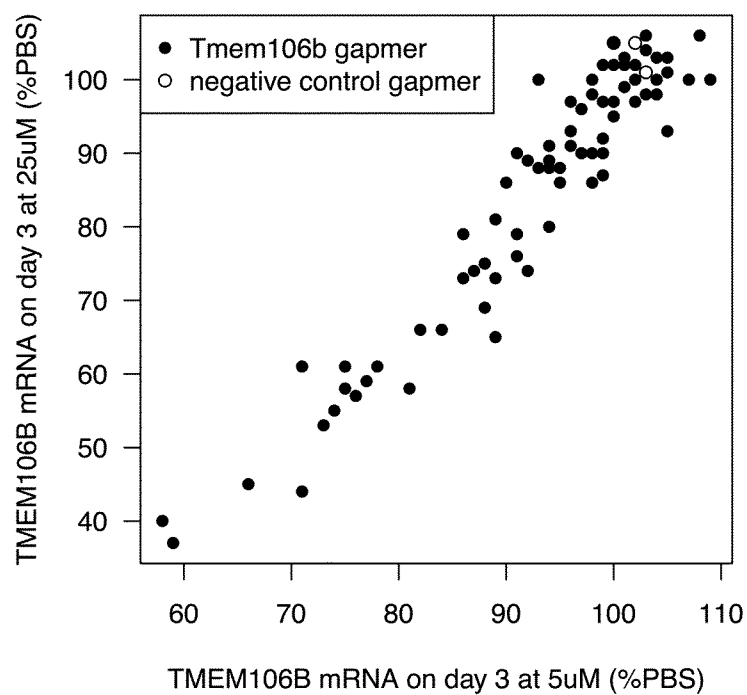
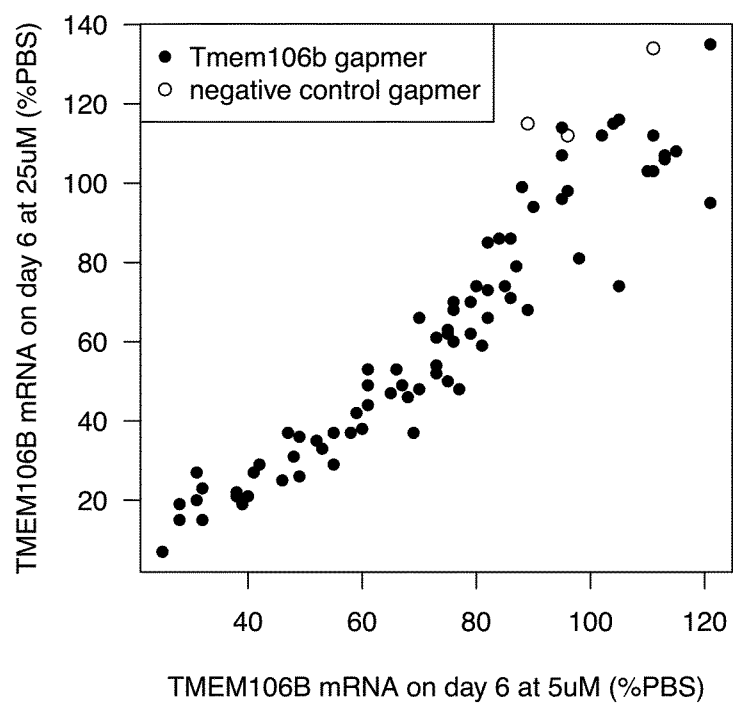
FIGURES**Figure 1****Figure 2**

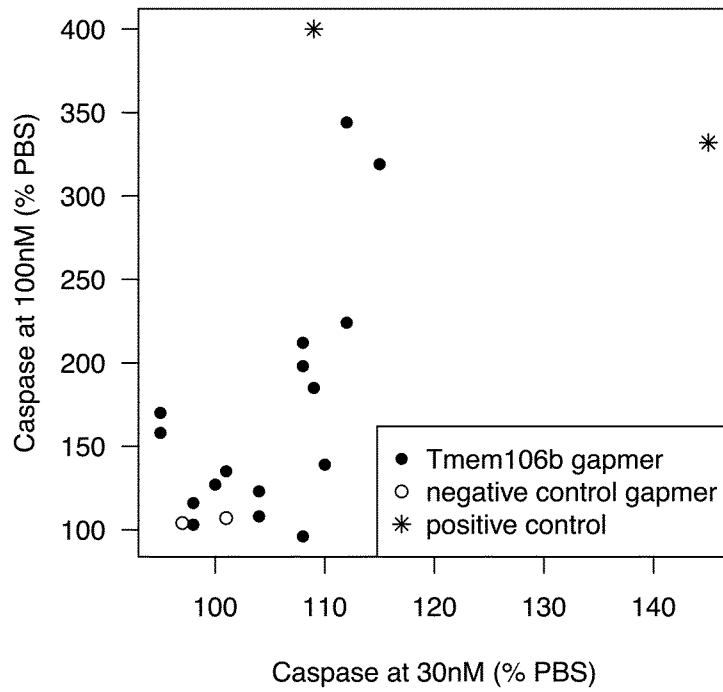
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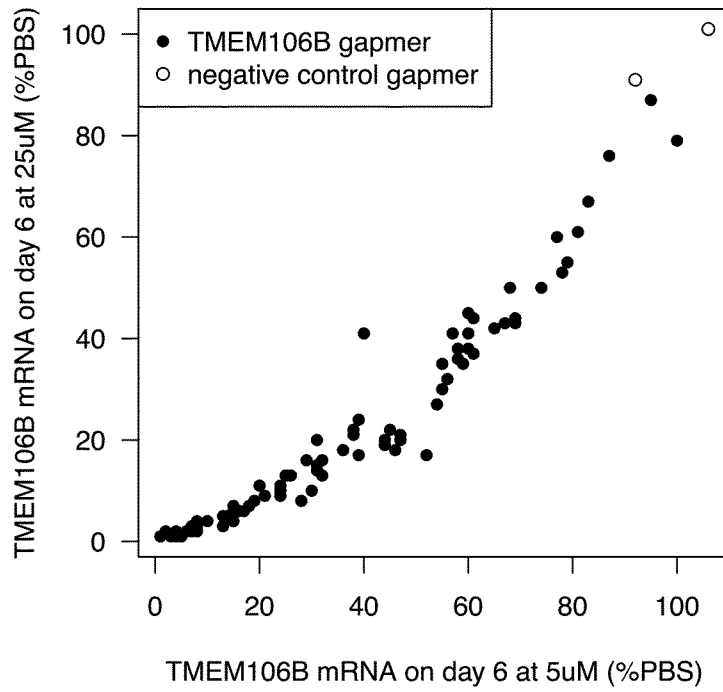
Figure 5

Figure 6

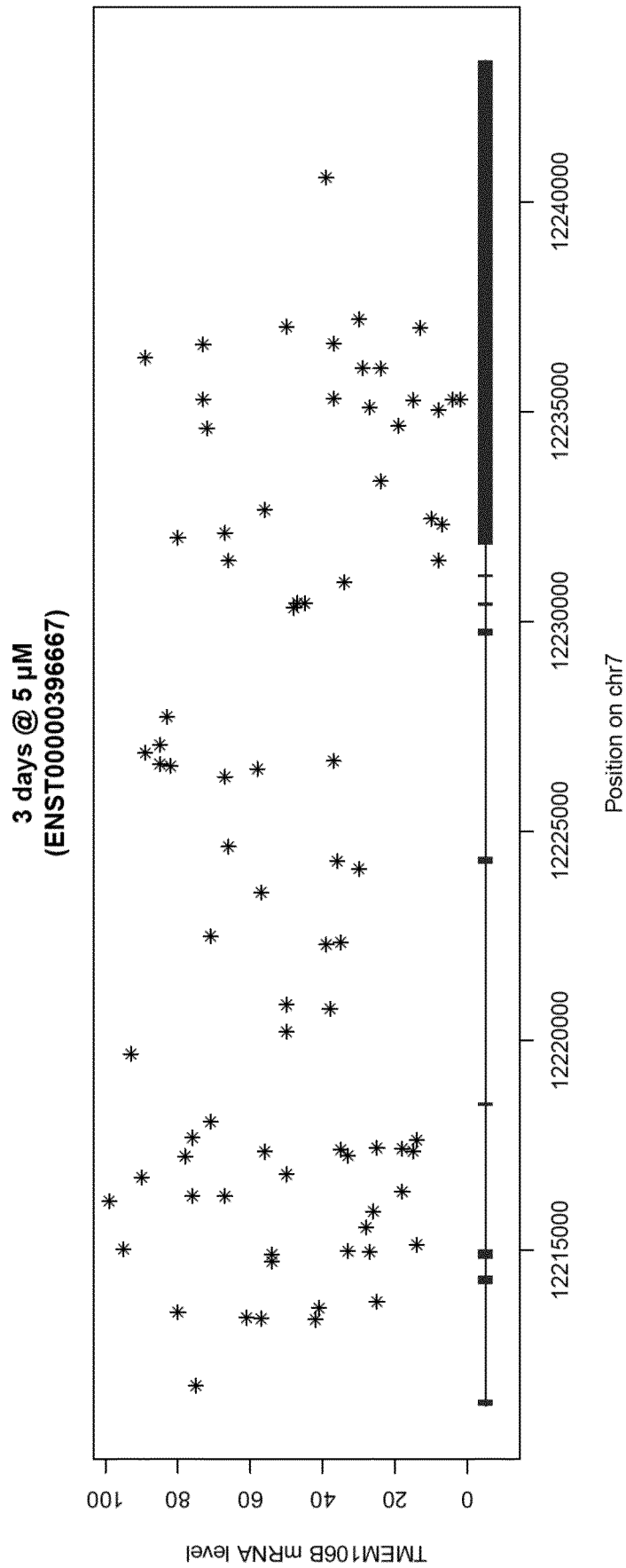


Figure 7A

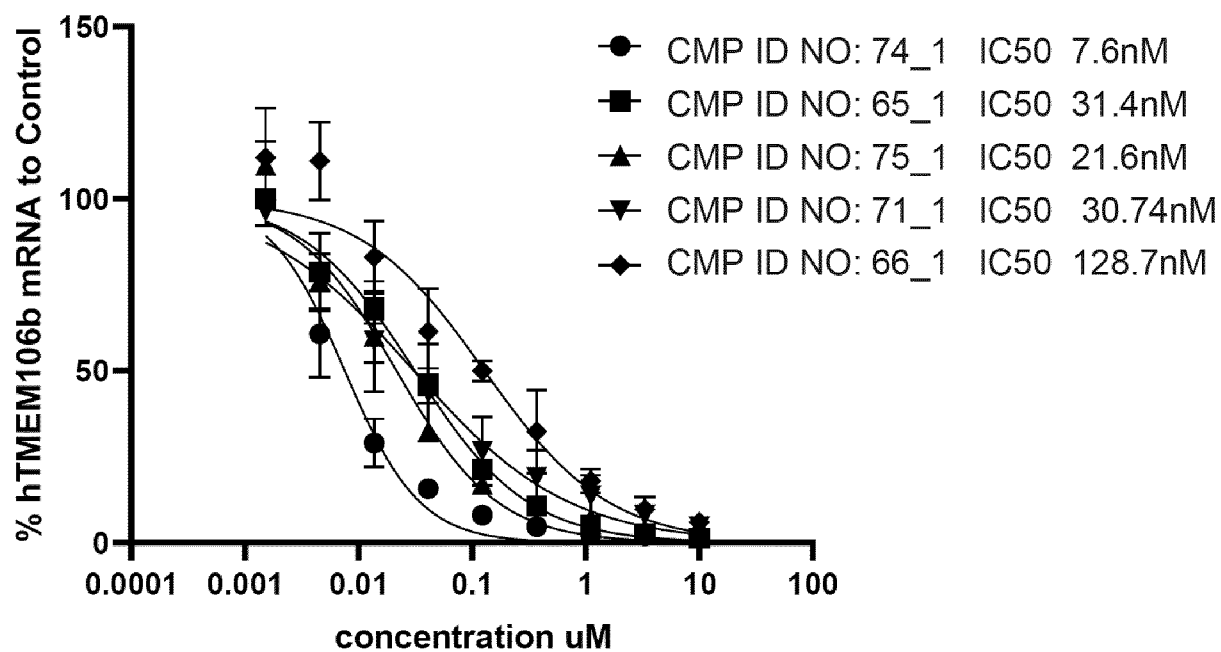


Figure 7B

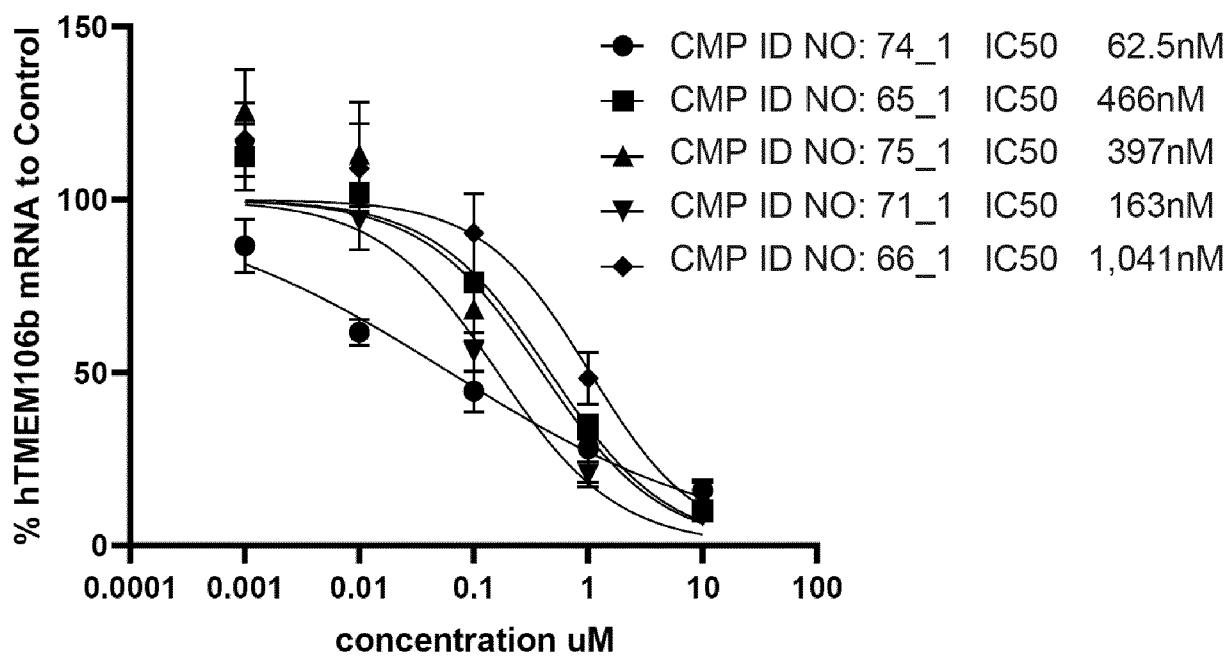


Figure 7C

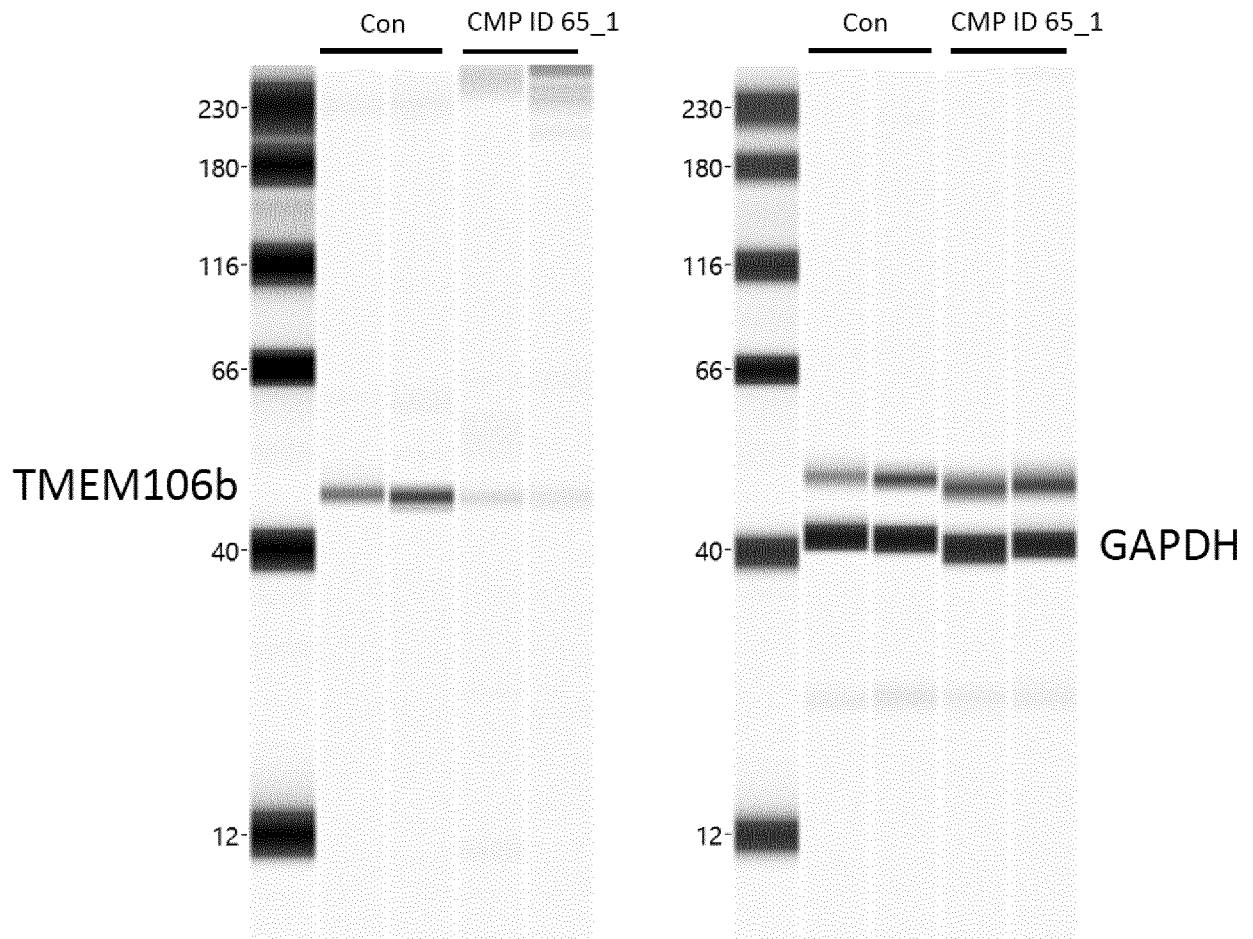


Figure 8A

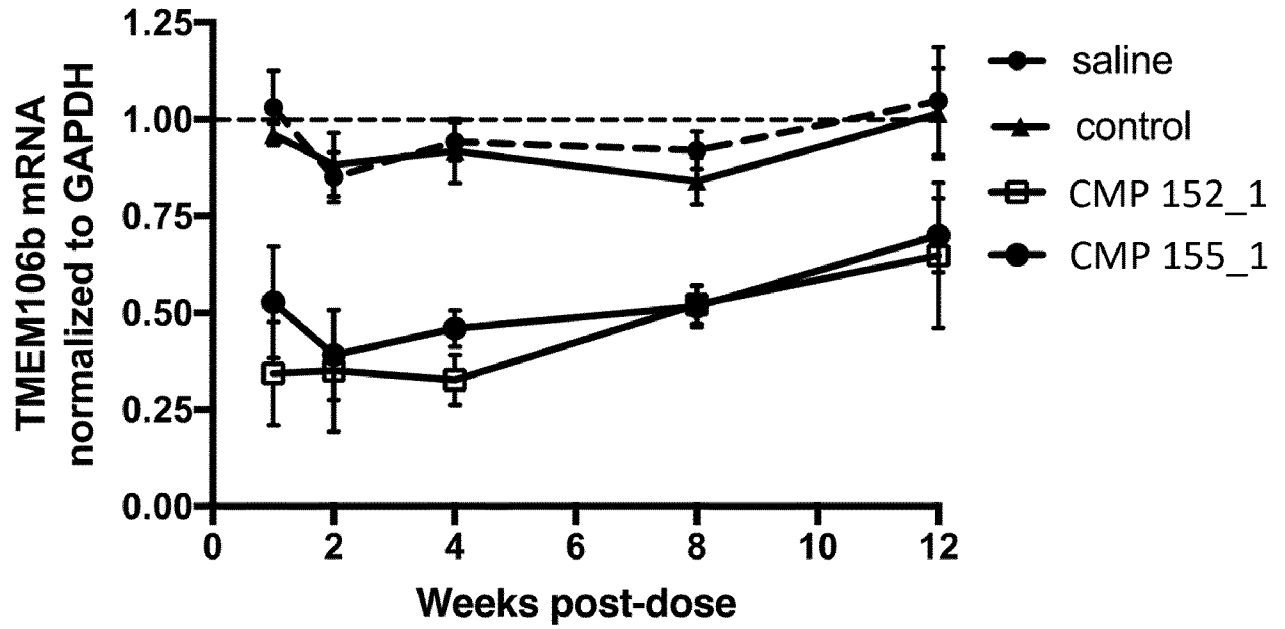


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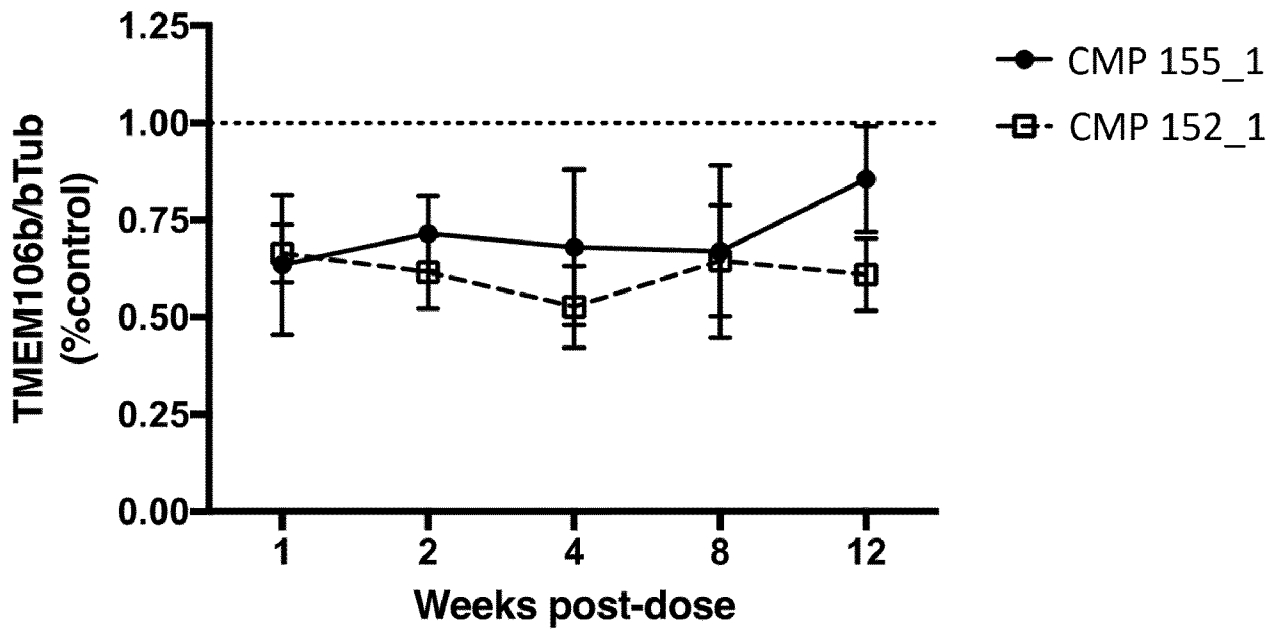


Figure 9

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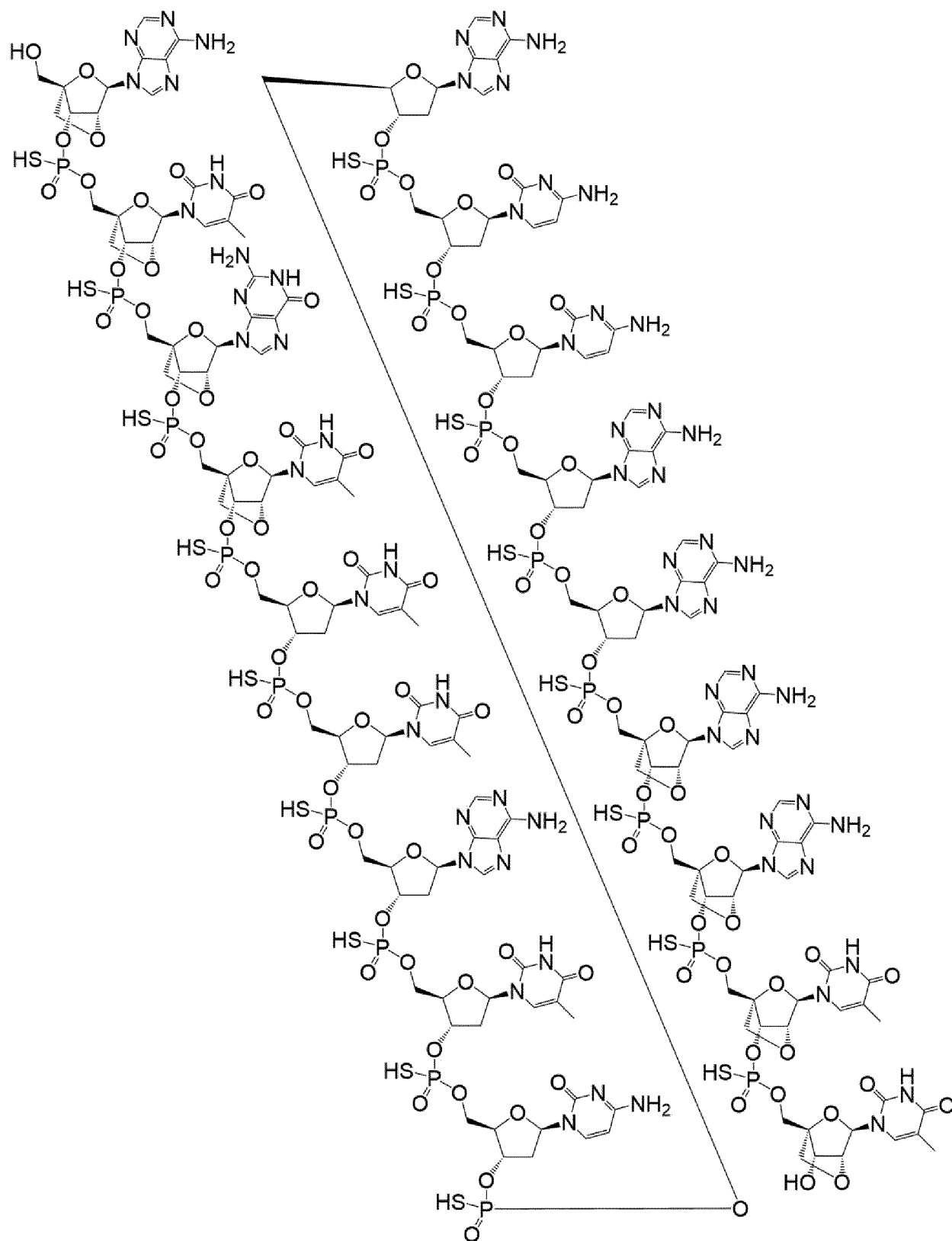


Figure 10

CMP ID NO: 66_1

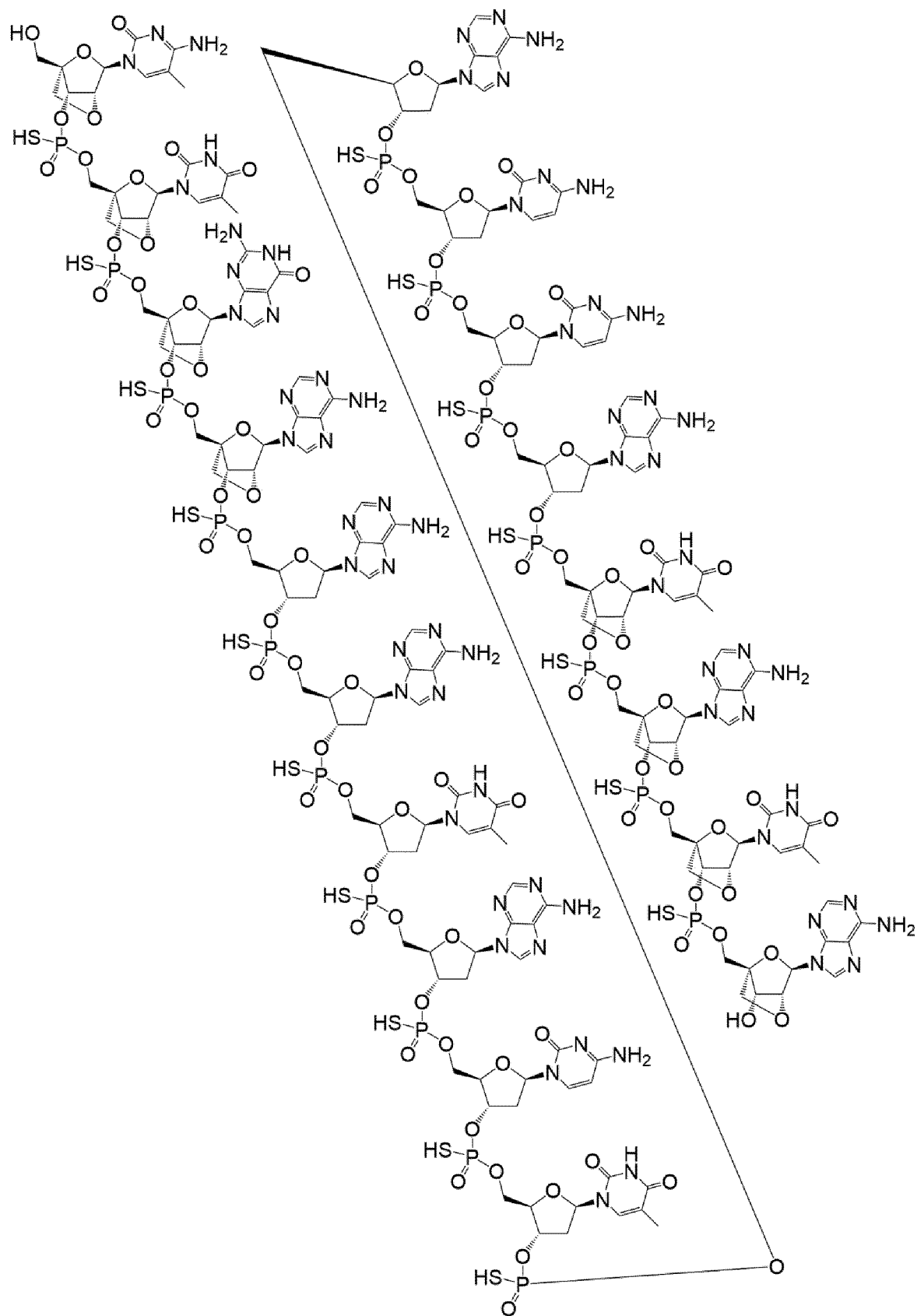


Figure 11

CMP ID NO: 71_1

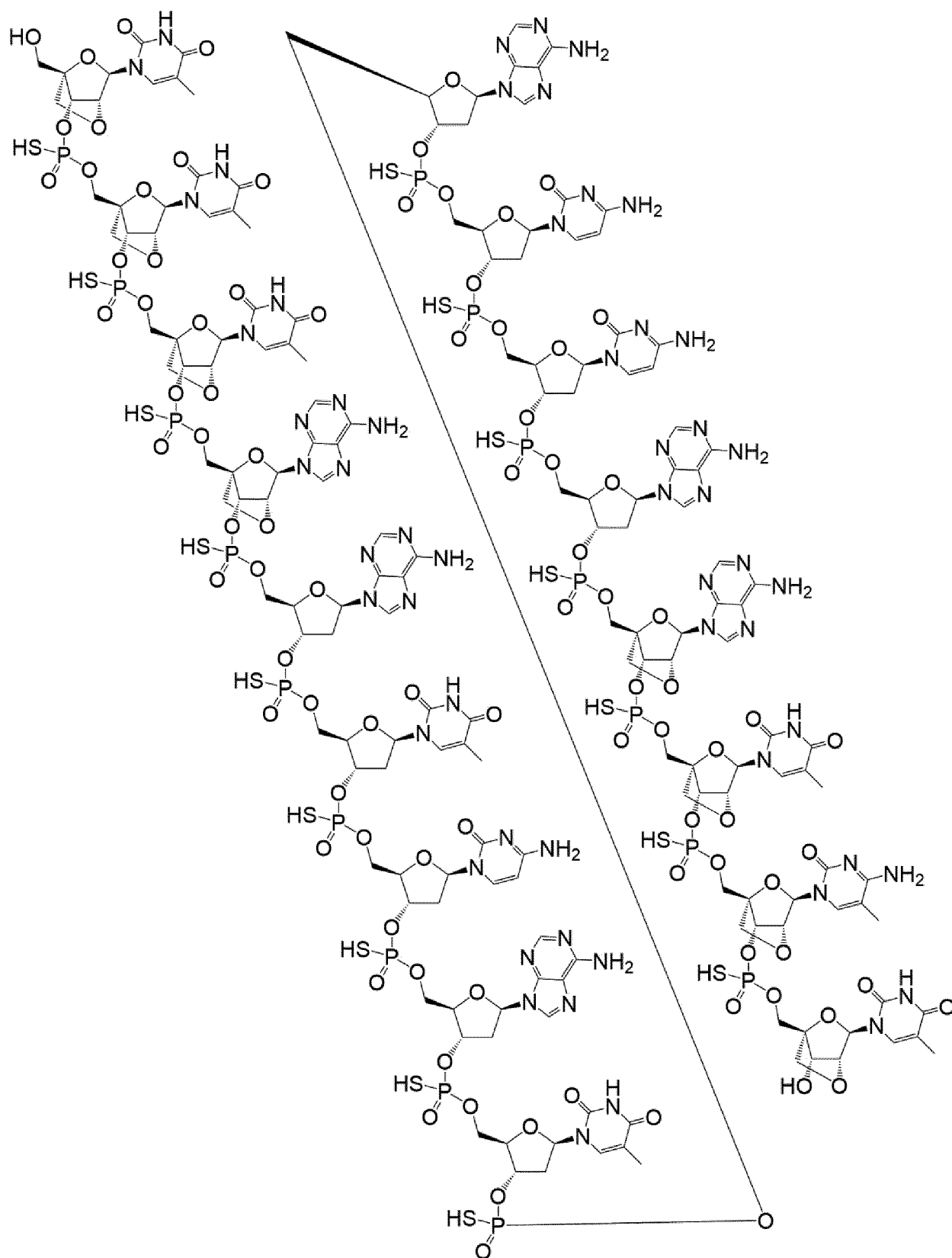


Figure 12

CMP ID NO: 74_1

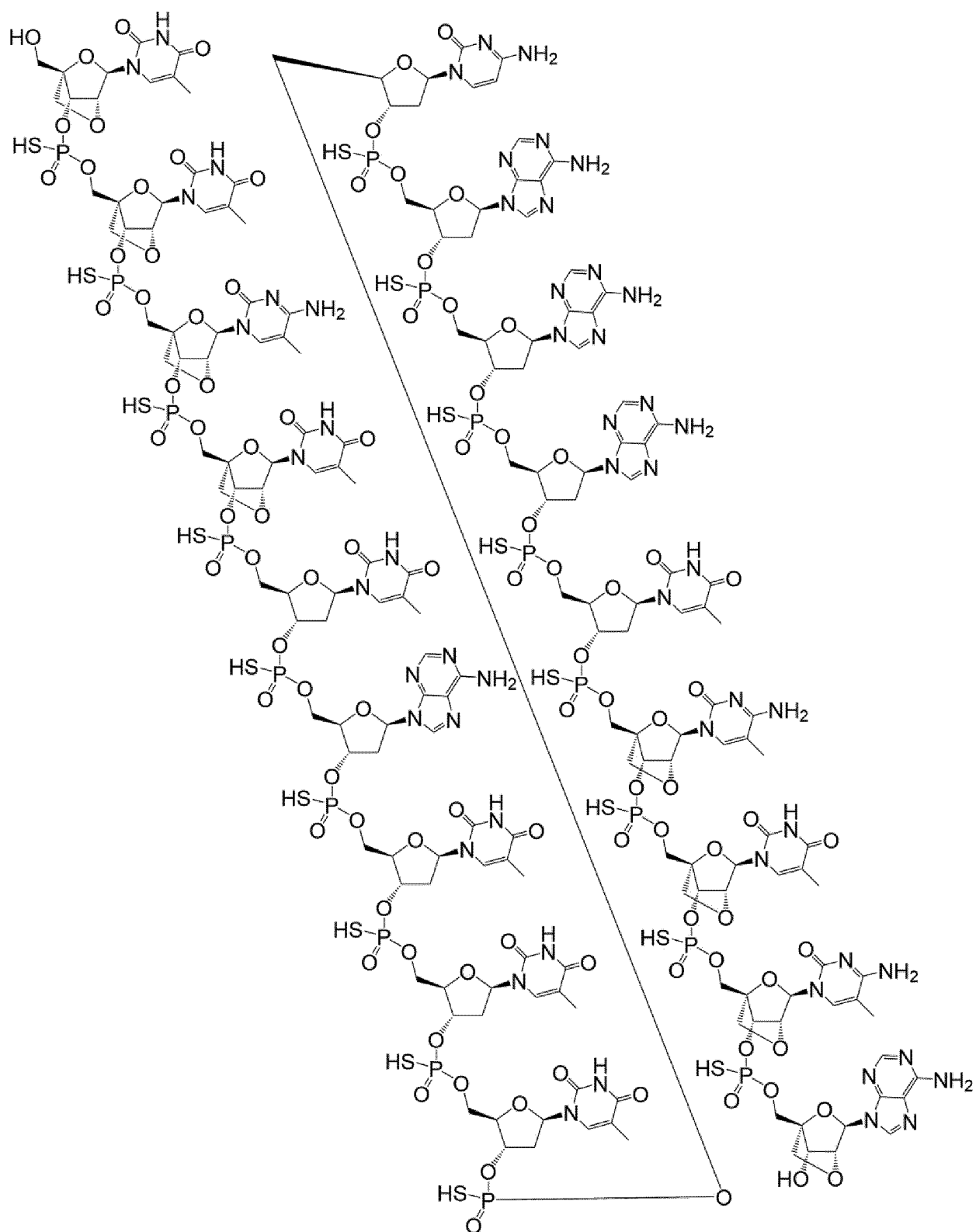


Figure 13

CMP ID NO: 75_1

